

CONTIG2667	3563_4425_fq_2	3563	17666	264	88	YDR079W	214	1.3(10)-17	Saccharomyces cerevisiae	[uri:ydr079w] [pn:cytochrome c oxidase assembly protein:hypothetical 13.2 kd protein in sed1-pdc2 intergenic region] [gn:per100_d444_I] [gicfc:2.8:12.16] [keggfc:4.2] [sgdfc:2.5.0.6.4.0:9.7.0] [db:gtsaccharomyces cerevisiae]
CONTIG1205	23478430_f1_1	3564	17667	465	155	YDR120C	160	2.0(10)-22	Saccharomyces cerevisiae	[uri:ydr120c] [pn:n2,n2-dimethylguanine tRNA methyltransferase;n2,n2-dimethylguanosine tRNA methyltransferase precursor] [gn:ttrm1:yd9727] [gicfc:2.8:10.6] [ec:2.1.1.32] [keggic:14.1] [sgdfc:4.6.0:9.7.0] [db:gtsaccharomyces cerevisiae]
CONTIG645	15829015_c3_3	3565	17668	744	248	YDR120C	646	2.1(10)-63	Saccharomyces cerevisiae	[uri:ydr120c] [pn:n2,n2-dimethylguanine tRNA methyltransferase;n2,n2-dimethylguanosine tRNA methyltransferase precursor] [gn:ttrm1:yd9727] [gicfc:2.8:10.6] [ec:2.1.1.32] [keggic:14.1] [sgdfc:4.6.0:9.7.0] [db:gtsaccharomyces cerevisiae]
CONTIG5076	1203416_c2_9	3566	17669	2013	671	YDR194C	524	1.8(10)-50	Saccharomyces cerevisiae	[uri:ydr194c] [pn:rnase helicase of the dead box family, mitochondrial:atp-dependent rna helicase mss116 precursor] [gn:mss116:yd9346] [gicfc:2.8:10.2] [keggfc:14.2] [sgdfc:4.9.0:9.7.0] [db:gtsaccharomyces cerevisiae]

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CONTIG4689	22298761_c3_11	3567	17670	564	188	YDR197W	139	6.7(10)-9	Saccharomyces cerevisiae	[ui:ydrl97w] [pn:cytochrome b translational activator protein cbs2] [gn:cbs2:cbs2:cbp7.yd19346] [gicfc:2.8:10.7] [keggfc:14.2] [sgdfc:5.3.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3239	995667_c2_7	3568	17671	711	237	YDR232W	715	1.0(10)-70	Saccharomyces cerevisiae	[ui:ydrl232w] [pn:5-aminolevulinate synthase:5-aminolevulinic acid synthase, mitochondrial precursor:delta-aminolevulinate synthase:delta-ala synthetase] [gn:hem1:yd9934] [gicfc:2.8:5.3:9.10:9.11] [ec:2.3.1.37] [keggfc:5.3] [sgdfc:1.7.]
CONTIG3239	9882667_c1_5	3569	17672	930	310	YDR232W	945	4.2(10)-95	Saccharomyces cerevisiae	[ui:ydrl232w] [pn:5-aminolevulinate synthase:5-aminolevulinic acid synthase, mitochondrial precursor:delta-aminolevulinate synthase:delta-ala synthetase] [gn:hem1:yd9934] [gicfc:2.8:5.3:9.10:9.11] [ec:2.3.1.37] [keggfc:5.3] [sgdfc:1.7.]
CONTIG4672	21640811_c1_8	3570	17673	1158	386	YDR234W	97	0.13	Saccharomyces cerevisiae	[ui:ydrl234w] [pn:homoaconitase:homoaconitase precursor:homoaconitate hydratase] [gn:lys4:yd9934] [gicfc:2.8:5.8:6.6] [ec:4.2.1.36] [keggfc:5.8] [sgdfc:1.1.1:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4880	34703879_c1_6	3571	17674	1977	659	YDR234W	2353	2.7(10)-244	Saccharomyces cerevisiae	[ui:yd234w] [pn:homoaconitase;homoaconitase precursor;homoaconitate hydratase] [gn:lys4;id9934] [gicfc:2.8;5.8;6.6] [ec:4.2.1.36] [keggfc:5.8] [sgdfc:1.1.19.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5547	13787567_c3_17	3572	17675	2328	776	YDR258C	2282	9.0(10)-237	Saccharomyces cerevisiae	[ui:yd258c] [pn:heat shock protein of clpb family of atp-dependent proteases, mitochondrial;mitochondrial heat shock protein 78 precursor] [gn:hsp78] [gicfc:12.7;2.8;10.11;13.2] [keggfc:14.2] [sgdfc:6.6;0.9;7.0;11.1.0] [db:gtc-saccha
CONTIG5125	24414078_c2_14	3573	17676	1215	405	YDR268W	977	1.8(10)-98	Saccharomyces cerevisiae	[ui:yd268w] [pn:tryptophanyl-tRNA synthetase, mitochondrial;tryptophanyl-tRNA ligase;trpsl [gn:mswl;id9954] [gicfc:2.8;5.14;10.6] [ec:6.1.1.2] [keggfc:5.14;10.1;10.2] [sgdfc:5.4;0.9;7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5518	9765627_c3_20	3574	17677	1047	349	YDR337W	439	1.8(10)-41	Saccharomyces cerevisiae	[ui:yd337w] [pn:ribosomal protein of the small subunit, mitochondrial;mitochondrial 40s ribosomal protein s28 precursor] [gn:mprps28;d9651] [gicfc:2.8;10.4] [keggfc:14.2] [sgdfc:5.1;0.9;7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4636	501381_f3_2	3575	17678	1077	359	YDR347W	163	5.9(10)-10	Saccharomyces cerevisiae	[ui:yd347w] [pn:ribosomal protein of the small subunit, mitochondrial:mitochondrial 40s ribosomal protein mrp1] [gn:mrp1:d9651] [gtcfc:2.8:10.4] [keggfc:14.2] [sgdgc:5.1:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2236	21650937_f1_1	3576	17679	627	209	YDR375C	795	3.3(10)-79	Saccharomyces cerevisiae	[ui:yd375c] [pn:mitochondrial protein of the cdc48/pas1/sec18:aaa family of atpases:bes1 protein] [gn:bcs1:d9481] [gtcfc:2.8:12.16] [keggfc:14.2] [sgdgc:6.4:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4291	16836540_f2_3	3577	17680	309	103	YDR375C	118	1.7(10)-6	Saccharomyces cerevisiae	[ui:yd375c] [pn:mitochondrial protein of the cdc48/pas1/sec18:aaa family of atpases:bes1 protein] [gn:bcs1:d9481] [gtcfc:2.8:12.16] [keggfc:14.2] [sgdgc:6.4:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3826	11038567_c2_3	3578	17681	813	271	YDR376W	345	1.6(10)-31	Saccharomyces cerevisiae	[ui:yd376w] [pn:similarity to human adrenodoxin reductase and ferredoxin-nadp+ reductase:nadph:adrenodoxin oxidoreductase homolog precursor:adrenodoxin reductase homolog][gn:arh1:d9481] [gtcfc:2.8:3.4:8.1:8.2] [keggfc:14.2] [sgdgc:1]

CONTIG1088	22378775_f3_1	3579	17682	609	203	YDR405W	279	1.6(10)-24	Saccharomyces cerevisiae	[ui:ydr405w] [pn:ribosomal protein of the large subunit, mitochondrial:mitochondrial 60s ribosomal protein 141 precursor:yml41]
										[gn:mpl41:tmp20:49509] [gtfc:2.8:10.4] [keggfc:14.2] [sgdgc:5.1.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2510	6640687_f1_1	3580	17683	495	165	YDR462W	316	1.8(10)-28	Saccharomyces cerevisiae	[ui:ydr462w] [pn:ribosomal protein yml28, mitochondrial]
										[gtfc:2.8:10.4] [keggfc:14.2] [sgdgc:5.1.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2838	4085965_c2_4	3581	17684	960	320	YER014W	327	3.7(10)-29	Saccharomyces cerevisiae	[ui:yer014w] [pn:protoporphyrinogen oxidase, mitochondrial:protoporphyrinogen oxidase:ppo] [gn:hem14]
										[gtfc:2.8:9.10:9.11] [ec:1.3.3.4] [keggfc:9.10] [sgdgc:1.7.1:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG5244	10156251_f3_10	3582	17685	621	207	YER014W	379	4.0(10)-35	Saccharomyces cerevisiae	[ui:yer014w] [pn:protoporphyrinogen oxidase, mitochondrial:protoporphyrinogen oxidase:ppo] [gn:hem14]
										[gtfc:2.8:9.10:9.11] [ec:1.3.3.4] [keggfc:9.10] [sgdgc:1.7.1:9.7.0] [db:gic-saccharomyces cerevisiae]

CONTIG1007	24320317_2_1	3583	17686	855	285	YER017C	575	7.0(10)-56	Saccharomyces cerevisiae	[ui:yer017c] [pn:protease of the sec18/cdc48/pas1 family of aipases:aaafafg3 protein:tat-binding homolog 10] [gn:afafg3:yta10] [gtcfc:2.8:10.11:12.16] [ec:3.4.24.-] [keggfc:14.1] [sgdfc:6.4.0:6.5.3:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5132	24508438_c2_11	3584	17687	1209	403	YER017C	959	4.5(10)-126	Saccharomyces cerevisiae	[ui:yer017c] [pn:protease of the sec18/cdc48/pas1 family of aipases:aaafafg3 protein:tat-binding homolog 10] [gn:afafg3:yta10] [gtcfc:2.8:10.11:12.16] [ec:3.4.24.-] [keggfc:14.1] [sgdfc:6.4.0:6.5.3:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG385	11750755_c3_4	3585	17688	687	229	YER026C	708	5.5(10)-70	Saccharomyces cerevisiae	[ui:yer026c] [pn:cdp-diacylglycerol serine o-phosphatidyltransferase:cdp-diacylglycerol--serine o-phosphatidyltransferase:phosphatidylserine synthase] [gn:cho1:pss1] [gtcfc:2.8:3.4:5.3:8.1:8.2:12.16] [ec:2.7.8.8] [keggfc:5.3:8.1]
CONTIG2766	10632776_c2_6	3586	17689	306	102	YER038W	128	1.6(10)-8	Saccharomyces cerevisiae	[ui:yer038w] [pn:cytochrome c oxidase assembly factor:protein precursor] [gn:pet17] [gtcfc:2.8:12.16] [keggfc:14.2] [sgdfc:6.4.0:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4186	6647807_f3_2	3587	17690	924	308	YER061C	534	1.5(10)-51	Saccharomyces cerevisiae	[ui:yer061c] [pn:3-oxoacyl-acyl-carrier-protein synthase homolog;beta-keto-acyl-acp synthase, mitochondrial] [gn:cem1] [gicfc:2.8.3.:3.4.8.1.8.2] [ec:2.3.1.41] [keggfc:3.1] [sgdgc:1.6.1.2.5.0.9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG4985	20897942_c3_9	3588	17691	282	94	YER061C	220	1.2(10)-17	Saccharomyces cerevisiae	[ui:yer061c] [pn:3-oxoacyl-acyl-carrier-protein synthase homolog;beta-keto-acyl-acp synthase, mitochondrial] [gn:cem1] [gicfc:2.8.3.:3.4.8.1.8.2] [ec:2.3.1.41] [keggfc:3.1] [sgdgc:1.6.1.2.5.0.9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG5605	486575_f1_2	3589	17692	2598	866	YER069W	2780	1.5(10)-289	Saccharomyces cerevisiae	[ui:yer069w] [pn:acetylglutamate kinase and acetylglutamyl-phosphate reductase] [gicfc:2.8.6.6] [keggfc:14.2] [sgdgc:1.1.1.9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG4952	26270942_c3_8	3590	17693	660	220	YER086W	671	4.7(10)-66	Saccharomyces cerevisiae	[ui:yer086w] [pn:anabolic serine and threonine dehydratase precursor;threonine dehydratase] [gn:ilv1] [gicfc:2.8.5.3.6.6] [ec:4.2.1.16] [keggfc:5.3] [sgdgc:1.1.1.9.7.0] [db:gic-saccharomyces cerevisiae]

CONTIG5168	32209802_f1_2	3591	17694	582	194	YER086W	565	8.0(10)-55	Saccharomyces cerevisiae	[ui:yer086w] [pn:anabolic serine and threonine dehydratase precursor:threonine deaminase] [gn:ilv1] [gicfc:2.8;5.3;6.6] [ec:4.2.1.16] [keggfc:5.3] [sgdfc:1.1.1;9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG5806	38877_f3_16	3592	17695	1245	415	YER141W	1031	3.2(10)-104	Saccharomyces cerevisiae	[ui:yer141w] [pn:cytochrome oxidase assembly factor:cytochrome c oxidase assembly protein] [gn:cox15] [gicfc:2.8;12.16] [keggfc:14.2] [sgdfc:6.4;9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG1344	3906275_f1_1	3593	17696	909	303	YER154W	478	1.3(10)-45	Saccharomyces cerevisiae	[ui:yer154w] [pn:cytochrome oxidase biogenesis protein:cytochrome oxidase biogenesis protein oxal1 precursor] [gn:oxal1;pet1402] [gicfc:2.8;12.16] [keggfc:14.2] [sgdfc:2.5;6.4;9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG3807	24484452_c1_7	3594	17697	1644	548	YER168C	927	3.5(10)-93	Saccharomyces cerevisiae	[ui:yer168c] [pn:tRNA nucleotidyltransferase:tRNA nucleotidyltransferase:tRNA adenylyltransferase:tRNA cca-pyrophosphorylase] [gn:ccal1nt1] [gicfc:2.8;10.1;10.2;10.6;4.1] [ec:2.7;7.25] [keggfc:14.1] [sgdfc:4.6;9.2;0.9.5.

CONTIG4129	32223908_c3_14	3595	17698	588	196	YER170W	501	4.7(10)-48	Saccharomyces cerevisiae	[ui:yer170w] [pn:adenylate kinase, mitochondrial:adenylate kinase 2:atp-amp transphosphorylase] [gn:adk2:pak3] [gtcfc:2.8:4.1:12.13:12.8] [ec:2.7.4.3] [keggfc:4.1] [sgdfc:1.3.8;3.1;0;9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4374	6347656_f2_1	3596	17699	2058	686	YFL036W	1308	1.5(10)-133	Saccharomyces cerevisiae	[ui:yfl036w] [pn: dna-directed rna polymerase, mitochondrial:dna-directed rna polymerase] [mitochondrial precursor] [gn:rp041] [gtcfc:2.8:4.1:4.2:10.2:10.8] [ec:2.7.7.6] [keggfc:4.1;4.2] [sgdfc:3.6.0;4.8;1;9.7.0] [db:gtc-saccharomyces ce]
CONTIG4904	19744788_c2_4	3597	17700	1014	338	YFL036W	748	3.2(10)-73	Saccharomyces cerevisiae	[ui:yfl036w] [pn: dna-directed rna polymerase, mitochondrial:dna-directed rna polymerase] [mitochondrial precursor] [gn:rp041] [gtcfc:2.8:4.1:4.2:10.2:10.8] [ec:2.7.7.6] [keggfc:4.1;4.2] [sgdfc:3.6.0;4.8;1;9.7.0] [db:gtc-saccharomyces ce]

CONTIG5682	35347688_c3_27	3598	17701	834	278	YFL036W	392	4.2(10)-35	Saccharomyces cerevisiae	[ui:yfl036w] [pn: dna-directed rna polymerase, mitochondrial: dna-directed rna polymerase, mitochondrial precursor] [gn: rpo41] [gicfc:2.8:4.1:4.2:10.2:10.8] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:3.6.0:4.8.1:9.7.0] [db:gtc-saccharomyces ce]
CONTIG5682	2113792_c2_25	3599	17702	2190	730	YFL036W	189	8.4(10)-11	Saccharomyces cerevisiae	[ui:yfl036w] [pn: dna-directed rna polymerase, mitochondrial: dna-directed rna polymerase, mitochondrial precursor] [gn: rpo41] [gicfc:2.8:4.1:4.2:10.2:10.8] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:3.6.0:4.8.1:9.7.0] [db:gtc-saccharomyces ce]
CONTIG1885	34406587_f2_1	3600	17703	720	240	YFL016C	268	4.7(10)-36	Saccharomyces cerevisiae	[ui:yfl016c] [pn: heat shock protein - chaperone protein precursor] [gn: mdj1] [gicfc:12.7:2.8:10.5:10.7:13.2] [keggfc:1:4.2] [sgdfc:6.1.0:9.7:0:11.1:0] [db:gtc-saccharomyces cerevisiae]
CONTIG5665	13862575_f1_1	3601	17704	267	89	YFR049W	98	2.5(10)-5	Saccharomyces cerevisiae	[ui:yfr049w] [pn: ribosomal protein, mitochondrial: mitochondrial 40s ribosomal protein ymr-31 precursor] [gn: ymt31] [gicfc:2.8:10.4] [keggfc:1:4.2] [sgdfc:5.1:0:9.7:0] [db:gtc-saccharomyces cerevisiae]

CONTIG5123	977140_c2_10	3602	17705	1860	620	YGL119W	1345	1.8(10)-137	Saccharomyces cerevisiae	[ui:ygl119w] [pn:ubiquinol cytochrome-c reductase complex assembly protein:protein precursor] [gn:abcl1] [gtcfc:2.8:12.16] [keggfc:14.2] [sgdfc:2.5:0:6.4:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5275	10574224_c1_14	3603	17706	219	73	YGL068W	229	3.2(10)-19	Saccharomyces cerevisiae	[ui:ygl068w] [pn:probable ribosomal protein 112:putative mitochondrial 60s ribosomal protein 17/12 precursor] [gtcfc:2.8:10.4] [keggfc:14.2] [sgdfc:5.1:0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5447	24407830_f1_3	3604	17707	543	181	YGR076C	233	1.2(10)-19	Saccharomyces cerevisiae	[ui:ygr076c] [pn:ribosomal protein ymr26;ymr25, mitochondrial/mitochondrial 60s ribosomal protein 125;ymr25] [gn:mrp125;ymr26] [gtcfc:2.8:10.4] [keggfc:14.2] [sgdfc:5.1:0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1387	19573387_c1_2	3605	17708	945	315	YGR094W	952	7.7(10)-96	Saccharomyces cerevisiae	[ui:ygr094w] [pn:valyl-tRNA synthetase:valyl-tRNA synthetase, mitochondrial precursor:valine-tRNA ligase:valrs][gn:vas1] [gtcfc:2.8:5.7:10.6] [kec:6.1:1.9] [keggfc:5.7:10.1:10.2] [sgdfc:5.4:0.9:2.0:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3315	3157502_f2_2	3606	17709	1284	428	YGR094W	1122	7.5(10)-114	Saccharomyces cerevisiae	[ui:ygr094w] [pn:valyl-tma synthetase;valyl-tma synthetase, mitochondrial precursor;valine--tma ligase;vals] [gn:vasl] [gtcfc:2.8;5.7;10.6] [ec:6.1.1.9] [keggfc:5.7;10.1;10.2] [sgdfc:5.4;0.9;2.0;9.7;0] [db:gtc-saccharomyces cerevi]
CONTIG3315	4102157_f1_1	3607	17710	1155	385	YGR094W	1601	1.3(10)-164	Saccharomyces cerevisiae	[ui:ygr094w] [pn:valyl-tma synthetase;valyl-tma synthetase, mitochondrial precursor;valine--tma ligase;vals] [gn:vasl] [gtcfc:2.8;5.7;10.6] [ec:6.1.1.9] [keggfc:5.7;10.1;10.2] [sgdfc:5.4;0.9;2.0;9.7;0] [db:gtc-saccharomyces cerevi]
CONTIG5713	13773450_f1_1	3608	17711	486	162	YGR171C	180	5.0(10)-13	Saccharomyces cerevisiae	[ui:ygr171c] [pn:methionyl-tma synthetase;methionyl-tma synthetase, mitochondrial:methionine-tma ligase;metrs] [gn:msml] [gtcfc:2.8;5.4;6.4;10.6] [ec:6.1.1.10] [keggfc:5.4;4.6;4.10.1;10.2] [sgdfc:5.4;0.9;7.0] [db:gtc-saccharomyces c]
CONTIG3802	4335052_f2_3	3609	17712	444	148	YGR174C	331	5.0(10)-30	Saccharomyces cerevisiae	[ui:ygr174c] [pn:ubiquinol-cytochrome c reductase assembly factor;protein precursor] [gn:cbp4] [gtcfc:2.8;12.16] [keggfc:14.2] [sgdfc:2.5;0.6;4.0;9.7;0] [db:gtc-saccharomyces cerevisiae]

b2x13522.y	23632941_c3_2	3610	17713	618	206	YGR207C	437	2.8(10)-41	Saccharomyces cerevisiae	[ui:ygr207c] [pn:electron-transferring flavoprotein, beta chain:probable electron transfer flavoprotein beta-subunit:beta- eff] [gn:eff-beta:g7742] [gtcfc:2.8] [keggfc: 14.2] [sgdfc:2.5:0:9.7.0] [db:gtc-saccharomyces cerevisiae]
b2x14802.y	16413507_c1_1	3611	17714	528	176	YGR207C	349	6.2(10)-32	Saccharomyces cerevisiae	[ui:ygr207c] [pn:electron-transferring flavoprotein, beta chain:probable electron transfer flavoprotein beta-subunit:beta- eff] [gn:eff-beta:g7742] [gtcfc:2.8] [keggfc: 14.2] [sgdfc:2.5:0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2016	787562_f3_1	3612	17715	702	234	YGR220C	396	6.5(10)-37	Saccharomyces cerevisiae	[ui:ygr220c] [pn:ribosomal protein of the large subunit, mitochondrial:mitochondrial 60s ribosomal protein 19 precursor:yml9] [gn:mp19:g8520] [gtcfc:2.8:10.4] [keggfc: 14.2] [sgdfc:5.1:0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2225	34267142_f1_1	3613	17716	522	174	YHL004W	322	4.5(10)-29	Saccharomyces cerevisiae	[ui:yhl004w] [pn:ribosomal protein of the small subunit, mitochondrial:mitochondrial 40s ribosomal protein] [gn:mp4] [gtcfc:2.8:10.4] [keggfc: 14.2] [sgdfc:5.1:0:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2859	30595705_c2_5	3614	17717	885	295	YHL004W	146	3.0(10)-8	Saccharomyces cerevisiae	[ui:yhr004w] [pn:ribosomal protein of the small subunit, mitochondrial:mitochondrial 40s ribosomal protein] [gn:mrp4] [gtcfc:2.8:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2395	1210300_c3_6	3615	17718	687	229	YHR008C	691	3.6(10)-68	Saccharomyces cerevisiae	[ui:yhr008c] [pn:superoxide dismutase:mn precursor, mitochondrial:superoxide dismutase precursor:mn] [gn:sod2] [gtcfc:2.8:12.12] [ec:1.15.1.1] [keggfc:14.1] [sgdfc:9.7.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4301	15660212_f2_4	3616	17719	204	68	YHR008C	91	0.00044	Saccharomyces cerevisiae	[ui:yhr008c] [pn:superoxide dismutase:mn precursor, mitochondrial:superoxide dismutase precursor:mn] [gn:sod2] [gtcfc:2.8:12.12] [ec:1.15.1.1] [keggfc:14.1] [sgdfc:9.7.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4301	15673286_f2_5	3617	17720	516	172	YHR008C	578	3.3(10)-56	Saccharomyces cerevisiae	[ui:yhr008c] [pn:superoxide dismutase:mn precursor, mitochondrial:superoxide dismutase precursor:mn] [gn:sod2] [gtcfc:2.8:12.12] [ec:1.15.1.1] [keggfc:14.1] [sgdfc:9.7.0:11.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5325	4335003_c2_13	3618	17721	543	181	YHR024C	310	1.5(10)-27	Saccharomyces cerevisiae	[ui:yhr024c] [pn:processing peptidase, catalytic 53kda:alpha subunit, mitochondrial:mitochondrial processing peptidase alpha subunit precursor:alpha-mpp] [gn:mas2:mit2] [gicfc:2.8:10.7] [ec:3.4.24.64] [keggfc:14.1] [sgdfc:6.3.0:9.7.0]
CONTIG5325	14455305_c1_7	3619	17722	1137	379	YHR024C	817	1.6(10)-81	Saccharomyces cerevisiae	[ui:yhr024c] [pn:processing peptidase, catalytic 53kda:alpha subunit, mitochondrial:mitochondrial processing peptidase alpha subunit precursor:alpha-mpp] [gn:mas2:mit2] [gicfc:2.8:10.7] [ec:3.4.24.64] [keggfc:14.1] [sgdfc:6.3.0:9.7.0]
CONTIG2505	20490811_f1_1	3620	17723	1257	419	YHR037W	1216	8.3(10)-124	Saccharomyces cerevisiae	[ui:yhr037w] [pn:1-pyrroline-5-carboxylate dehydrogenase:delta-1-pyrroline-5-carboxylate dehydrogenase precursor:p5c dehydrogenase] [gn:put2] [gicfc:2.8:5.1:5.10:6.6] [ec:1.5.1.12] [keggfc:5.1:5.10] [sgdfc:1.1.1:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG1990	819687_f2_2	3621	17724	1170	390	YHR120W	542	1.5(10)-51	Saccharomyces cerevisiae	[ui:yhr120w] [pn:dnat mismatch repair protein, mitochondrial:muts protein homolog 1] [gn:msh1] [gicfc:2.8:10.8] [keggfc:14.2] [sgdfc:3.7.0:9.7.0] [db:gic-saccharomyces cerevisiae]

CONTIG3662	30270253_c2_7	3622	17725	264	88	YHR120W	179	1.3(10)-12	Saccharomyces cerevisiae	[ui:yr120w] [pn:dnase mismatch repair protein, mitochondrial:muts protein homolog 1] [gn:msh1]
CONTIG2483	25065556_c1_3	3623	17726	717	239	YHR147C	437	2.8(10)-41	Saccharomyces cerevisiae	[ui:yhr147c] [pn:ribosomal protein of the large subunit, mitochondrial:mitochondrial 60s ribosomal protein 16 precursor:yml6] [gn:mp16] [gtcfc:2.8:0.4] [keggfc:14.2] [sgdfc:5.1.0:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG2293	40636_c1_3	3624	17727	972	324	YIL043C	587	3.7(10)-57	Saccharomyces cerevisiae	[ui:yil043c] [pn:cytochrome-b5 reductase:putative nadh-cytochrome b5 reductase:p35] [gn:chr1:cbr5:cbr] [gtcfc:2.8:7.1] [ec:1.6.2.2] [keggfc:4.4] [sgdfc:2.5.0:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG624	20899163_f2_2	3625	17728	342	114	YJL208C	330	6.4(10)-30	Saccharomyces cerevisiae	[ui:yjl208c] [pn:nuclease, mitochondrial:mitochondrial nuclease] [gn:nuc1:j0310:hre329] [gtcfc:2.8:4.4:10.10] [ec:3.1.30.-] [keggfc:14.1] [sgdfc:1.3.6:9.7.0] [db:gic-saccharomyces cerevisiae]
b3x14607_y	23866630_c3_2	3626	17729	519	173	YJL208C	559	3.5(10)-54	Saccharomyces cerevisiae	[ui:yjl208c] [pn:nuclease, mitochondrial:mitochondrial nuclease] [gn:nuc1:j0310:hre329] [gtcfc:2.8:4.4:10.10] [ec:3.1.30.-] [keggfc:14.1] [sgdfc:1.3.6:9.7.0] [db:gic-saccharomyces cerevisiae]

CONTIG1101	24476527_c1_2	3627	17730	594	198	YJL180C	287	2.2(10)-25	Saccharomyces cerevisiae	[ui:yj1180c] [pn:f10-atpase complex assembly protein:atp12 protein precursor] [gn:atp12;0486] [gicfc:2.8;12.16] [keggc:14.2] [sgdsc:6.4;0.9;7.0] [db:gic-saccharomyces cerevisiae]
CONTIG4516	4017160_c1_9	3628	17731	951	317	YJL133W	442	8.6(10)-42	Saccharomyces cerevisiae	[ui:yj133w] [pn:rna splicing protein and member of the mitochondrial carrier family:mcf:mitochondrial rna splicing protein mrs3] [gn:mrs3;06751] [gicfc:2.8;10.2] [keggc:14.2] [sgdsc:4.9;0.9;7.0] [db:gic-saccharomyces cerevisiae]
CONTIG5288	4322777_c2_15	3629	17732	2220	740	YJL102W	1303	5.0(10)-133	Saccharomyces cerevisiae	[ui:yj102w] [pn:translation elongation factor, mitochondrial:elongation factor g, mitochondrial 2 precursor:mcf-g-2] [gn:mcf2;06826] [gicfc:2.8;10.7] [keggc:14.2] [sgdsc:5.2;0.9;7.0] [db:gic-saccharomyces cerevisiae]
CONTIG55801	781312_c1_25	3630	17733	843	281	YJL063C	175	2.1(10)-13	Saccharomyces cerevisiae	[ui:yj063c] [pn:ribosomal protein 117, mitochondrial:mitochondrial 60s ribosomal protein 18;ym18] [gn:mrp18;j1125;hrd238] [gicfc:2.8;10.4] [keggc:14.2] [sgdsc:5.1;0.9;7.0] [db:gic-saccharomyces cerevisiae]

CONTIG3687	19609687_f1_1	3631	17734	1806	602	YJR016C	2114	5.7(10)-219	Saccharomyces cerevisiae	[ui:yjr016c] [pn:dihydroxy-acid dehydratase;dhydroxy-acid dehydratase precursor;dad:2,3-dihydroxy acid hydrolase] [gn:ii:v3;j 450] [gicfc:2.8:5:7.6:6.9:51] [ec:4.2.1.9] [keggfc:5.7:9:51][sgdfc:1.1.19.7.0] [db:gic-saccharomyces cerev
CONTIG5200	23674202_c1_10	3632	17735	1965	655	YJR045C	1663	3.6(10)-171	Saccharomyces cerevisiae	[ui:yjr045c] [pn:mitochondrial heat shock protein 70-related protein;mitochondrial heat shock protein ssc 1 precursor;endonuclease scei 75 kd subunit] [gn:sscl:ens1;j 1639] [gicfc:12.7:2.8:10.2:10.5:10.7:13.2] [keggfc:1.4:2][sgdfc:4.9:0]
CONTIG3304	36204187_c3_9	3633	17736	1551	517	YJR045C	1998	1.1(10)-206	Saccharomyces cerevisiae	[ui:yjr045c] [pn:mitochondrial heat shock protein 70-related protein;mitochondrial heat shock protein ssc 1 precursor;endonuclease scei 75 kd subunit] [gn:sscl:ens1;j 1639] [gicfc:12.7:2.8:10.2:10.5:10.7:13.2] [keggfc:1.4:2][sgdfc:4.9:0]
CONTIG4485	4689000_f1_2	3634	17737	363	121	YJR048W	479	1.0(10)-45	Saccharomyces cerevisiae	[ui:yjr048w] [pn:cytochrome c isoform 1:cytochrome c, iso-1] [gn:cycl:j 653][gicfc:2.8] [keggfc:14.2][sgdfc:2.5:0.9:7.0] [db:gic-saccharomyces cerevisiae]
CONTIG4669	3940677_c3_10	3635	17738	921	307	YJR095W	956	3.0(10)-96	Saccharomyces cerevisiae	[ui:yjr095w] [pn:regulator of acetyl-coa synthetase activity] [gn:acr1;j 1921][gicfc:2.8:12.13] [keggfc:14.2][sgdfc:1.5:2.9:7.0] [db:gic-saccharomyces cerevisiae]

CONTIG5093	312_f2_2	3636	17739	813	271	YJR113C	458	1.7(10)-43	Saccharomyces cerevisiae	[ui:yr113c] [pn:similarity to bacterial, chloroplast and mitochondrial ribosomal protein s7:putative 40s ribosomal protein yjr113c] [gn:j2020] [gicfc:2.8:10.4] [keggc:14.2] [sgdic:5.1.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3874	15658430_c3_10	3637	17740	774	258	YJR144W	566	6.2(10)-55	Saccharomyces cerevisiae	[ui:yr144w] [pn:mitochondrial genome maintenance protein/mitochondrial genome maintenance protein mgm101 precursor] [gn:mgm101:mgm9;j2181] [gicfc:2.8] [keggc:14.2] [sgdic:9.7.0] [db:gtc-saccharomyces cerevisiae]
b1x12579.y	36500900_c1_2	3638	17741	561	187	YKL194C	463	5.2(10)-44	Saccharomyces cerevisiae	[ui:yk1194c] [pn:threonine--tRNA ligase, mitochondrial:threonyl-tRNA synthetase, mitochondrial precursor:threonine--tRNA ligase:thrs1] [gn:mst1] [gicfc:2.8:5.3:10.6] [keggc:5.3:10.1:10.2] [sgdic:5.4:0.9:7.0] [db:gtc-sacc
CONTIG5757	178936_f1_1	3639	17742	984	328	YKL150W	835	2.0(10)-83	Saccharomyces cerevisiae	[ui:yk150w] [pn:cytochrome-b5 reductase:nadh-cytochrome b5 reductase precursor:p34 / p32] [gn:mcr1:ykl605] [gicfc:2.8:7.1] [keggc:4.4] [sgdic:2.5.0:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1385	24870933_c1_5	3640	17743	612	204	YKL142W	202	2.2(10)-16	Saccharomyces cerevisiae	[uri:ykl142w] [pn:ribosomal protein, mitochondrial:mitochondrial 40s ribosomal protein mrp8] [gn:mrp8;ykl13] [gicfc:2.8:10.4] [keggfc:14.2] [sgdfc:5.1:0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5410	12615636_c3_18	3641	17744	1800	600	YKL134C	1115	4.2(10)-113	Saccharomyces cerevisiae	[uri:ykl134c] [pn:mitochondrial intermediate peptidase:hypothetical zinc metalloproteinase ykl134c] [gicfc:10.7:2.8] [ec:3.4.24.-] [keggfc:14.1] [sgdfc:6.3:0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5780	5094437_f2_21	3642	17745	519	173	YKL134C	237	6.2(10)-19	Saccharomyces cerevisiae	[uri:ykl134c] [pn:mitochondrial intermediate peptidase:hypothetical zinc metalloproteinase ykl134c] [gicfc:10.7:2.8] [ec:3.4.24.-] [keggfc:14.1] [sgdfc:6.3:0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5465	15017827_f3_4	3643	17746	1053	351	YKL120W	909	2.7(10)-91	Saccharomyces cerevisiae	[uri:ykl120w] [pn:similarity to mitochondrial uncoupling proteins:mcf:mitochondrial carrier protein pmf1 [gn:pmf1;ykl1522] [gicfc:2.8] [keggfc:14.2] [sgdfc:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3351	1188257_f3_3	3644	17747	795	265	YKL087C	501	4.7(10)-48	Saccharomyces cerevisiae	[uri:ykl087c] [pn:holocytochrome c1 synthase:cytochrome c1 heme lyase:cc1_h1] [gn:cyt2] [gicfc:2.8:9.12:10.7] [ec:4.4.1.-] [keggfc:14.1] [sgdfc:1.7.2:6.3:0:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3460	14625285_f3_3	3645	17748	1116	372	YKR066C	728	4.2(10)-72	Saccharomyces cerevisiae	[uii:ykr066c] [pn:cytochrome-c peroxidase precursor:cytochrome c peroxidase precursor:cpo] [gn:cpo1:ccp:cpo] [gicfc:2.8:12.12] [ec:1.11.1.5] [keggfc:14.1] [sgdfc:9.7.0:11.3.0][db:gic-saccharomyces cerevisiae]
CONTIG5793	35189387_c2_20	3646	17749	936	312	YKR066C	550	3.1(10)-53	Saccharomyces cerevisiae	[uii:ykr066c] [pn:cytochrome-c peroxidase precursor:cytochrome c peroxidase precursor:cpo] [gn:cpo1:ccp:cpo] [gicfc:2.8:12.12] [ec:1.11.1.5] [keggfc:14.1] [sgdfc:9.7.0:11.3.0][db:gic-saccharomyces cerevisiae]
CONTIG859	26257692_c3_1	3647	17750	921	307	YLR067C	127	6.0(10)-5	Saccharomyces cerevisiae	[uii:ylr067c] [pn:required for stability and translation of cox1 mRNA:pet309 protein precursor] [gn:pet309:12.189] [gicfc:2.8:10.2:10.7] [keggfc:14.2] [sgdfc:4.12.0:5.3.0:9.7.0][db:gic-saccharomyces cerevisiae]
CONTIG2753	167508_c3_5	3648	17751	804	268	YLR069C	768	2.5(10)-76	Saccharomyces cerevisiae	[uii:ylr069c] [pn:translation elongation factor g, mitochondrial elongation factor g, mitochondrial 1 precursor:mef-g-1] [gn:mef1] [gicfc:2.8:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.7.0][db:gic-saccharomyces cerevisiae]
b3x14382.x	34428141_c2_2	3649	17752	630	210	YLR069C	765	5.0(10)-76	Saccharomyces cerevisiae	[uii:ylr069c] [pn:translation elongation factor g, mitochondrial 1 precursor:mef-g-1] [gn:mef1] [gicfc:2.8:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.7.0][db:gic-saccharomyces cerevisiae]

CONTIG4884	23945307_f3_2	3650	17753	2271	757	YLR139C	136	1.3(10)-5	Saccharomyces cerevisiae	[uiylr139c] [pn:suppresses lethality of ssm4 deletion:sis1 protein] [gn:ssm1::1621] [gtfc:2.8:10.2] [keggc:14.2] [sgdc:4.12.09.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2451	24298302_f1_1	3651	17754	1446	482	YLR142W	1009	7.0(10)-102	Saccharomyces cerevisiae	[uiylr142w] [pn:proline oxidase precursor] [gn:put1::17019606] [gtfc:2.8.53.6.6] [ec:1.5.3.-] [keggc:14.1] [sgdc:1.1.1.1.14.9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4430	9853302_f1_1	3652	17755	1449	483	YLR163C	1248	3.3(10)-127	Saccharomyces cerevisiae	[uiylr163c] [pn:mitochondrial processing peptidase:mitochondrial processing peptidase beta subunit precursor:beta-mpp:pep] [gn:mas1::mif1::19632] [gtfc:2.8.10.7] [ec:3.4.24.64] [keggc:14.1] [sgdc:6.3.0.9.7.0] [db:gtc-saccharomyces_c]
CONTIG692	4898961_c3_3	3653	17756	468	156	YLR168C	368	6.0(10)-34	Saccharomyces cerevisiae	[uiylr168c] [pn:probably involved in intramitochondrial protein sorting:msf1 protein] [gtfc:2.8.10.7.11.1] [keggc:14.2] [sgdc:6.2.0.9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2059	42707_c3_5	3654	17757	240	80	YLR203C	119	1.2(10)-6	Saccharomyces cerevisiae	[uiylr203c] [pn:possibly involved in translational activation of cox1 and cob mRNA:mss51 protein] [gn:mss51::18167] [gtfc:2.8.10.7] [keggc:14.2] [sgdc:5.3.0.9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3403	23867908_c1_7	3655	17758	300	100	YLR203C	124	3.5(10)-7	Saccharomyces cerevisiae	[ui:ylr203c] [pn:possibly involved in translational activation of cox I and cob mRNA:mss51 protein] [gn:mss51:18 67] [gicfc:2.8:10.7] [keggfc:14 2] [sgdic:5.3:0.9:7.0] [db:gic-saccharomyces cerevisiae]
CONTIG3403	19000_c1_6	3656	17759	672	224	YLR203C	620	1.2(10)-60	Saccharomyces cerevisiae	[ui:ylr203c] [pn:possibly involved in translational activation of cox I and cob mRNA:mss51 protein] [gn:mss51:18 67] [gicfc:2.8:10.7] [keggfc:14 2] [sgdic:5.3:0.9:7.0] [db:gic-saccharomyces cerevisiae]
b9x10g13.y	4898505_c2_2	3657	17760	567	189	YLR259C	798	1.6(10)-79	Saccharomyces cerevisiae	[ui:ylr259c] [pn:heat shock protein - chaperone, mitochondrial heat shock protein 60 precursor:stimulator factor i 66 kd component:p66:cpn60] [gn:hsp60;mi4:184 79] [gicfc:12.7:2.8:10.5:10.7:13.2] [keggfc:14 2] [sgdic:6.1:0.9:7.0:11.1].
CONTIG3815	13711563_f2_2	3658	17761	834	278	YLR355C	920	1.8(10)-92	Saccharomyces cerevisiae	[ui:ylr355c] [pn:ketol-acid reductoisomerase:ketol-acid reductoisomerase precursor:acetohydroxy-acid reductoisomerase:alpha-keto-beta-hydroxyacil reductoisomerase] [gn:ilv5 9638] [gicfc:2.8:5.7:6.6:9.5] [ec:1.1.1.86] [keggfc:5.7:9].

CONTIG5098	14144091_12_3	3659	17762	210	70	YLR355C	271	1.1(10)-23	Saccharomyces cerevisiae	[ui.yl355c] [pn:ketol-acid reductoisomerase:ketol-acid reductoisomerase] [precursor:acetohydroxy-acid reductoisomerase:alpha-keto-beta-hydroxyacyl reductoisomerase] [gn:ilv5;19638] [gicfc:2.8:5.7:6.9:5] [ec:1.1.1.86] [keggfc:5.7:9]
CONTIG131	333784438_c1_3	3660	17763	510	170	YLR382C	170	1.1(10)-11	Saccharomyces cerevisiae	[ui.yl382c] [pn:leucine--tRNA ligase precursor, mitochondrial:leucyl-tRNA synthetase, mitochondrial [precursor:leucine--tRNA ligase:leurs] [gn:nam2;msl1:13502] [gicfc:2.8:5.7:10.2:10.6] [ec:6.1.1.4] [keggfc:5.7:10.1:10.2] [sgdfc:4.9.0]
CONTIG4375	22459702_f3_6	3661	17764	372	124	YLR382C	236	1.0(10)-18	Saccharomyces cerevisiae	[ui.yl382c] [pn:leucine--tRNA ligase precursor, mitochondrial:leucyl-tRNA synthetase, mitochondrial [gn:nam2;msl1:13502] [gicfc:2.8:5.7:10.2:10.6] [ec:6.1.1.4] [keggfc:5.7:10.1:10.2] [sgdfc:4.9.0]

CONTIG3253	16689694_02_5	3662	17765	1515	505	YLR382C	1341	4.7(10)-137	Saccharomyces cerevisiae	[ui:ylr382c] [pn:leucine-tRNA ligase precursor, mitochondrial:leucyl-tRNA synthetase, mitochondrial precursor:leucine-tRNA synthetase, mitochondrial [gn:nam2-msl] [13502] [gicfc:2.8:5.7:10.2:10.6] [fec:6.1.1.4] [keggfc:5.7:10.1:10.2] [sgdfc:4.9.0]
CONTIG4120	26195187_f3_5	3663	17766	621	207	YLR393W	324	2.7(10)-29	Saccharomyces cerevisiae	[ui:ylr393w] [pn:f1f10 aipase complex assembly protein:protein] [gn:aip10] [gicfc:2.8:12.16] [keggfc:14.2] [sgdfc:6.4:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3359	1178567_f3_3	3664	17767	513	171	YLR439W	153	1.2(10)-10	Saccharomyces cerevisiae	[ui:ylr439w] [pn:ribosomal protein, mitochondrial,mitochondrial 60s ribosomal protein 14 precursor:yml4] [gn:mp14:j9753] [gicfc:2.8:10.4] [keggfc:14.2] [sgdfc:5.1:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3871	24814713_c1_8	3665	17768	675	225	YML078W	549	4.0(10)-53	Saccharomyces cerevisiae	[ui:yml078w] [pn:cyclophilin:peptidyl/prolyl isomerase, mitochondrial:peptidyl-prolyl cis-trans isomerase c precursor:ppase:rotamase:cyclophil in c:ppi-iii] [gn:cpr3:cyp3] [gicfc:2.8:0.5:10.7:12.7] [ec:5.2.1.8] [keggfc:14.1] [sgdfc:6.-525-

CONTIG5562	4334651_c3_13	3666	17769	846	282	YML025C	396	6.5(10)-37	Saccharomyces cerevisiae	[ui:yml025c] [pn:ribosomal protein, mitochondrial putative l4p like ribosomal protein] [gicfc:2.8:10.4] [keggfc:14.2] [sgdfc:5.1:0.9:7.0] [db:gic-saccharomyces cerevisiae]
CONTIG5744	2400410_c2_22	3667	17770	645	215	YML021C	472	5.7(10)-45	Saccharomyces cerevisiae	[ui:yml021c] [pn:uracil-dna glycosylase precursor] [gn:ung1] [gicfc:2.8:10.1:10.2:10.8:14.1] [ec:3.2.2.-] [keggfc:14.1] [sgdfc:3.7:0.9:5.0:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG1523	24616002_c3_3	3668	17771	405	135	YMR023C	283	2.6(10)-24	Saccharomyces cerevisiae	[ui:ymr023c] [pn:mitochondrial gtpase involved in expression of cox1:mitochondrial gtpase mss1 precursor] [gn:mss1:pet53:ym971] [gicfc:2.8:10.2:10.7] [keggfc:14.2] [sgdfc:4.9:0.5:2.0:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG3233	5094182_f3_3	3669	17772	1227	409	YMR023C	700	4.0(10)-69	Saccharomyces cerevisiae	[ui:ymr023c] [pn:mitochondrial gtpase involved in expression of cox1:mitochondrial gtpase mss1 precursor] [gn:mss1:pet53:ym971] [gicfc:2.8:10.2:10.7] [keggfc:14.2] [sgdfc:4.9:0.5:2.0:9.7.0] [db:gic-saccharomyces cerevisiae]

CONTIG5743	29923_130_f2_9	3670	17773	1266	422	YMR024W	449	1.6(10)-42	Saccharomyces cerevisiae	[ui:ymr024w] [pn:ribosomal protein of the large subunit, mitochondrial:mitochondrial 60s ribosomal protein 13 precursor:ym13] [gn:mrp13:ym9711] [gtcfc:2.8:10.4] [keggfc:14.2] [sgdgc:5.10:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5040	4729557_c3_15	3671	17774	498	166	YMR035W	450	1.2(10)-42	Saccharomyces cerevisiae	[ui:ymr035w] [pn:mitochondrial inner membrane protease subunit:mitochondrial inner membrane protease subunit 2] [gn:imp2:ym9973] [gtcfc:2.8:10.11:10.7:11.1] [ec:3.4.99.-] [keggfc:14.1] [sgdgc:6.2.0:6.3.0:9.7.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5507	4725027_f3_6	3672	17775	774	258	YMR038C	420	1.8(10)-39	Saccharomyces cerevisiae	[ui:ymr038c] [pn:regulation of lysine biosynthesis:homocitrate dehydratase] [gn:lys7:ym9532] [gtcfc:5.8:1:2.2.8] [ec:4.2.-.] [keggfc:14.1] [sgdgc:1.4.1:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2077	26345250_f2_1	3673	17776	1155	385	YMR089C	1539	4.9(10)-158	Saccharomyces cerevisiae	[ui:ymr089c] [pn:protease of the sec18/cdc48/pas1 family of ATPases:aaa:mitochondrial respiratory chain complexes assembly protein real:rat-binding homolog] [gn:rcal.yta12:ym9582] [gtcfc:2.8:10.11:12.16] [ec:3.4.24.-] [keggfc:14.1]

CONTIG3564	29335008_f2_2	3674	177777	315	105	YNMR089C	273	9.5(10)-23	Saccharomyces cerevisiae	[ui:ymr089c] [pn:protease of the sec18/cdc48/pas1 family of atpases;aa:mitochondrial respiratory chain complexes assembly protein rec1:tat-binding homolog 12] [gn:rec1;ya12;ym9582] [gricfc:2.8:10.11:12.16] [ec:3.4.24.-] [keggfc:14.1]
CONTIG1243	900305_f3_2	3675	17778	555	185	YNMR150C	538	5.7(10)-52	Saccharomyces cerevisiae	[ui:ymr150c] [pn:protease, mitochondrial;mitochondrial inner membrane protease subunit 1] [gn:imp1;pcr2858;ym9375] [gricfc:2.8:10.11:11.1] [ec:3.4.99.-] [keggfc:14.1] [sgdgc:6.2.0:6.3.0:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG5578	21879093_f1_1	3676	17779	3006	1002	YNMR189W	3211	0	Saccharomyces cerevisiae	[ui:ymr189w] [pn:glycine decarboxylase subunit;glycine dehydrogenase;decarboxylating precursor;glycine decarboxylase;glycine cleavage system P- protein] [gn:gcv2;gsd2;ym9646] [gricfc:2.8:5.31 [ec:1.4.4.2] [keggfc:5.3] [sgdgc:1.1.4.9.7.]
CONTIG2692	36515911_q2_5	3677	17780	474	158	YNMR193W	172	3.5(10)-13	Saccharomyces cerevisiae	[ui:ymr193w] [pn:ribosomal protein of the large subunit, mitochondrial;mitochondrial 60s ribosomal protein 124 precursor;yml24] [gn:mpr124;ym9646] [gricfc:2.8:10.4] [keggfc:14.2] [sgdgc:5.1.0:9.7.0] [db:gic-saccharomyces cerevisiae]

CONTIG4790	24416057_f2_4	3678	17781	375	125	YMR225C	186	1.2(10)-14	Saccharomyces cerevisiae	[ui:ymr225c] [pn:ribosomal protein ymr44, mitochondrial:mitochondrial 60s ribosomal protein l44:yml44] [gn:mrp[44:ymr44:ym959] [gicfc:2.8:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG1699	33672643_f1_1	3679	17782	579	193	YMR228W	213	2.5(10)-17	Saccharomyces cerevisiae	[ui:ymr228w] [pn:ma polymerase specific factor, mitochondrial:mitochondrial replication protein mtfl:rf1023:mitochondrial specificity factor] [gn:mtfl:ym959] [gicfc:2.8:10.2:10.8] [keggfc:14.2] [sgdfc:3.7.0:4.8.1:9.7.0] [db:gic-sacc]
CONTIG3740	79526_c1_13	3680	17783	912	304	YMR244W	761	1.3(10)-75	Saccharomyces cerevisiae	[ui:ymr244w] [pn:similarity to ncaa3 and sun4 protein] [gicfc:2.8] [keggfc:14.2] [sgdfc:2.5.0:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG3274	35947500_f3_2	3681	17784	204	68	YMR286W	96	4.0(10)-5	Saccharomyces cerevisiae	[ui:ymr286w] [pn:ribosomal protein mitochondrial:mitochondrial 60s ribosomal protein l33:yml33] [gn:mrp[33:ym8021] [gicfc:2.8:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.7.0] [db:gic-saccharomyces cerevisiae]

CONTIG5730	12772760_B_8	3682	17785	1911	637	YMR287C	132	9.1(10)-9	Saccharomyces cerevisiae	[ui:ymr287c] [pn:3"-5" exonuclease for rna 3" ss-tail, mitochondrial:mitochondrial biogenesis msu protein] [gn:msu1;ym8021] [gtfc:2.8:4.4:10.10] [keggfc:14.2] [sgdfc:1.3.6.9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5730	4017186_f3_9	3683	17786	1575	525	YMR287C	176	1.0(10)-20	Saccharomyces cerevisiae	[ui:ymr287c] [pn:3"-5" exonuclease for rna 3" ss-tail, mitochondrial:mitochondrial biogenesis msu protein] [gn:msu1;ym8021] [gtfc:2.8:4.4:10.10] [keggfc:14.2] [sgdfc:1.3.6.9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5419	20078556_f2_3	3684	17787	2124	708	YMR302C	557	2.7(10)-117	Saccharomyces cerevisiae	[ui:ymr302c] [pn:involved in early maturation of pre-rrm4a12 protein] [gn:rrm4a12;prp12;ym9952] [gtfc:2.8:10.3] [keggfc:14.2] [sgdfc:4.3.0.9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5419	2236262_f3_8	3685	17788	459	153	YMR302C	113	1.3(10)-5	Saccharomyces cerevisiae	[ui:ymr302c] [pn:involved in early maturation of pre-rrm4a12 protein] [gn:rrm4a12;prp12;ym9952] [gtfc:2.8:10.3] [keggfc:14.2] [sgdfc:4.3.0.9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG557	22273311_c3_2	3686	17789	783	261	YNL315C	448	2.0(10)-42	Saccharomyces cerevisiae	[ui:ynl315c] [pn:f1f0-atpase complex assembly protein:atp11 protein precursor] [gn:atp11:n0357] [gtcfc:2.8:12.16] [keggc:14.2] [sgfc:6.4:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3405	13945135_c3_9	3687	17790	870	290	YNL252C	527	8.5(10)-51	Saccharomyces cerevisiae	[ui:ynl252c] [pn:ribosomal protein yml30, mitochondrial:mitochondrial 60s ribosomal protein [yml30] precursor:yml30] [gn:mpf30:n0864] [gtcfc:2.8:10.4] [keggc:14.2] [sgfc:5.1:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2737	14531262_c2_4	3688	17791	1641	547	YNL237W	758	2.2(10)-90	Saccharomyces cerevisiae	[ui:ynl237w] [pn:weak similarity to mitochondrial electron transport proteins:ytp1 protein] [gn:ytp1:n1129] [gtcfc:2.8:12.6] [keggc:14.2] [sgfc:2.5:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1625	333362500_f2_1	3689	17792	972	324	YNL169C	574	8.9(10)-56	Saccharomyces cerevisiae	[ui:ynl169c] [pn:phosphatidylserine decarboxylase proenzyme 1 precursor] [gn:psd1:n1692] [gtcfc:2.8:3.4.5.3:8.1:8.2:10.2] [ec:4.1.1.65] [keggc:5.3:8.1] [sgfc:1.6:1:1.6:4.9:7.0] [db:gtc-saccharomyces]

CONTIG3682	12929655_f3_4	3690	17793	1392	464	YNL137C	607	2.7(10)-59	Saccharomyces cerevisiae	[ui:ynl137c] [pn:ribosomal protein, mitochondrial:nam9 protein precursor] [gn:nam9;n121:n1840] [gicfc:2.8:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG4489	5272257_f2_6	3691	17794	309	103	YNL066W	293	5.2(10)-26	Saccharomyces cerevisiae	[ui:ynl066w] [pn:involved in the aging process;proteasome component sun4] [gn:sun4;n241;ynl241lw] [gicfc:2.8:12.13] [keggfc:14.2] [sgdfc:9.7.0:11.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5792	6665902_c3_40	3692	17795	1050	350	YNR041C	884	1.3(10)-88	Saccharomyces cerevisiae	[ui:ynr041c] [pn:para-hydroxybenzoate--polypropenyltransferase:para-hydroxybenzoate--precursor:phb:polypropenyltransferase] [gn:cog2;r3419] [gicfc:2.8:7.1:9.10:9.11:9.12:11.3] [ec:2.5.1.-] [keggfc:7.2:9.13] [sgdfc:1.]
CONTIG5748	1250135_c3_23	3693	17796	1494	498	YOL140W	1053	1.6(10)-106	Saccharomyces cerevisiae	[ui:yol140w] [pn:acetylornithine aminotransferase:acetylornithine aminotransferase precursor:acoot] [gn:arg8] [gicfc:2.8:5.1:6:6.6] [ec:2.6.1.1] [keggfc:5.16] [sgdfc:1.1.1:9.7.0] [db:gic-saccharomyces cerevisiae]

CONTIG4945	38887_c3_12	3694	17797	1002	334	YOL096C	727	5.5(10)-72	Saccharomyces cerevisiae	[ui:yo 096c] [pn:3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase;hexaprenyldihydroxybenzoate methyltransferase;hexaprenylbenzoprecursor:dihydroxyhexaprenylbenzoate methylestertransferase;3,4-dihydroxy-5-hexaprenylbenzoatemethyltransferase;dhhb meth
CONTIG5635	34378252_c1_14	3695	17798	1626	542	YOL033W	1090	7.7(10)-118	Saccharomyces cerevisiae	[ui:yo 033w] [pn:glutamyl-tRNA synthetase, mitochondrial;glutamate-tRNA ligase;glurS] [gn:mse1] [gcfc:2.8.5 1.9.10 10.6] [ec:6.1.1.17] [keggc:5.1.9.10 10.1 1.0.2] [sgdfc:5.4.0 9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG529	1458318_f1_1	3696	17799	429	143	YOL023W	398	1.6(10)-36	Saccharomyces cerevisiae	[ui:yo 023w] [pn:translation initiation factor 2, mitochondrial;initiation factor if-2, mitochondrial precursor;if-2m1] [gn:ifm1] [gcfc:2.8 10.7] [keggc:14.2] [sgdfc:5.2.0 9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG529	21682937_f3_6	3697	17800	1449	483	YOL023W	931	1.3(10)-93	Saccharomyces cerevisiae	[ui:yo 023w] [pn:translation initiation factor 2, mitochondrial;initiation factor if-2, mitochondrial precursor;if-2m1] [gn:ifm1] [gcfc:2.8 10.7] [keggc:14.2] [sgdfc:5.2.0 9.7.0] [db:gic-saccharomyces cerevisiae]

CONTIG5796	25397577_f1_8	3698	17801	1287	429	YOL009C	300	4.7(10)-44	Saccharomyces cerevisiae	[ui:yo1009c] [pn:involved in mitochondrial inheritance] [gn:mdm12] [gicfc:2.8] [keggfc:14.2] [sgdfc:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG623	25506942_f1_1	3699	17802	756	252	YOR017W	177	1.8(10)-12	Saccharomyces cerevisiae	[ui:yo17w] [pn:component of mitochondrial translation system;putative mitochondrial translation system component pet127] [gn:pet127.or26] [gicfc:2.8.10.7] [keggfc:14.2] [sgdfc:5.3.0:9.7.0] [db:gic-saccharomyces cerevisiae]
b9x11t72.x	21954437_c3_2	3700	17803	783	261	YOR017W	208	8.4(10)-16	Saccharomyces cerevisiae	[ui:yo17w] [pn:component of mitochondrial translation system;putative mitochondrial translation system component pet127] [gn:pet127.or26] [gicfc:2.8.10.7] [keggfc:14.2] [sgdfc:5.3.0:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG4846	2772530_c1_9	3701	17804	318	106	YOR020C	312	5.2(10)-28	Saccharomyces cerevisiae	[ui:yo20c] [pn:chaperonin, mitochondrial:10 kd heat shock protein, mitochondrial:hsp10:10 kd chaperonin] [gn:hsp10-cpn10:or26] [gicfc:12.7.2.8:10.7.1.1] [keggfc:14.2] [sgdfc:6.2.0:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG987	880017_f3_1	3702	17805	429	143	YOR065W	561	2.1(10)-54	Saccharomyces cerevisiae	[ui:yo65w] [pn:cytochrome c1:cytochrome c1, heme protein precursor] [gn:ccl1:cyt1] [gicfc:2.8] [keggfc:14.2] [sgdfc:2.5.0:9.7.0] [db:gic-saccharomyces cerevisiae]

CONTIG2506	20007785_c1_4	3703	17806	549	183	YOR150W	510	5.4(10)-49	Saccharomyces cerevisiae	[ui:yor150w] [pn:similarity to ribosomal protein 113] [gtcfc:2.8:10.4] [keggc:14.2] [sgdfc:5.1.0:9.7.0]
CONTIG5467	3023443_c2_17	3704	17807	693	231	YOR158W	218	4.7(10)-18	Saccharomyces cerevisiae	[ui:yor158w] [pn:ribosomal protein, mitochondrial:mitochondrial 40S ribosomal protein precursor] [gn:pet123] [gtcfc:2.8:10.4] [keggc:14.2] [sgdfc:5.1.0:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG5788	29462502_f3_10	3705	17808	1206	402	YOR176W	1254	7.7(10)-128	Saccharomyces cerevisiae	[ui:yor176w] [pn:ferrochelatase precursor:protoheme ferrolyase:heme synthetase] [gn:hem15] [gtcfc:2.8:9:10.9:11:12:6] [ec:4.99.1.1] [keggc:9.10] [sgdfc:1.7.1:1.8.1:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG4202	26618966_f2_2	3706	17809	663	221	YOR187W	664	2.6(10)-65	Saccharomyces cerevisiae	[ui:yor187w] [pn:translation elongation factor tu, mitochondrial:elongation factor tu, mitochondrial precursor] [gn:tuf1] [gtcfc:2.8:10.7] [keggc:14.2] [sgdfc:5.2:0:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG2136	35199025_q2_2	3707	17810	480	160	YOR196C	483	3.8(10)-46	Saccharomyces cerevisiae	[ui:yor196c] [pn:lipoyc acid synthase:lipoyc acid synthetase] [precursor:lip-syn] [gn:lip5] [gtcfc:2.8:9:10.9:11] [keggc:14.2] [sgdfc:1.7.1:9.7.0] [db:gic-saccharomyces cerevisiae]

CONTIG2598	32032812_c3_2	3708	17811	1275	425	YOR201C	297	1.1(10)-40	Saccharomyces cerevisiae	[ui:yor201c] [pn:rma guanosine-2'-o--methyltransferase;ribose methyltransferase:mitochondrial large ribosomal rna ribose methylase] [gr:pet56] [gicfc:2.8;3.7;5.11;5.14;9.12;10.3] [ec:2.1.1.-] [keggfc:3.7;5.11;5.14;9.13] [sgdfc:4.2.0;]
CONTIG1196	1304582_f1_1	3709	17812	1065	355	YOR211C	705	1.2(10)-69	Saccharomyces cerevisiae	[ui:yor211c] [pn:dynamin-like protein:mgm1 protein precursor] [gn:mgm1:yor50-1] [gicfc:2.8] [keggfc:14.2] [sgdfc:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG3428	31542562_f3_2	3710	17813	1026	342	YOR211C	332	1.2(10)-44	Saccharomyces cerevisiae	[ui:yor211c] [pn:dynamin-like protein:mgm1 protein precursor] [gn:mgm1:yor50-1] [gicfc:2.8] [keggfc:14.2] [sgdfc:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG4453	302111575_f3_2	3711	17814	372	124	YOR211C	280	2.0(10)-23	Saccharomyces cerevisiae	[ui:yor211c] [pn:dynamin-like protein:mgm1 protein precursor] [gn:mgm1:yor50-1] [gicfc:2.8] [keggfc:14.2] [sgdfc:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG2021	19743805_f3_1	3712	17815	1161	387	YOR274W	692	2.7(10)-68	Saccharomyces cerevisiae	[ui:yor274w] [pn:isopentenyl-diphosphate:tRNA isopentenyltransferase:ipp transferase:ipp] [gn:mod5] [gicfc:2.8;10.1:10.2;10.6:14.1] [ec:2.5.1.8] [keggfc:14.1] [sgdfc:4.6;0.9.2.0.9.5.0.9.7.0] [db:gic-saccharomyces cerevisiae]

CONTIG3071	4381436_f3_3	3713	17816	963	321	YOR330C	426	9.0(10)-39	Saccharomyces cerevisiae	[ui:yor330c] [pn:dnad-directed dna polymerase gamma catalytic subunit, mitochondrial:dnatpolymerase catalytic subunit][gn:mip1] [gtcfc:2.8:4.1:4.2:10.8][ec:2.7.7.7] [keggfc:4.1:4.2][sgdgc:3.6.0:9.7]
CONTIG5060	21963277_c3_7	3714	17817	2232	744	YOR330C	1455	3.8(10)-149	Saccharomyces cerevisiae	[ui:yor330c] [pn:dnad-directed dna polymerase gamma catalytic subunit, mitochondrial:dnatpolymerase catalytic subunit][gn:mip1] [gtcfc:2.8:4.1:4.2:10.8][ec:2.7.7.7] [keggfc:4.1:4.2][sgdgc:3.6.0:9.7]
CONTIG4036	34251377_c1_5	3715	17818	1155	385	YOR334W	780	1.3(10)-77	Saccharomyces cerevisiae	[ui:yor334w] [pn:rnasplicing protein and member of the mitochondrial carrier family:mcf:mitochondrial msplicing protein mrs2 precursor][gn:mrs2:yor333c] [gtcfc:2.8:10.2][keggfc:14.2] [sgdgc:4.9.0:9.7.0][db:gic-saccharomyces cer
CONTIG4238	14648436_c3_8	3716	17819	1482	494	YOR355W	329	1.8(10)-29	Saccharomyces cerevisiae	[ui:yor355w] [pn:nam9-1 suppressor:protein] [gn:gds1][gtcfc:2.8] [keggfc:14.2][sgdgc:9.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG2959	31258541_f2_2	3717	17820	183	61	YPL215W	92	0.00067	Saccharomyces cerevisiae	[ui:ypl215w] [pn:required for assembly of cytochrome bc1 complex:protein precursor][gn:cbp3] [gtcfc:2.8:12.16][keggfc:14.2] [sgdgc:6.4.0:9.7.0][db:gic-saccharomyces cerevisiae]

CONTIG3142	781256_f2_2	3718	17821	1008	336	YPL215W	736	6.0(10)-73	Saccharomyces cerevisiae	[ui:yp11215w] [pn:required for assembly of cytochrome bc1 complex:protein precursor]
									[gn:ebp3] [gicfc:2.8;12;16] [keggfc:14;2] [sgdfc:6.4;0;9.7.0] [db:gic-saccharomyces cerevisiae]	
CONTIG2108	10663437_f1_1	3719	17822	639	213	YPL173W	161	1.2(10)-11	Saccharomyces cerevisiae	[ui:yp1173w] [pn:ribosomal protein yml40, mitochondrial/mitochondrial 60s ribosomal protein l40:yml40]
									[gn:mpl40] [gicfc:2.8;10.4] [keggfc:14;2] [sgdfc:5.1.0;9.7.0] [db:gic-saccharomyces cerevisiae]	
CONTIG5191	15097650_q3_11	3720	17823	336	112	YPL172C	199	2.7(10)-15	Saccharomyces cerevisiae	[ui:yp1172c] [pn:farnesylyl transferase:cytochrome c oxidase assembly protein precursor]
									[gn:cox10] [gicfc:2.8;3.1;9.10;9.11;12;16] [keggfc:14;2] [sgdfc:1.6;3.1;7.1;6.4;0;9.7.0] [db:gic-saccharomyces cerevisiae]	
CONTIG5559	33773507_f3_13	3721	17824	1167	389	YPL172C	899	3.2(10)-90	Saccharomyces cerevisiae	[ui:yp1172c] [pn:farnesylyl transferase:cytochrome c oxidase assembly protein precursor]
									[gn:cox10] [gicfc:2.8;3.1;9.10;9.11;12;16] [keggfc:14;2] [sgdfc:1.6;3.1;7.1;6.4;0;9.7.0] [db:gic-saccharomyces cerevisiae]	

CONTIG4714	33400257_f2_2	3722	17825	825	275	YPL132W	764	6.5(10)-76	Saccharomyces cerevisiae	[ui:yp[132w] [pn:cytochrome-c oxidase assembly protein:cytochrome c oxidase assembly protein cox 11] [gn:cox1:1:pi[13w] [gicfc:2.8.9;10.9.11:12.16] [keggfc:14.2] [sgdgc:1.7.1:6.4:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4972	22867143_c1_9	3723	17826	1683	561	YPL104W	678	8.5(10)-67	Saccharomyces cerevisiae	[ui:yp[104w] [pn:aspartate--tRNA ligase, mitochondrial:aspartyl-tRNA synthetase, mitochondrial:aspartate-tRNA ligase:asprs][gn:msd1:1p[5w] [gicfc:2.8.5;2.10.6] [ec:6.1.1.12] [keggfc:5.2;10.1:10.2] [sgdgc:5.4.0:9.7.0] [db:gtc-saccha
CONTIG4559	34171950_c2_5	3724	17827	255	85	YPL097W	100	0.00016	Saccharomyces cerevisiae	[ui:yp[097w] [pn:tyrosyl-tRNA synthetase:tyrosyl-tRNA synthetase, mitochondrial precursor:tyrosine-tRNA ligase:tyrss][gn:msy1:1p[1w] [gicfc:2.8.5;15;10.6] [ec:6.1.1.1] [keggfc:5.1;5;10.1:10.2] [sgdgc:5.4.0:9.7.0] [db:gtc-saccharomyce
CONTIG578	976587_c1_3	3725	17828	537	179	YPL097W	249	1.1(10)-20	Saccharomyces cerevisiae	[ui:yp[097w] [pn:tyrosyl-tRNA synthetase:tyrosyl-tRNA synthetase, mitochondrial precursor:tyrosine-tRNA ligase:tyrss][gn:msy1:1p[1w] [gicfc:2.8.5;15;10.6] [ec:6.1.1.1] [keggfc:5.1;5;10.1:10.2] [sgdgc:5.4.0:9.7.0] [db:gtc-saccharomyce

CONTIG5813	3912836_c2_44	3726	17829	1164	388	YPL040C	591	8.4(10)-57	Saccharomyces cerevisiae	[ui:yp 040c] [pn:isoleucine-tRNA ligase, mitochondrial:isoleucyl-tRNA synthetase, mitochondrial:isoleucine--tRNA ligase:illers] [gn:ism1:p7102] [gicfc:2.8;5.7;10.6] [ec:6.1.1.5] [keggfc:5.7;10.1;10.2] [sgdgc:5.4.0.9;7.0] [db:gic-sacch]
CONTIG5813	258387_cl_33	3727	17830	1821	607	YPL040C	1204	1.5(10)-122	Saccharomyces cerevisiae	[ui:yp 040c] [pn:isoleucine-tRNA ligase, mitochondrial:isoleucyl-tRNA synthetase, mitochondrial:isoleucine--tRNA ligase:illers] [gn:ism1:p7102] [gicfc:2.8;5.7;10.6] [ec:6.1.1.5] [keggfc:5.7;10.1;10.2] [sgdgc:5.4.0.9;7.0] [db:gic-sacch]
CONTIG5153	11181552_f2_3	3728	17831	2166	722	YPL029W	1113	6.7(10)-113	Saccharomyces cerevisiae	[ui:yp 029w] [pn:atp-dependent RNA helicase, mitochondrial:mitochondrial atp-dependent RNA helicase suv3 precursor] [gn:suv3;1pb2w] [gicfc:2.8;4;4.10.10;10.2:10.3;10.7] [keggfc:14;2] [sgdgc:1.3.6.4.2.0;4.9.0;5.3.0;9.7.0] [db:gic-sacch]
CONTIG3664	1550_c2_8	3729	17832	630	210	YPL013C	279	1.6(10)-24	Saccharomyces cerevisiae	[ui:yp 013c] [pn:ribosomal protein S16, mitochondrial] [gicfc:2.8;10.4] [keggfc:14;2] [sgdgc:5.1.0;9.7.0] [db:gic-saccharomyces cerevisiae]

CONTIG5198	31913311_c1_8	3730	17833	1302	434	YPR024W	1043	1.8(10)-105	Saccharomyces cerevisiae	[ui:yp024w] [pn:protease of the sec18/cdc48/pas1 family of aipases:aaayme1 protein:tat-binding homolog 11:osd1 protein] [gn:yme1.yta11:osd1.yp9367] [gicfc:2.8:10.11:12.16] [ec:3.4.24.-] [keggfc:14..1] [sgdfc:6.4.0:6.5.3:9.7.0] [db:gt]
CONTIG816	33492754_02_5	3731	17834	909	303	YPR024W	978	1.3(10)-98	Saccharomyces cerevisiae	[ui:yp024w] [pn:protease of the sec18/cdc48/pas1 family of aipases:aaayme1 protein:tat-binding homolog 11:osd1 protein] [gn:yme1.yta11:osd1.yp9367] [gicfc:2.8:10.11:12.16] [ec:3.4.24.-] [keggfc:14..1] [sgdfc:6.4.0:6.5.3:9.7.0] [db:gt]
CONTIG5155	5353307_f1_1	3732	17835	606	202	YPR037C	351	3.7(10)-32	Saccharomyces cerevisiae	[ui:yp037c] [pn:similarity to erv1p and rat air protein] [gicfc:2.8] [keggfc:14..2] [sgdfc:9.7.0] [db:gicsaccharomyces cerevisiae]
CONTIG4428	14100281_f3_4	3733	17836	357	119	YPR047W	167	8.9(10)-12	Saccharomyces cerevisiae	[ui:yp047w] [pn:phenylalanine-tRNA ligase alpha chain, mitochondrial] [gn:msf1] [gicfc:2.8:5.15:10.6:10.7:11.1] [ec:6.1.1.20] [keggfc:5.15:10.1:10.2] [sgdfc:5.4.0:6.2.0:9.7.0] [db:gicsaccharomyces cerevisiae]

CONTIG5336	26265627_c2_12	3734	17837	918	306	YPR047W	871	3.0(10)-87	Saccharomyces cerevisiae	[ui:ypr047w] [pm:phenylalanine-tRNA ligase alpha chain, mitochondrial] [gn:mst1] [gicfc:2.8:5:15:10.6:10.7:11.1] [ec:6.1.1.20] [keggc:5.15:10.1:10.2] [sgdfc:5.4.0:6.2.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2365	16431388_c3_5	3735	17838	528	176	YPR155C	119	2.0(10)-15	Saccharomyces cerevisiae	[ui:ypr155c] [pn:control of mitochondrial synthesis of ATP6P and ATP8P] [gn:nca2] [gicfc:2.8] [keggc:14.2] [sgdfc:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5107	156261_c3_10	3736	17839	1605	535	YPR155C	193	5.7(10)-12	Saccharomyces cerevisiae	[ui:ypr155c] [pn:control of mitochondrial synthesis of ATP6P and ATP8P] [gn:nca2] [gicfc:2.8] [keggc:14.2] [sgdfc:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5523	21914062_f1_3	3737	17840	387	129	YPR166C	292	6.7(10)-26	Saccharomyces cerevisiae	[ui:ypr166c] [pn:ribosomal protein S14, mitochondrial 40S ribosomal protein Mrp2] [gn:mp2,p9325] [gicfc:2.8:10.4] [keggc:14.2] [sgdfc:5.1.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4269	12288260_c1_3	3738	17841	1242	414	YDL107W	266	2.8(10)-38	Saccharomyces cerevisiae	[ui:ydl107w] [pn:ser/thr protein kinase, Mss2 protein] [gn:mss2,d2340] [gicfc:2.8:12.13] [keggc:14.2] [sgdfc:2.5.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3724	1586_f3_2	3739	17842	1452	484	YEL053C	247	1.8(10)-18	Saccharomyces cerevisiae	[ui:yel053c] [pn:glucose-repressible protein, glucose repressible protein] [gn:mak1] [gicfc:2.8] [keggc:14.2] [sgdfc:2.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4466	26345312_f3_4	3740	17843	579	193	YEL053C	94	0.05199	Saccharomyces cerevisiae	[ui:yel053c] [pn:glucose-repressible protein;glucose repressive protein] [gn:mak10] [gtcfc:2.8] [keggfc:14.2] [sgdfc:2.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4070	20759813_c3_8	3741	17844	528	176	YGR062C	133	1.8(10)-8	Saccharomyces cerevisiae	[ui:ygr062c] [pn:required for activity of mitochondrial cytochrome oxidase:cytochrome c oxidase assembly protein cox18 precursor] [gn:cox18;g4532] [gtcfc:2.8] [keggfc:14.2] [sgdfc:2.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5713	26199067_f3_8	3742	17845	525	175	YGR062C	187	1.7(10)-14	Saccharomyces cerevisiae	[ui:ygr062c] [pn:required for activity of mitochondrial cytochrome oxidase:cytochrome c oxidase assembly protein cox18 precursor] [gn:cox18;g4532] [gtcfc:2.8] [keggfc:14.2] [sgdfc:2.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4949	959687_f1_2	3743	17846	246	82	YLL009C	102	9.3(10)-6	Saccharomyces cerevisiae	[ui:yll009c] [pn:interacts genetically with sco1 and sco2 in cytochrome oxidase assembly] [gn:cox17] [gtcfc:2.8;12.16;12.6] [keggfc:14.2] [sgdfc:1.8.1.2.5.0.6.4.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
b1x17891.y	6033442_f1_1	3744	17847	519	173	YML125C	454	4.5(10)-43	Saccharomyces cerevisiae	[ui:yml125c] [pn:strong similarity to cytochrome-b5- and nitrate reductases] [gtcfc:2.8] [keggfc:14.2] [sgdfc:2.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1595	2054517_c1_4	3745	17848	660	220	YMR073C	186	4.0(10)-19	Saccharomyces cerevisiae	[ui:ymr073c] [pn:weak similarity to c-terminal part of cytochrome b5 and b2] [gicfc:2.8] [keggfc:14.2] [sgdfc:2.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG2926	36444568_c2_5	3746	17849	852	284	YMR145C	759	2.2(10)-75	Saccharomyces cerevisiae	[ui:ymr145c] [pn:strong similarity to nadh dehydrogenase:ubiquinone:hypothetical 62.8 kd protein in mds1-swp1 intergenic region] [gn:ym9375] [gicfc:2.8:9.12] [keggfc:14.2] [sgdfc:2.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5718	12271933_c2_20	3747	17850	582	194	YMR165C	333	2.2(10)-33	Saccharomyces cerevisiae	[ui:ymr165c] [pn:involved in plasmid maintenance, respiration and cell proliferation:smp2 protein] [gn:smp2:ym8520] [gicfc:2.8:12.8] [keggfc:14.2] [sgdfc:2.5.0:3.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG3321	4375675_c3_32	3748	17851	1203	401	YNL118C	662	9.0(10)-65	Saccharomyces cerevisiae	[ui:ynl118c] [pn:suppressor protein of a yeast per mutant:psu1 protein] [gn:psu1:n1917] [gicfc:2.8] [keggfc:14.2] [sgdfc:2.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5628	24266511_f1_4	3749	17852	1905	635	YOR356W	1905	8.0(10)-197	Saccharomyces cerevisiae	[ui:yor356w] [pn:strong similarity to human electron transfer flavoprotein-ubiquinone oxidoreductase:strong similarity to human electron transfer flavoprotein-ubiquinone oxidoreductase] [gicfc:2.8:9.12] [keggfc:14.2] [sgdfc:2.5.0] [db:gic-saccharomyces cerevisiae]

b3x16938.y	14536001_q3_5	3750	17853	336	112	YPR004C	147	6.7(10)-10	Saccharomyces cerevisiae	[ui:ypr004c] [pn:strong similarity to electron transfer flavoproteins alpha chain] [gtcfc:2.8] [keggfc: 14.2] [sgdfc:2.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4428	13864407_f3_3	3751	17854	861	287	YPR048W	347	4.5(10)-31	Saccharomyces cerevisiae	[ui:ypr048w] [pn:similarity to m.domestica nadph-ferrihemoprotein reductase and mammalian nitric-oxide synthases] [grcfc:2.8] [keggfc: 14.2] [sgdfc:2.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4428	22034632_f1_2	3752	17855	1068	356	YPR048W	628	1.7(10)-61	Saccharomyces cerevisiae	[ui:ypr048w] [pn:similarity to m.domestica nadph-ferrihemoprotein reductase and mammalian nitric-oxide synthases] [grcfc:2.8] [keggfc: 14.2] [sgdfc:2.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4071	22540967_f3_5	3753	17856	2067	689	YKL182W	2276	3.8(10)-236	Saccharomyces cerevisiae	[ui:ykl182w] [pn:fatty-acyl-coa synthase, beta chain:fatty acid synthase, subunit beta:contains 3-hydroxypalmitoyl-acyl-carrier-protein dehydratase enoyl-acyl-carrier-protein reductase (nadh) acyl-carrier-protein acetyltransferase acyl]
CONTIG3036	3944006_f3_3	3754	17857	1185	395	YKL182W	1029	1.1(10)-102	Saccharomyces cerevisiae	[ui:ykl182w] [pn:fatty-acyl-coa synthase, beta chain:fatty acid synthase, subunit beta:contains 3-hydroxypalmitoyl-acyl-carrier-protein dehydratase enoyl-acyl-carrier-protein reductase (nadh) acyl-carrier-protein acetyltransferase acyl]

CONTIG2315	23938329_c1_3	3755	17858	909	303	YKL182W	968	3.5(10)-96	Saccharomyces cerevisiae	[ui:ycl1182w] [pn:fatty-acyl-coa synthase, beta chain:fatty acid synthase, subunit beta:contains 3-hydroxypalmitoyl-acyl-carrier-protein dehydratase enoyl-acyl-carrier-protein reductase (nadh) acyl-carrier-protein acetyltransferase acyl]
CONTIG2544	1959375_c2_5	3756	17859	1209	403	YPL231W	1211	2.1(10)-122	Saccharomyces cerevisiae	[ui:yp1231w] [pn:fatty-acyl-coa synthase, alpha chain:fatty acid synthase, subunit alpha:contains:ec 1.1.1.100, and ec 2.3.1.41] [gn:fas2] [gtcfc:3.1:3.4:8.1:8.2:12.16] [ec:2.3.1.86] [keggfc:3.1] [sgdgc:1.6.1:6.4.0:9.2.0] [db:gtc-sacc]
CONTIG3183	269442_f1_1	3757	17860	1242	414	YPL231W	1286	1.3(10)-130	Saccharomyces cerevisiae	[ui:yp1231w] [pn:fatty-acyl-coa synthase, alpha chain:fatty acid synthase, subunit alpha:contains:ec 1.1.1.100, and ec 2.3.1.41] [gn:fas2] [gtcfc:3.1:3.4:8.1:8.2:12.16] [ec:2.3.1.86] [keggfc:3.1] [sgdgc:1.6.1:6.4.0:9.2.0] [db:gtc-sacc]
CONTIG3183	30096938_f3_5	3758	17861	222	74	YPL231W	132	3.1(10)-7	Saccharomyces cerevisiae	[ui:yp1231w] [pn:fatty-acyl-coa synthase, alpha chain:fatty acid synthase, subunit alpha:contains:ec 1.1.1.100, and ec 2.3.1.41] [gn:fas2] [gtcfc:3.1:3.4:8.1:8.2:12.16] [ec:2.3.1.86] [keggfc:3.1] [sgdgc:1.6.1:6.4.0:9.2.0] [db:gtc-sacc]

CONTIG3995	36366563_c1_8	3759	17862	1131	377	YPL231W	1256	2.6(10)-127	Saccharomyces cerevisiae	[ui:yp 231w] [pn:fatty-acyl-coa synthase, alpha chain:fatty acid synthase, subunit alpha:contains:sec 1.1.1.100, and ec 2.3.1.41] [gn:fas2] [gicfc:3.1:3.4.8.1:8.2:12.16] [ec:2.3.1.86] [keggfc:3.1] [sgdfc:1.6.1:6.4.0:9.2.0] [db:gtc-sacc]
CONTIG679	26376953_2_3	3760	17863	240	80	YPL231W	320	3.2(10)-27	Saccharomyces cerevisiae	[ui:yp 231w] [pn:fatty-acyl-coa synthase, alpha chain:fatty acid synthase, subunit alpha:contains:sec 1.1.1.100, and ec 2.3.1.41] [gn:fas2] [gicfc:3.1:3.4.8.1:8.2:12.16] [ec:2.3.1.86] [keggfc:3.1] [sgdfc:1.6.1:6.4.0:9.2.0] [db:gtc-sacc]
CONTIG679	24610787_f3_4	3761	17864	1095	365	YPL231W	1397	5.5(10)-143	Saccharomyces cerevisiae	[ui:yp 231w] [pn:fatty-acyl-coa synthase, alpha chain:fatty acid synthase, subunit alpha:contains:sec 1.1.1.100, and ec 2.3.1.41] [gn:fas2] [gicfc:3.1:3.4.8.1:8.2:12.16] [ec:2.3.1.86] [keggfc:3.1] [sgdfc:1.6.1:6.4.0:9.2.0] [db:gtc-sacc]

CONTIG2925	20347787_c3_6	3762	17865	1185	395	YDL090C	231	4.2(10)-18	Saccharomyces cerevisiae	[ui:yd 090c] [pn:protein farnesyltransferase, beta subunit:caax farnesyltransferase beta subunit:ras proteins prenyltransferase:flase-beta] [gn:ram1:dpr1:ste16:scg2:d2412] [gtcfc:3.1:7.1:9.12:10]
b3x16082_x	1994166_f2_1	3763	17866	288	96	YDL090C	135	2.2(10)-8	Saccharomyces cerevisiae	[ui:yd 090c] [pn:protein farnesyltransferase, beta subunit:caax farnesyltransferase beta subunit:ras proteins prenyltransferase:flase-beta] [gn:ram1:dpr1:ste16:scg2:d2412] [gtcfc:3.1:7.1:9.12:10]
CONTIG3892	14344057_f1_1	3764	17867	1425	475	YDL040C	1042	2.2(10)-105	Saccharomyces cerevisiae	[ui:yd 040c] [pn:protein n-acetyltransferase subunit:n-terminal alpha-amino, acetyltransferase 1] [gn:nat1:aaal :d2720] [gtcfc:3.1:10.7:14.1] [ec:2.3.1.88] [keggfc:14.1] [sgdfc:1.6.3.5.5.0:6.3.0:9.2.

CONTIG4324	24881577_c2_9	3765	17868	807	269	YDL040C	237	7.2(10)-19	Saccharomyces cerevisiae	[ui:yd1040c] [pn:protein n-acetyltransferase subunit:n-terminal alpha-amino, acetyltransferase 1: amino-terminal, alpha-nati :aaal :d2720] [gn:nat1 :ec:2.3.1.88] [gicfc:3.1:10.7:14.1] [keggfc:14.1] [sgdgc:1.6.3:5.5:0.6.3.0:9.2.]
CONTIG5041	10663925_f3_4	3766	17869	1080	360	YDR331W	1086	4.9(10)-110	Saccharomyces cerevisiae	[ui:yd331w] [pn:essential for gpi anchor attachment:hypothetical 4.7.4 kd protein in pas3 3" region] [gn:gpi8_d9798] [gicfc:3.1:10.7:12.16] [keggfc:14.2] [sgdgc: 1.6.3:6.3:0.9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1277	24042550_g3_3	3767	17870	408	136	YDR410C	196	1.2(10)-19	Saccharomyces cerevisiae	[ui:yd410c] [pn:farnesyl cysteine carboxyl-methyltransferase:protein- s isoprenylcysteine o- methyltransferase:isoprenylcysteine carboxylmethyltransferase] [gn:ste14:d9461] [gicfc:3.1:10.7] [ec:2.1.1.100] [keggfc:14.1] [sgdgc:1.6.3:6.3]
CONTIG3528	25549090_o2_5	3768	17871	843	281	YDR410C	191	3.3(10)-15	Saccharomyces cerevisiae	[ui:yd410c] [pn:farnesyl cysteine carboxyl-methyltransferase:protein- s isoprenylcysteine o- methyltransferase:isoprenylcysteine carboxylmethyltransferase] [gn:ste14:d9461] [gicfc:3.1:10.7] [ec:2.1.1.100] [keggfc:14.1] [sgdgc: 1.6.3:6.3]

CONTIG2198	21517168_f2_1	3769	17872	912	304	YER015W	723	1.3(10)-71	Saccharomyces cerevisiae	[ui:yer015w] [pn:long-chain-fatty-acid--coa ligase:long-chain-fatty-acid--coa ligase 2:long-chain acyl-coa synthetase 2:fatty acid activator 2] [gn:faa2;fam1] [gicfc:3.1.3:2:12.2:12.6] [ec:6.2.1.3] [keggfc:3.2] [sgdfc:1.6.3:1.6.5:8.4]
CONTIG3922	4773937_f1_1	3770	17873	975	325	YER015W	389	2.2(10)-35	Saccharomyces cerevisiae	[ui:yer015w] [pn:long-chain-fatty-acid--coa ligase:long-chain-fatty-acid--coa ligase 2:long-chain acyl-coa synthetase 2:fatty acid activator 2] [gn:faa2;fam1] [gicfc:3.1.3:2:12.2:12.6] [ec:6.2.1.3] [keggfc:3.2] [sgdfc:1.6.3:1.6.5:8.4]
CONTIG4532	12625281_f1_1	3771	17874	1380	460	YER015W	971	7.5(10)-98	Saccharomyces cerevisiae	[ui:yer015w] [pn:long-chain-fatty-acid--coa ligase:long-chain-fatty-acid--coa ligase 2:long-chain acyl-coa synthetase 2:fatty acid activator 2] [gn:faa2;fam1] [gicfc:3.1.3:2:12.2:12.6] [ec:6.2.1.3] [keggfc:3.2] [sgdfc:1.6.3:1.6.5:8.4]
CONTIG4868	820425_f3_4	3772	17875	186	62	YER015W	128	2.7(10)-7	Saccharomyces cerevisiae	[ui:yer015w] [pn:long-chain-fatty-acid--coa ligase:long-chain-fatty-acid--coa ligase 2:long-chain acyl-coa synthetase 2:fatty acid activator 2] [gn:faa2;fam1] [gicfc:3.1.3:2:12.2:12.6] [ec:6.2.1.3] [keggfc:3.2] [sgdfc:1.6.3:1.6.5:8.4]

CONTIG5092	10976502_c1_10	3773	17876	1851	617	YER015W	718	4.9(10)-71	Saccharomyces cerevisiae	[ui:yer015w] [pn:long-chain-fatty-acid--coa ligase:long-chain-fatty-acid--coa ligase 2:long-chain acyl-coa synthetase 2:fatty acid activator 2] [gn:faa2:fam1] [gicfc:3.1.3:2:12.2:12.6] [ec:6.2.1.3] [keggfc:3.2] [sgdgc:1.6.3:1.6.5:8.4]
CONTIG5818	23447052_f1_3	3774	17877	765	255	YER015W	167	2.1(10)-16	Saccharomyces cerevisiae	[ui:yer015w] [pn:long-chain-fatty-acid--coa ligase:long-chain-fatty-acid--coa ligase 2:long-chain acyl-coa synthetase 2:fatty acid activator 2] [gn:faa2:fam1] [gicfc:3.1.3:2:12.2:12.6] [ec:6.2.1.3] [keggfc:3.2] [sgdgc:1.6.3:1.6.5:8.4]
CONTIG5818	30173825_f2_15	3775	17878	1494	498	YER015W	919	2.5(10)-92	Saccharomyces cerevisiae	[ui:yer015w] [pn:long-chain-fatty-acid--coa ligase:long-chain-fatty-acid--coa ligase 2:long-chain acyl-coa synthetase 2:fatty acid activator 2] [gn:faa2:fam1] [gicfc:3.1.3:2:12.2:12.6] [ec:6.2.1.3] [keggfc:3.2] [sgdgc:1.6.3:1.6.5:8.4]
b2x15869.x	13788931_f2_1	3776	17879	483	161	YGL155W	137	1.0(10)-8	Saccharomyces cerevisiae	[ui:ygl155w] [pn:geranylgeranyltransferase beta subunit:type i proteins geranylgeranyltransferase beta subunit:type i protein geranylgeranyltransferase beta subunit:gerase-i-beta:pggt:ras proteins geranylgeranyltransferase beta subunit]

b1x18944.y	866677_c2_1	3777	17880	477	159	YGL155W	206	2.5(10)-16	Saccharomyces cerevisiae	[ui:yg 155w] [pn:geranylgeranyltransferase beta subunit:type i proteins geranylgeranyltransferase beta subunit:protein geranyl-geranyltransferase beta subunit:ggtase-i-beta:pgt:ras proteins geranylgeranyltransferase beta subunit
CONTIG5696	14492952_f2_5	3778	17881	525	175	YHR013C	538	5.7(10)-52	Saccharomyces cerevisiae	[ui:yhr013c] [pn:protein n-acetyltransferase subunit:n-terminal acetyltransferase complex subunit:arrest-defective protein 1] [gn:ard1][gfcf:3.1:10.7:12.8] [keggfc:4.2] [sgdic:1.6.3.3.8.0.6.3.0.9.2.0] [db:gtc-saccharomyces cerevis
b3x16013.y	21963942_f1_1	3779	17882	294	98	YHR013C	182	3.1(10)-14	Saccharomyces cerevisiae	[ui:yhr013c] [pn:protein n-acetyltransferase subunit:n-terminal acetyltransferase complex subunit:arrest-defective protein 1] [gn:ard1][gfcf:3.1:10.7:12.8] [keggfc:4.2] [sgdic:1.6.3.3.8.0.6.3.0.9.2.0] [db:gtc-saccharomyces cerevis
CONTIG2298	12791267_f2_1	3780	17883	543	181	YJL031C	116	3.3(10)-9	Saccharomyces cerevisiae	[ui:yj031c] [pn:geranylgeranyl transferase, alpha chain:type ii proteins geranylgeranyltransferase alpha subunit:type ii protein geranyl-geranyltransferase alpha subunit:ggtase-ii-alpha:pgt:ypf1/sec4 proteins geranylgeranyltransferas

CONTIG1168	21485635_c3_3	3781	17884	792	264	YJR066W	202	1.1(10)-18	Saccharomyces cerevisiae	[ui:yj066w] [pn:phosphatidylinositol 3-kinase:phosphatidylinositol 3-kinase: tor1:pi3-kinase:pidins-3-kinase:pi3k] [gn:tor1:dr1:j1803] [gicfc:3.1:8.1:10.7:12.8] [ec:2.7.1.137] [keggfc:8.1] [sgdic:1.6.3.3.8.0.5.5.0] [db:gic-saccharomy]
b2x15416_x	31273942_f2_1	3782	17885	816	272	YJR066W	832	1.6(10)-81	Saccharomyces cerevisiae	[ui:yj066w] [pn:phosphatidylinositol 3-kinase:phosphatidylinositol 3-kinase: tor1:pi3-kinase:pidins-3-kinase:pi3k] [gn:tor1:dr1:j1803] [gicfc:3.1:8.1:10.7:12.8] [ec:2.7.1.137] [keggfc:8.1] [sgdfc:1.6.3.3.8.0.5.5.0] [db:gic-saccharomy]
CONTIG1565	16220261_c3_2	3783	17886	444	148	YKL019W	214	1.3(10)-17	Saccharomyces cerevisiae	[ui:yk019w] [pn:protein farnesyltransferase, alpha subunit:protein farnesyltransferase alpha subunit:caax farnesyltransferase alpha subunit:ras proteins prenyltransferase:flase-alpha] [gn:ramp2] [gicfc:3.1:7.1:9.12.10.7:11.3] [ec:2.5.

CONTIG1565	4688312_c3_1	3784	17887	231	77	YKL019W	153	1.2(10)-10	Saccharomyces cerevisiae	[ui:yk1019w] [pn:protein farnesylyltransferase, alpha subunit:proteins farnesylyltransferase, ras proteins prenyltransferase:flase-alpha] [gn:ram2] [gicfc:3.1:7.1:9.12:10.7.11.3] [ec:2.5.]
CONTIG1936	24665901_c1_4	3785	17888	471	157	YLR088W	324	1.3(10)-28	Saccharomyces cerevisiae	[ui:yh088w] [pn:required for attachment of gpi anchor onto proteins:gaa1 protein] [gn:gaa1:end2:19449] [gicfc:3.1:10.7:12.16:12.6] [keggfc:14.2] [sgdgc:1.6.3:6.3:0.8:7.0:9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG410	24797067_c3_1	3786	17889	726	242	YLR195C	637	1.8(10)-62	Saccharomyces cerevisiae	[ui:ylr195c] [pn:n-myristoyltransferase:glycylpeptide n-tetradecanoyltransferase:n-myristoyl-coa:protein n-myristoyltransferase:nmt] [gn:nmt:cdc2:18167] [gicfc:3.1:10.7:14.1] [ec:2.3.1.97] [keggfc:14.1]
b9x13972.y	4070152_c1_2	3787	17890	630	210	YMR013C	129	1.3(10)-7	Saccharomyces cerevisiae	[ui:ym013c] [pn:dolichol kinase] [gn:sec59:ym8270] [gicfc:3.1:7.1:11.3:12.15:12.16] [ec:2.7.1.108] [keggfc:7.2] [sgdgc:1.6.3:3.4.0:9.4.0] [db:gic-saccharomyces cerevisiae]

CONTIG2707	4688932_c3_6	3788	17891	972	324	YMR246W	886	7.7(10)-89	Saccharomyces cerevisiae	[ui:ymr246w] [pn:long-chain-fatty-acid--coa ligase;long-chain-fatty-acid--coa ligase 4:long-chain acyl-coa synthetase 4:fatty acid activator 4] [gn:faa4;ym9408] [gtcfc:3.1:3.2:3.4:8.1:8.2:12.2] [ec:6.2.1.3] [keggfc:3.2] [sgdgc:1.6.1.]
CONTIG4397	984700_f3_2	3789	17892	1038	346	YOR317W	1076	5.7(10)-109	Saccharomyces cerevisiae	[ui:yor317w] [pn:long-chain-fatty-acid--coa ligase;long-chain-fatty-acid--coa ligase 1:long-chain acyl-coa synthetase 1:fatty acid activator 1] [gn:faa1;06136] [gtcfc:3.1:3.2:12.2] [ec:6.2.1.3] [keggfc:3.2] [sgdgc:1.6.3:1.6.5] [db:gt]
CONTIG5608	12689637_c1_12	3790	17893	2031	677	YOR370C	1133	5.2(10)-115	Saccharomyces cerevisiae	[ui:yor370c] [pn:geranylgeranyltransferase regulatory subunit:rab proteins geranylgeranyltransferase component:arab escort protein:rep] [gn:msi4:mrs6] [gtcfc:3.1:10.7] [keggfc:14.2] [sgdgc:1.6.3:6.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4727	25571936_f2_1	3791	17894	630	210	YPR176C	650	7.9(10)-64	Saccharomyces cerevisiae	[ui:ypr176c] [pn:geranylgeranyltransferase type ii beta subunit:type ii proteins geranylgeranyltransferase beta subunit:type ii protein geranylgeranyltransferase beta subunit:egtase-ii-beta] [gtcfc:1.6.3:6.3.0] [keggfc:14.2] [sgdgc:1.6.1.1] [db:gtc-saccharomyces cerevisiae]

CONTIG5261	30478927_f1_3	3792	17895	426	142	YPR176C	155	7.7(10)-11	Saccharomyces cerevisiae	[ui:ypr176c] [pn:geranylgeranyltransferase type ii beta subunit:type ii proteins geranylgeranyltransferase beta subunit:type ii protein geranylgeranyltransferase beta subunit:ggatase-ii-beta:pggt:ypt1/sec4 proteins geranylgeranyltransferase-ii-beta]
CONTIG764	25976412_f1_1	3793	17896	672	224	YDR058C	441	1.1(10)-41	Saccharomyces cerevisiae	[ui:ydr058c] [pn:lipase 2:triacylglycerol lipase] [gn:igf2.ydg609] [gicfc:3.2.8.1] [ec:3.1.1.3] [keggfc:8.1] [sgdfc:1.6.2] [db:gic-saccharomyces cerevisiae]
CONTIG2680	20394002_f1_1	3794	17897	861	287	YJL068C	629	1.3(10)-61	Saccharomyces cerevisiae	[ui:yj068c] [pn:strong similarity to human esterase d:hypothetical 33.9 kd esterase in sep160-nmr18 intergenic region] [gn:j1102:hre299] [gicfc:3.2] [ec:3.1.1.1] [keggfc: 14.1] [sgdfc:1.6.2] [db:gic-saccharomyces cerevisiae]
CONTIG156	9979142_f1_1	3795	17898	621	207	YKR031C	203	7.7(10)-15	Saccharomyces cerevisiae	[ui:ykr031c] [pn:phospholipase d:meiosis-specific sporulation protein] [gn:spo14] [gicfc:3.2:12.15] [keggfc:14.2] [sgdfc:1.6.2:3.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG2461	23652262_c1_3	3796	17899	1089	363	YKR031C	973	5.0(10)-97	Saccharomyces cerevisiae	[ui:ykr031c] [pn:phospholipase d:meiosis-specific sporulation protein] [gn:spo14] [gicfc:3.2:12.15] [keggfc:14.2] [sgdfc:1.6.2:3.4.0] [db:gic-saccharomyces cerevisiae]

CONTIG4483	9806677_c1_14	3797	17900	603	201	YKR031C	488	3.5(10)-45	Saccharomyces cerevisiae	[ui:ykr031c] [pn:phospholipase d:meiosis-specific sporulation protein] [gn:spo14] [gicfc:3.2;12.15] [keggfc:14.2] [sgdfc:1.6.2;3.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG4483	11959836_03_18	3798	17901	838	286	YKR031C	218	6.0(10)-21	Saccharomyces cerevisiae	[ui:ykr031c] [pn:phospholipase d:meiosis-specific sporulation protein] [gn:spo14] [gicfc:3.2;12.15] [keggfc:14.2] [sgdfc:1.6.2;3.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG5808	9789126_f1_3	3799	17902	1593	531	YLR020C	368	7.0(10)-34	Saccharomyces cerevisiae	[ui:yhr020c] [pn:similarity to triacylglycerol lipase] [gicfc:3.2] [keggfc:14.2] [sgdfc:1.6.2] [db:gic-saccharomyces cerevisiae]
CONTIG3882	892182_c2_5	3800	17903	1239	413	YMR006C	707	7.2(10)-70	Saccharomyces cerevisiae	[ui:ymr006c] [pn:strong similarity to pib1p] [gicfc:3.2] [keggfc:14.2] [sgdfc:1.6.2] [db:gic-saccharomyces cerevisiae]
CONTIG620	26760173_02_5	3801	17904	186	62	YMR006C	117	3.8(10)-6	Saccharomyces cerevisiae	[ui:ymr006c] [pn:strong similarity to pib1p] [gicfc:3.2] [keggfc:14.2] [sgdfc:1.6.2] [db:gic-saccharomyces cerevisiae]
CONTIG5474	6665938_c1_10	3802	17905	1833	611	YMR008C	1218	5.0(10)-124	Saccharomyces cerevisiae	[ui:ymr008c] [pn:lysophospholipase:lysophospholipase precursor:phospholipase b] [gn:pbl1;ym8270] [gicfc:3.2;8.4;11.1] [keggfc:1.6.2;9.1.0] [sgdfc:8.4] [db:gic-saccharomyces cerevisiae]

CONTIG5527	22360301_f1_1	3803	17906	1914	638	YMR008C	1603	8.0(10)-165	Saccharomyces cerevisiae	[ui:ymr008c] [pn:lysophospholipase:lysophospholipase precursor:phospholipase b] [gn:plbl:ymr008c] [gicfc:3.2:8.4:11.1] [ec:3.1.1.5] [keggfc:8.4] [sgdfc:1.6.2.9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG620	33417768_c2_6	3804	17907	627	209	YMR008C	285	3.1(10)-24	Saccharomyces cerevisiae	[ui:ymr008c] [pn:lysophospholipase:lysophospholipase precursor:phospholipase b] [gn:plbl:ymr008c] [gicfc:3.2:8.4:11.1] [ec:3.1.1.5] [keggfc:8.4] [sgdfc:1.6.2.9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4295	20507697_c2_6	3805	17908	990	330	YNIL012W	484	3.1(10)-46	Saccharomyces cerevisiae	[ui:ynil012w] [pn:transcriptional regulator involved in sporulation,sporulation protein spo1] [gn:spo1:n2858] [gicfc:3.2:10.1:10.2:12.15:12.8] [keggfc:14.2] [sgdfc:1.6.2:3.4.0:3.8.0:4.8:29.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3890	25627002_f2_1	3806	17909	1587	529	YOL011W	1135	3.2(10)-115	Saccharomyces cerevisiae	[ui:yol011w] [pn:strong similarity to phospholipases] [gicfc:3.2] [keggfc:14.2] [sgdfc: 6.2] [db:gtc-saccharomyces cerevisiae]
CONTIG3994	24641561_c1_6	3807	17910	609	203	YOL011W	217	7.0(10)-17	Saccharomyces cerevisiae	[ui:yol011w] [pn:strong similarity to phospholipases] [gicfc:3.2] [keggfc:14.2] [sgdfc: 1.6.2] [db:gtc-saccharomyces cerevisiae]

CONTIG5072	3751_c2_4	3808	17911	2142	714	YOL011W	928	2.7(10)-93	Saccharomyces cerevisiae	[ui:yo 011w] [pn:strong similarity to phospholipases] [gtcfc:3.2] [keggfc:14.2] [sgdfc:1.6.2] [db:gic-saccharomyces cerevisiae]
CONTIG2195	20319377_f3_3	3809	17912	306	102	YGR175C	321	1.0(10)-28	Saccharomyces cerevisiae	[ui:ygr175c] [pn:squalene monoxygenase;squalene epoxidase;se] [gn:erg1] [gtcfc:3.4:8:1:8:2:9:13:12:16] [ec:1.14.99.7] [keggfc:3.4:9:11] [sgdfc:1.6.1:9:4.0] [db:gic-saccharomyces cerevisiae]
CONTIG2588	5875938_f2_1	3810	17913	255	85	YHR072W	286	3.0(10)-24	Saccharomyces cerevisiae	[ui:yhr072w] [pn:lanosterol synthase;oxidosqualene--lanosterol cyclase;2,3-epoxysqualene--lanosterol cyclase:2,3-epoxysqualene:osc] [gn:erg7] [gtcfc:3.4:8:1:8:2:12:16] [ec:5.4.99.7] [keggfc:3.4] [sgdfc:1.6.1:9:4.0] [db:gic-saccharomyces cerevisiae]
CONTIG515	21932809_c1_1	3811	17914	747	249	YHR072W	765	5.0(10)-76	Saccharomyces cerevisiae	[ui:yhr072w] [pn:lanosterol synthase;oxidosqualene--lanosterol cyclase:2,3-epoxysqualene--lanosterol cyclase:osc] [gn:erg7] [gtcfc:3.4:8:1:8:2:12:16] [ec:5.4.99.7] [keggfc:3.4] [sgdfc:1.6.1:9:4.0] [db:gic-saccharomyces cerevisiae]

CONTIG3232	4772512_f3_5	3812	17915	1218	406	YHR190W	1129	1.3(10)-114	Saccharomyces cerevisiae	[ui:yhr190w] [pn:farnesyldiphosphate synthetase:ss:fpp:farnesyltransferase:squalene synthetase:ss:fpss:farnesyltransferase] [gn:erg9][gicfc:3.4.8.1.8.2.9.13.12.16][ec:2.5.1.21][keggfc:3.4.9.11][sgdfc:1.6.1.9.4.0][db:gicsaccharomyces cerev]
CONTIG5151	23570892_3_7	3813	17916	1224	408	YJL167W	1366	1.1(10)-139	Saccharomyces cerevisiae	[ui:yj167w] [pn:farnesylpyrophosphate synthetase:farnesylpyrophosphate synthetase:ss:farnesyl diphosphate synthetase:dimethylallyltransferase / geranyltransferase] [gn:fpp1:fdsl:bot3:erg20:j0525][gicfc:3.4.8.1:
CONTIG2477	35369020_f2_1	3814	17917	942	314	YLR450W	961	8.6(10)-97	Saccharomyces cerevisiae	[ui:ylr450w] [pn:3-hydroxy-3-methylglutaryl-coenzyme a reductase 2:hmg-coa reductase 2] [gn:hmg2:19324][gicfc:3.4.8.1.8.2.12.16][ec:1.1.1.34][keggfc:3.4][sgdfc:1.6.1.9.4.0][db:gicsaccharomyces cerevisiae]
CONTIG4037	24220450_e3_5	3815	17918	1014	338	YLR450W	279	3.2(10)-23	Saccharomyces cerevisiae	[ui:ylr450w] [pn:3-hydroxy-3-methylglutaryl-coenzyme a reductase 2:hmg-coa reductase 2] [gn:hmg2:19324][gicfc:3.4.8.1.8.2.12.16][ec:1.1.1.34][keggfc:3.4][sgdfc:1.6.1.9.4.0][db:gicsaccharomyces cerevisiae]

CONTIG4037	10823550_q2_3	3816	17919	870	290	YLR450W	350	8.3(10)-31	Saccharomyces cerevisiae	[ui:ylr450w] [pn:3-hydroxy-3-methylglutaryl-coenzyme a reductase 2-hmg-coa reductase 2] [gn:hmg2;19324] [gicfc:3.4:8:1:8:2:12.16] [ec:1.1.1.34] [keggfc:3.4] [sgdfc:1.6.1:9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG1965	28242313_c3_5	3817	17920	402	134	YMR208W	164	1.6(10)-11	Saccharomyces cerevisiae	[ui:ymr208w] [pn:mevalonate kinase:mvk] [gn:rar1;erg12;ym8261] [gicfc:3.4:10.2] [ec:2.7.1.36] [keggfc:3.4] [sgdfc:1.6:4:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5199	22353426_f1_2	3818	17921	654	218	YMR208W	448	2.0(10)-42	Saccharomyces cerevisiae	[ui:ymr208w] [pn:mevalonate kinase:mvk] [gn:rar1;erg12;ym8261] [gicfc:3.4:10.2] [ec:2.7.1.36] [keggfc:3.4] [sgdfc:1.6:4:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG2617	11177088_c3_7	3819	17922	1230	410	YMR220W	694	1.7(10)-68	Saccharomyces cerevisiae	[ui:ymr220w] [pn:phosphomevalonate kinase] [gn:erg8;ym9939] [gicfc:3.4:8:1:8:2] [ec:2.7.4.2] [keggfc:3.4] [sgdfc:1.6:1:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5378	9882002_c2_18	3820	17923	765	255	YMR220W	517	9.8(10)-50	Saccharomyces cerevisiae	[ui:ymr220w] [pn:phosphomevalonate kinase] [gn:erg8;ym9939] [gicfc:3.4:8:1:8:2] [ec:2.7.4.2] [keggfc:3.4] [sgdfc:1.6:1:9.2.0] [db:gic-saccharomyces cerevisiae]

CONTIG5601	20890782_f2_8	3821	17924	1050	350	YNR043W	1039	2.3(10)-110	Saccharomyces cerevisiae	[ui:ymr043w] [pn:diphosphomevalonate decarboxylase;mevalonate pyrophosphate decarboxylase] [gn:erg19;mpd:n3427] [gicfc:3.4:8.1.8.2] [ec:4.1.1.33] [keggfc:3.4] [sgdfc:1.6.1] [db:gic-saccharomyces cerevisiae]
CONTIG1153	25579387_c3_1	3822	17925	186	62	YPL117C	206	8.8(10)-17	Saccharomyces cerevisiae	[ui:ypl117c][pn:isopentenyl-diphosphate delta-isomerase;ipp isomerase][gn:id11:b012:iph10c] [gicfc:3.4:8.1.8.2.9.13] [ec:5.3.3.2] [keggfc:3.4.9.11] [sgdfc:1.6.1.9.2.0] [db:gic-saccharomyces cerevisiae]
b2x15112.y	24472625_f2_1	3823	17926	543	181	YPL117C	491	5.5(10)-47	Saccharomyces cerevisiae	[ui:ypl117c][pn:isopentenyl-diphosphate delta-isomerase;ipp isomerase][gn:id11:b012:iph10c] [gicfc:3.4:8.1.8.2.9.13] [ec:5.3.3.2] [keggfc:3.4.9.11] [sgdfc:1.6.1.9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG3968	35429566_f2_2	3824	17927	465	155	YAR044W	427	2.7(10)-39	Saccharomyces cerevisiae	[ui:yar044w][pn:similarity to human oxysterol binding protein;osbp:osh1 protein] [gn:osh1:swh1] [gicfc:3.4:8.1.8.2.10.2] [keggfc:1.4.2] [sgdfc:1.6.1.4.8.3] [db:gic-saccharomyces cerevisiae]

CONTIG1728	16509562_f1_1	3825	17928	693	231	YBR029C	635	3.1(10)-62	Saccharomyces cerevisiae	[ui:ybr029c] [pn:cdp-diacylglycerol synthase:phosphatidate cytidylyltransferase:cdp-diglyceride synthetase:cdp-diacylglycerol pyrophosphorylase:cdp-diacylglycerol synthase] [gn:cds1.cdg1.ybr031.3] [gicfc:3.4:8.1:8.2:12.16] [ec:2.7.7.41]
CONTIG2244	10558385_c1_7	3826	17929	738	246	YBR029C	517	9.8(10)-50	Saccharomyces cerevisiae	[ui:ybr029c] [pn:cdp-diacylglycerol synthase:phosphatidate cytidylyltransferase:cdp-diglyceride synthetase:cdp-diacylglycerol pyrophosphorylase:cdp-diacylglycerol synthase] [gn:cds1.cdg1.ybr031.3] [gicfc:3.4:8.1:8.2:12.16] [ec:2.7.7.41]
CONTIG3755	35413942_f2_2	3827	17930	270	90	YBR159W	225	1.1(10)-18	Saccharomyces cerevisiae	[ui:ybr159w] [pn:similarity to human 17-beta-hydroxysteroid dehydrogenase:hypothetical 38.7 kd protein in rp5-cdc28 intergenic region] [gn:ybr1209] [gicfc:3.4:8.1:8.2] [keggfc:14.2] [sgdfc:1.6.1] [db:gic-saccharomyces cerevisiae]

CONTIG1747	20117314_c1_2	3828	17931	675	225	YBR159W	633	5.0(10)-62	Saccharomyces cerevisiae	[ui:ybr159w] [pn:similarity to human 17-beta-hydroxysteroid dehydrogenase:hypothetical 38.7 kd protein in rpb2-cdc28 intergenic region] [gn:ybri209] [gicfc:3.4:8.1:8.2] [keggfc:14.2] [sgdfc:1.6.] [db:gic-saccharomyces cerevisiae]
CONTIG5601	22523251_c1_20	3829	17932	750	250	YDL142C	300	9.6(10)-27	Saccharomyces cerevisiae	[ui:ydl142c] [pn:phosphatidylglycerophosphate synthase] [gn:pgs] [gicfc:3.4:8.1:8.2] [keggfc:14.2] [sgdfc:1.6.] [db:gic-saccharomyces cerevisiae]
CONTIG4549	12140636_c1_7	3830	17933	942	314	YDL052C	654	3.0(10)-64	Saccharomyces cerevisiae	[ui:ydl052c] [pn:fatty acyltransferase;possible 1-acyl-sn-glycerol-3-phosphate acyltransferase] [gn:sc1] [gicfc:3.4:8.1:8.2] [ec:2.3.1.51] [keggfc:8.1] [sgdfc:1.6.] [db:gic-saccharomyces cerevisiae]
CONTIG3968	35417136_f2_1	3831	17934	1254	418	YDL019C	927	3.5(10)-93	Saccharomyces cerevisiae	[ui:ydl019c] [pn:similarity to osh1p] [gicfc:3.4:8.1:8.2] [keggfc:14.2] [sgdfc:1.6.] [db:gic-saccharomyces cerevisiae]
CONTIG4505	24344501_f2_3	3832	17935	2349	783	YDL019C	676	1.5(10)-75	Saccharomyces cerevisiae	[ui:ydl019c] [pn:similarity to osh1p] [gicfc:3.4:8.1:8.2] [keggfc:14.2] [sgdfc:1.6.] [db:gic-saccharomyces cerevisiae]

CONTIG5157	26798437_03_10	3833	17936	369	123	YDR062W	252	7.7(10)-21	Saccharomyces cerevisiae	[ui:yd062w] [pn:serine c-palmitoyltransferase subunit:serine palmitoyltransferase 2:long chain base biosynthesis protein 2:spt 2] [gn:icb2:scs1;yd9609] [gicfc:3.4.8.1:8.2.8.5] [ec:2.3.1.50] [keggfc:8.5] [sgdfc:1.6.1] [db:gic-saccharo]
CONTIG5157	35173137_c2_6	3834	17937	936	312	YDR062W	1025	1.3(10)-103	Saccharomyces cerevisiae	[ui:yd062w] [pn:serine c-palmitoyltransferase subunit:serine palmitoyltransferase 2:long chain base biosynthesis protein 2:spt 2] [gn:icb2:scs1;yd9609] [gicfc:3.4.8.1:8.2.8.5] [ec:2.3.1.50] [keggfc:8.5] [sgdfc:1.6.1] [db:gic-saccharo]
CONTIG2898	15626_f3_2	3835	17938	336	112	YDR062W	187	8.4(10)-14	Saccharomyces cerevisiae	[ui:yd062w] [pn:serine c-palmitoyltransferase subunit:serine palmitoyltransferase 2:long chain base biosynthesis protein 2:spt 2] [gn:icb2:scs1;yd9609] [gicfc:3.4.8.1:8.2.8.5] [ec:2.3.1.50] [keggfc:8.5] [sgdfc:1.6.1] [db:gic-saccharo]

CONTIG887	19710752_c2_4	3836	17939	858	286	YDR208W	470	3.8(10)-44	Saccharomyces cerevisiae	[ui:ydr208w] [pn:similarity to human pip 5'-kinase;probable phosphatidylinositol-4-phosphate 5'-kinase mss4;1 -phosphatidylinositol-4-phosphate kinase;pi5k;pidins:4p-5'-kinase;diphosphoinositide kinase] [gn:mss4;yd8142a] [gtcfc:3.4:8.1.8]
b9x12u09.x	50627_c1_1	3837	17940	582	194	YDR208W	446	1.7(10)-41	Saccharomyces cerevisiae	[ui:ydr208w] [pn:similarity to human pip 5'-kinase;probable phosphatidylinositol-4-phosphate 5'-kinase mss4;1 -phosphatidylinositol-4-phosphate kinase;pi5k;pidins:4p-5'-kinase;diphosphoinositide kinase] [gn:mss4;yd8142a] [gtcfc:3.4:8.1.8]
CONTIG546	4038905_c2_4	3838	17941	1011	337	YGL126W	115	6.0(10)-15	Saccharomyces cerevisiae	[ui:ygl126w] [pn:inositol phospholipid synthesis protein;scs3 protein] [gr:ses3;g2868] [gtcfc:3.4:8.1:8.2] [keggfc:14.2] [sgdfc:1.6.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1217	11117665_f1_1	3839	17942	726	242	YGL055W	283	2.2(10)-24	Saccharomyces cerevisiae	[ui:ygl055w] [pn:stearoyl-coa desaturase I:stearoyl-coa desaturase I:fatty acid desaturase 1] [gn:ole1] [gtcfc:3.4:8.1:8.2:12.16] [ec:1.14.99.5] [keggfc:14.1] [sgdfc:1.6.1:9.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5698	4800011_f2_11	3840	17943	927	309	YGL055W	866	1.0(10)-86	Saccharomyces cerevisiae	[ui:yg[055w] [pn:stearoyl-coa desaturase:acyl-coa desaturase 1:fatty acid desaturase 1][gn:ole1][gicfc:3.4.8:1.8.2:12.16][ec:1.14.99.5][keggfc:[4.1][sgdfc:1.6.1:9.4.0][db:gic-saccharomyces cerevisiae]
CONTIG5698	6642807_f1_1	3841	17944	381	127	YGL055W	304	1.1(10)-26	Saccharomyces cerevisiae	[ui:yg[055w] [pn:stearoyl-coa desaturase:acyl-coa desaturase 1:fatty acid desaturase 1][gn:ole1][gicfc:3.4.8:1.8.2:12.16][ec:1.14.99.5][keggfc:[4.1][sgdfc:1.6.1:9.4.0][db:gic-saccharomyces cerevisiae]
CONTIG506	204700_f1_2	3842	17945	795	265	YGL012W	802	6.2(10)-80	Saccharomyces cerevisiae	[ui:yg[012w] [pn:sterol c-24-reductase:c-24:28 sterol reductase][gn:erg4_yg022][gicfc:3.4.8:1.8:2][ec:1.1...][keggfc:14.1][sgdfc:1.6.1][db:gic-saccharomyces cerevisiae]
CONTIG4272	31336678_f2_2	3843	17946	903	301	YGL001C	1083	1.0(10)-109	Saccharomyces cerevisiae	[ui:yg[001c] [pn:putative 3-beta-hydroxysteroid dehydrogenase:putative 3-beta hydroxy-5-sene steroid dehydrogenase / steroid delta-isomerase:3beta-hsd:progesterone reductase][gicfc:3.4:3.6:3.7:8.1:8:2][keggfc:3.6:3.7][sgdfc:1.6.1][

CONTIG5167	22063392_c3_16	3844	17947	648	216	YGR007W	391	2.2(10)-36	Saccharomyces cerevisiae	[ui:ygr007w] [pn:choline phosphate cytidylyltransferase:protein] [gn:muq] [gicfc:3.4.8.1.8.2] [keggfc:14.2] [sgdfc:1.6.] [db:gic-saccharomyces cerevisiae]
CONTIG3381	12506943_c2_2	3845	17948	960	320	YGR037C	122	2.6(10)-7	Saccharomyces cerevisiae	[ui:ygr037c] [pn:acyl-coenzyme-a-binding protein:diazepam binding inhibitor:acyl-coa-binding protein:acb] [gn:acb] :acb [gicfc:3.4.8.1.8.2.1.2.2] [keggfc:14.2] [sgdfc:1.6.1:1.6.5] [db:gic-saccharomyces cerevisiae]
CONTIG4951	6814008_f1_1	3846	17949	234	78	YGR037C	270	1.5(10)-23	Saccharomyces cerevisiae	[ui:ygr037c] [pn:acyl-coenzyme-a-binding protein:diazepam binding inhibitor:acyl-coa-binding protein:acb] [gn:acb] :acb [gicfc:3.4.8.1.8.2.1.2.2] [keggfc:14.2] [sgdfc:1.6.1:1.6.5] [db:gic-saccharomyces cerevisiae]
CONTIG1332	953392_c3_3	3847	17950	921	307	YGR060W	854	1.8(10)-85	Saccharomyces cerevisiae	[ui:ygr060w] [pn:c-4 sterol methyl oxidase:c-4 methyl sterol oxidase] [gn:erg25;fet6] [gicfc:3.4.8.1.8.2.1.2.16] [ec:1.1.9.4.0] [keggfc:14.1] [sgdfc:1.6.1:9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG4151	6853437_f2_2	3848	17951	969	323	YGR060W	910	2.2(10)-91	Saccharomyces cerevisiae	[ui:ygr060w] [pn:c-4 sterol methyl oxidase:c-4 methyl sterol oxidase] [gn:erg25;fet6] [gicfc:3.4.8.1.8.2.1.2.16] [ec:1.1.9.4.0] [keggfc:14.1] [sgdfc:1.6.1:9.4.0] [db:gic-saccharomyces cerevisiae]

CONTIG3701	4375802_c2_5	3849	17952	318	106	YGR060W	246	5.0(10)-21	Saccharomyces cerevisiae	[ui:gr060w] [pn:c-4 sterol methyl oxidase;c-4 methyl sterol oxidase] [gn:erg25;fei6] [gicfc:3.4.8.1:8.2:12.16] [ec:1..-..] [keggfc:14.1] [sgdfc:1.6.1:9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG1185	23495718_c2_2	3850	17953	660	220	YGR157W	123	3.0(10)-13	Saccharomyces cerevisiae	[ui:gr157w] [pn:phosphatidyl/ethanolamine n-methyltransferase] [gn:pem1;cho2:g6673] [gicfc:3.4.5.3:8.1:8.2:12.16] [ec:2.1.1.17] [keggfc:5.3] [sgdfc:1.6.1:9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG3467	171877_c3_5	3851	17954	672	224	YGR157W	199	8.8(10)-15	Saccharomyces cerevisiae	[ui:gr157w] [pn:phosphatidyl/ethanolamine n-methyltransferase] [gn:pem1;cho2:g6673] [gicfc:3.4.5.3:8.1:8.2:12.16] [ec:2.1.1.17] [keggfc:5.3] [sgdfc:1.6.1:9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG5637	34492200_f3_7	3852	17955	1116	372	YGR170W	596	4.0(10)-57	Saccharomyces cerevisiae	[ui:gr170w] [pn:phosphatidylserine decarboxylase 2:phosphatidylserine decarboxylase proenzyme 2 precursor] [gn:psd2] [gicfc:3.4.5.3:8.1:8.2:12.16] [ec:4.1.1.65] [keggfc:5.3:8.1] [sgdfc:1.6.1:9.4.0] [db:gic-saccharomyces cerevisiae]

CONTIG5637	36064812_f1_1	3853	17956	720	240	YGR170W	531	4.0(10)-50	Saccharomyces cerevisiae	[ui:ygr170w] [pn:phosphatidylserine decarboxylase 2:phosphatidylserine precursor] [gn:psd2] [gicfc:3.4;5.3;8.1;8.2;12.16] [ec:4.1.1.65] [keggfc:5.3;8.1] [sgdfc:1.6.1:9.4.0] [db:gic-saccharomyces cerevisiae]
b2x18670.x	2401038_f2_1	3854	17957	576	192	YGR170W	290	2.5(10)-24	Saccharomyces cerevisiae	[ui:ygr170w] [pn:phosphatidylserine decarboxylase 2:phosphatidylserine precursor] [gn:psd2] [gicfc:3.4;5.3;8.1;8.2;12.16] [ec:4.1.1.65] [keggfc:5.3;8.1] [sgdfc:1.6.1:9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG5670	33337762_f1_5	3855	17958	1377	459	YGR202C	957	2.2(10)-96	Saccharomyces cerevisiae	[ui:ygr202c] [pn:cholinephosphate cytidylyltransferase:phosphorylcholine transferase:ct] [gn:pct1;cc1:cctg7729] [gicfc:3.4;6.3;8.1;8.2;12.16] [ec:2.7.7.15] [keggfc:6.3;8.1] [sgdfc:1.6.1:9.4.0] [db:gic-saccharomyces cerevisiae]

CONTIG3973	156567_f2_3	3856	17959	1455	485	YGR216C	287	4.9(10)-32	Saccharomyces cerevisiae	[ui:ygr216c] [pn:required for n-acetylglucosaminyl phosphatidylinositol synthesis:hypothetical 70.4 kd protein in nab1-a-crml intergenic region] [gn:gpi1] [gtcfc:3.4:8.1:8.2] [keggfc:14.2] [sgdfc:1.6.1] [db:gtc-saccharomyces cerevisiae]
CONTIG30	17033563_c1_4	3857	17960	534	178	YHR001W	486	1.8(10)-46	Saccharomyces cerevisiae	[ui:yhr001w] [pn:similarity to kes1p:hypothetical 49.8 kd protein in rpl14b-gpa1 intergenic region] [gtcfc:3.4:8.1:8.2:8.5] [keggfc:14.2] [sgdfc:1.6.1:1.6.6] [db:gtc-saccharomyces cerevisiae]
CONTIG56	1723200_f2_1	3858	17961	642	214	YHR001W	535	1.2(10)-51	Saccharomyces cerevisiae	[ui:yhr001w] [pn:similarity to kes1p:hypothetical 49.8 kd protein in rpl14b-gpa1 intergenic region] [gtcfc:3.4:8.1:8.2:8.5] [keggfc:14.2] [sgdfc:1.6.1:1.6.6] [db:gtc-saccharomyces cerevisiae]
CONTIG5249	14665887_f2_1	3859	17962	2538	846	YHR073W	982	4.0(10)-136	Saccharomyces cerevisiae	[ui:yhr073w] [pn:similarity to osh1p, ydl019c and mammalian oxysterol-binding protein:hypothetical 113.8 kd protein in erg7-rmd2 intergenic region] [gtcfc:3.4:8.1:8.2] [keggfc:14.2] [sgdfc:1.6.1] [db:gtc-saccharomyces cerevisiae]

CONTIG5694	14250878_c2_21	3860	17963	699	233	YIR035C	570	2.3(10)-55	Saccharomyces cerevisiae	[ui:yir035c] [pn:similarity to human corticosteroid 11-beta-dehydrogenase:hypothetical oxidoreductase in lys1-hyr1 intergenic region] [gicfc:3.4.8.1:8.2] [ec:1.1.1.-] [keggfc:14.1] [sgdfc:1.6.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5694	51342_c1_18	3861	17964	798	266	YIR035C	540	3.6(10)-52	Saccharomyces cerevisiae	[ui:yir035c] [pn:similarity to human corticosteroid 11-beta-dehydrogenase:hypothetical oxidoreductase in lys1-hyr1 intergenic region] [gicfc:3.4.8.1:8.2] [ec:1.1.1.-] [keggfc:14.1] [sgdfc:1.6.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5615	23600262_f1_1	3862	17965	1218	406	YJL196C	177	2.5(10)-11	Saccharomyces cerevisiae	[ui:yjl196c] [pn:fatty acid elongation protein:hypothetical 36.2 kd protein in ubp12-cdc6 intergenic region] [gncel1:j0343] [gicfc:3.4.8.1:8.2] [keggfc:14.2] [sgdfc:1.6.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4808	2767125_c1_8	3863	17966	318	106	YIR073C	222	1.8(10)-18	Saccharomyces cerevisiae	[ui:yir073c] [pn:methylene-fatty-acyl-phospholipid synthase:unsaturated phospholipid methyltransferase] [gn:pem2:opj3;jl824] [gicfc:3.4.8.1:8.2;12.16] [ec:2.1.1.16] [keggfc:14.1] [sgdfc:1.6.1.9.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1917	16972215_c1_5	3864	17967	1014	338	YKL203C	1241	4.4(10)-125	Saccharomyces cerevisiae	[ui:ykl203c] [pn:phosphatidylinositol 3-kinase:phosphatidylinositol 3-kinase:tor2:pi3-kinase:pidins-3-kinase:pi3k] [gn:tor2:dr2] [gicfc:3.4.8.1:8.2:12.8] [ec:2.7.1.137] [keggfc:8.1] [sgdfc:1.6.1.3.1.0:3.8.0] [db:gic-saccharomyces cer]
CONTIG58	35167202_c1_1	3865	17968	852	284	YKL203C	778	9.0(10)-76	Saccharomyces cerevisiae	[ui:ykl203c] [pn:phosphatidylinositol 3-kinase:phosphatidylinositol 3-kinase:tor2:pi3-kinase:pidins-3-kinase:pi3k] [gn:tor2:dr2] [gicfc:3.4.8.1:8.2:12.8] [ec:2.7.1.137] [keggfc:8.1] [sgdfc:1.6.1.3.1.0:3.8.0] [db:gic-saccharomyces cer]
CONTIG869	16494055_c3_2	3866	17969	552	184	YKL203C	311	4.0(10)-26	Saccharomyces cerevisiae	[ui:ykl203c] [pn:phosphatidylinositol 3-kinase:phosphatidylinositol 3-kinase:tor2:pi3-kinase:pidins-3-kinase:pi3k] [gn:tor2:dr2] [gicfc:3.4.8.1:8.2:12.8] [ec:2.7.1.137] [keggfc:8.1] [sgdfc:1.6.1.3.1.0:3.8.0] [db:gic-saccharomyces cer]

b9x10w65,y	31413532_f1_1	3867	17970	606	202	YKL203C	775	1.8(10)-75	Saccharomyces cerevisiae	[ui:ykl203c] [pn:phosphatidylinositol 3-kinase;phosphatidylinositol 3-kinase:pi3-kinase;pidins-3-tor2;pi3-kinase;pidins-3-kinase:pi3k1][gn:tor2;dr2][gctfc:3.4.8.1.8.2;12.8][ec:2.7.1.137][keggfc:8.1][sgdfc:1.6.1.3.1.0.3.8.0][db:gtc-saccharomyces cer]
CONTIG2802	21906312_f1_1	3868	17971	1083	361	YKR003W	956	3.0(10)-96	Saccharomyces cerevisiae	[ui:ykr003w][pn:similarity to kes1p, hes1p and osh1p;hypothetical 51.6 kd protein in pap1-mrp13 intergenic region][gn:yk102][gctfc:3.4.8.1.8.2][keggfc:14.2][sgdfc:1.6.1][db:gtc-saccharomyces cerevisiae]
CONTIG2802	14665632_f3_3	3869	17972	327	109	YKR003W	244	2.8(10)-20	Saccharomyces cerevisiae	[ui:ykr003w][pn:similarity to kes1p, hes1p and osh1p;hypothetical 51.6 kd protein in pap1-mrp13 intergenic region][gn:yk102][gctfc:3.4.8.1.8.2][keggfc:14.2][sgdfc:1.6.1][db:gtc-saccharomyces cerevisiae]
CONTIG3959	85753_f3_5	3870	17973	1122	374	YLR056W	879	1.2(10)-93	Saccharomyces cerevisiae	[ui:ylr056w][pn:c-5 sterol desaturase][gn:erg3;syf1:2150][gctfc:3.4.8.1.8.2][ec:1.1.1.1][keggfc:1.4.1][sgdfc:1.6.1.9.4.0][db:gic-saccharomyces cerevisiae]
CONTIG5660	14953268_f2_9	3871	17974	1926	642	YLR133W	648	6.2(10)-72	Saccharomyces cerevisiae	[ui:ylr133w][pn:choline kinase][gn:ck11;ck11:1310;19606][gctfc:3.4.8.1.8.2][ec:2.7.1.32][keggfc:8.1][sgdfc:1.6.1.9.2.0][db:gic-saccharomyces cerevisiae]

CONTIG5233	506262_c1_8	3872	17975	969	323	YML131W	460	1.1(10)-43	Saccharomyces cerevisiae	[ui:ym1131w] [pn:similarity to human leukotriene b4 1.2-hydroxydehydrogenase] [gicfc:3.4.8.1:8.2] [keggfc:14.2] [sgdfc:1.6.1] [db:gic-saccharomyces cerevisiae]
CONTIG3880	23609675_f1_1	3873	17976	1164	388	YML008C	1288	1.8(10)-131	Saccharomyces cerevisiae	[ui:ym1008c] [pn:sadenosyl-methionine delta-24-sterol-c-methyltransferase:delta-24-sterol c-methyltransferase] [gn:erg6;scd6;ise1;isi1;ym9571] [gicfc:3.4.8.1:8.2] [ec:2.1.1.41] [keggfc:14.1] [sgdfc:1.6.1] [db:gic-saccharomyces cerev]
CONTIG1458	1055313_f1_1	3874	17977	840	280	YMR296C	462	6.5(10)-44	Saccharomyces cerevisiae	[ui:ymr296c] [pn:serine c-palmitoyltransferase subunit:serine palmitoyltransferase 1:long chain base biosynthesis protein 1;spt1] [gn:icb1] [gicfc:3.4.8.1:8.2:8.5] [ec:2.3.1.50] [keggfc:8.5] [sgdfc:1.6.1] [db:gic-saccharomyces cerevi]
CONTIG3044	24647501_f2_3	3875	17978	534	178	YNL280C	270	3.1(10)-23	Saccharomyces cerevisiae	[ui:ynl280c] [pn:c-14 sterol reductase] [gn:erg24;nd593] [gicfc:3.4.8.1:8.2] [ec:1.1--] [keggfc:14.1] [sgdfc:1.6.1] [db:gic-saccharomyces cerevisiae]
CONTIG1381	242010_f2_3	3876	17979	726	242	YNL111C	191	3.3(10)-15	Saccharomyces cerevisiae	[ui:ynl111c] [pn:cytochrome b5] [gn:cytb5;n1949] [gicfc:3.4.8.1:8.2] [keggfc:14.2] [sgdfc:1.6.1] [db:gic-saccharomyces cerevisiae]

CONTIG3299	12995686_f3_2	3877	17980	1290	430	YNL045W	1010	5.5(10)-102	Saccharomyces cerevisiae	[ui:ynl045w] [pn:strong similarity to human leukotriene-a4 hydrolase;probable leukotriene a-4 hydrolase;lt:a-4 hydrolase;leukotriene a:4 hydrolase] [gn:n2535] [gtcfc:3.4.8.1:8.2] [ec:3.3.2.6] [keggfc:8.6] [sgdgc: 1.6.1] [db:gic-saccharo
CONTIG3906	13953535_f2_5	3878	17981	357	119	YNL045W	135	4.2(10)-8	Saccharomyces cerevisiae	[ui:ynl045w] [pn:strong similarity to human leukotriene-a4 hydrolase;probable leukotriene a-4 hydrolase;lt:a-4 hydrolase;leukotriene a:4 hydrolase] [gn:n2535] [gtcfc:3.4.8.1:8.2] [ec:3.3.2.6] [keggfc:8.6] [sgdgc: 1.6.1] [db:gic-saccharo
CONTIG4024	26432750_c3_6	3879	17982	1260	420	YNR019W	677	3.5(10)-92	Saccharomyces cerevisiae	[ui:ynr019w] [pn:acyl-coa sterol acyltransferase;sterol o-acyltransferase 2;sterol-ester synthase 2] [gn:are2:sal1:n3206] [gtcfc:3.4.3.5:8.1:8.2:12.15] [ec:2.3.1.26] [keggfc:3.5] [sgdgc: 1.6.1:3.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG5797	10582762_c3_30	3880	17983	1335	445	YPL145C	191	3.7(10)-121	Saccharomyces cerevisiae	[ui:ypl145c] [pn:involved in ergosterol biosynthesis;kes1 protein] [gr:kes1:lp3cp2614] [gtcfc:3.4.8.1:8.2:12.10] [keggfc: 14.2] [sgdgc: 1.6.1:8.3.0:9.2.0] [db:gic-saccharomyces cerevisiae]

CONTIG5810	4407203_c3_36	3881	17984	798	266	YPL076W	251	1.5(10)-21	Saccharomyces cerevisiae	[ui:yp1076w] [pn:n-acetylglucosaminyl-phosphatidylinositol biosynthetic protein:n-acetylglucosaminyl-phosphatidylinositol biosynthetic protein gp12] [gn:gpi2;gc14;[p19w][gtfc:3.4:8.1:8.2] [keggc:14.2][sgfc:1.6.1] [db:gic-saccharo
CONTIG2518	20586442_f2_2	3882	17985	498	166	YPL069C	223	1.3(10)-18	Saccharomyces cerevisiae	[ui:yp1069c] [pn:geranylgeranyl diphosphate synthase] [gn:bts1][gtfc:3.4:8.1:8.2] [keggc:14.2][sgfc:1.6.1] [db:gic-saccharomyces cerevisiae]
CONTIG4222	20578786_c2_13	3883	17986	486	162	YPL069C	148	5.0(10)-10	Saccharomyces cerevisiae	[ui:yp1069c] [pn:geranylgeranyl diphosphate synthase] [gn:bts1][gtfc:3.4:8.1:8.2] [keggc:14.2][sgfc:1.6.1] [db:gic-saccharomyces cerevisiae]
CONTIG3382	14097510_B3_4	3884	17987	747	249	YPR113W	550	3.1(10)-53	Saccharomyces cerevisiae	[ui:yp113w] [pn:cdp diacylglycerol--inositol 3-phosphatidyltransferase;cdp-diacylglycerol--inositol 3-phosphatidyltransferase;phosphatidylinositol synthase] [gn:pis1;pis8283][gtfc:3.4:8.1:8.2:12.16][ec:2.7.8.11] [keggc:8.1] [s
CONTIG4607	26204657_f1_1	3885	17988	456	152	YBR034C	601	1.2(10)-58	Saccharomyces cerevisiae	[ui:ybr034c] [pn:hnmp methyltransferase;hnmp arginine n-methyltransferase;odp1 protein] [gn:hmt1:odp1:ymr0220][gtfc:3.7.5.11:5.14.9.12:10.1:10.2:10.7] [ec:2.1.1.-][keggc:3.7.5.11:5.14.9.13][sgfc:6.3.0:9.5.0] [db:gic-sacch

CONTIG4607	26441635_11_2	3886	17989	591	197	YBR034C	506	1.3(10)-48	Saccharomyces cerevisiae	[ui:ybr034c] [pn:hnrrp methyltransferase;hnrrp arginine n-methyltransferase;odpl protein] [gn:hm1:odpl1:rm1:ybr0320] [gicfc:3.7:5.11.5.14:9.12:10.1:10.2: 10.7] [ec:2.1.1.-] [keggfc:3.7.5.11.5.14:9.13] [sgdfc:6.3.0:9.5.0] [db:gic-sacch]
CONTIG5565	23848387_f2_6	3887	17990	999	333	YPL266W	1320	7.9(10)-135	Saccharomyces cerevisiae	[ui:yp1266w] [pn:rna:adenine-n6,n6-dimethyltransferase;dimethyladenosine transferase;s-adenosyl:trna dimethyltransferase;18s rRNA dimethylase] [gn:dim1] [gicfc:3.7.5.11.5.14:9.12:10.1:10.2: 10.3] [ec:2.1.1]
CONTIG2392	21989575_c1_2	3888	17991	948	316	YAR015W	931	1.3(10)-93	Saccharomyces cerevisiae	[ui:yar015w] [pn:phosphoribosylamidoimidazole-succinocarboxamide synthase;saicar synthetase] [gn:ade1] [gicfc:4.1] [ec:6.3.2.6] [keggfc:4.1] [sgdfc:1.3.1] [db:gic-saccharomyces cerevisiae]
CONTIG5717	196076_c2_15	3889	17992	393	131	YDL150W	147	1.1(10)-9	Saccharomyces cerevisiae	[ui:ydl150w] [pn: dna-directed rna polymerase iii, 47 kd subunit:dna-directed rna polymerase iii 47 kd polypeptide:c53:rna polymerase c subunit 4] [gn:rpc4:rp053:d1557] [gicfc:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdf

CONTIG2231	2507812_f2_1	3890	17993	771	257	YDL140C	904	1.5(10)-89	Saccharomyces cerevisiae	[ui:yd1140c] [pn: dna-directed rna polymerase ii, 215 kd subunit: dna-directed rna polymerase ii largest subunit:b220] [gn: rpb1:rpo21:rpb220:sua8:d2150] [gicfc:4.1:4.2:10.1:10.2] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.8.1:9.5.0] [db:gic]
CONTIG2835	11761285_c3_10	3891	17994	1116	372	YDL140C	1462	7.0(10)-150	Saccharomyces cerevisiae	[ui:yd1140c] [pn: dna-directed rna polymerase ii, 215 kd subunit: dna-directed rna polymerase ii largest subunit:b220] [gn: rpb1:rpo21:rpb220:sua8:d2150] [gicfc:4.1:4.2:10.1:10.2] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.8.1:9.5.0] [db:gic]
CONTIG2835	22662842_c3_9	3892	17995	735	245	YDL140C	1099	1.5(10)-110	Saccharomyces cerevisiae	[ui:yd1140c] [pn: dna-directed rna polymerase ii, 215 kd subunit: dna-directed rna polymerase ii largest subunit:b220] [gn: rpb1:rpo21:rpb220:sua8:d2150] [gicfc:4.1:4.2:10.1:10.2] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.8.1:9.5.0] [db:gic]
CONTIG5417	31683333_f3_6	3893	17996	1341	447	YDL140C	669	1.8(10)-64	Saccharomyces cerevisiae	[ui:yd1140c] [pn: dna-directed rna polymerase ii, 215 kd subunit: dna-directed rna polymerase ii largest subunit:b220] [gn: rpb1:rpo21:rpb220:sua8:d2150] [gicfc:4.1:4.2:10.1:10.2] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.8.1:9.5.0] [db:gic]

CONTIG810	10833318_f1_1	3894	17997	732	244	YDL140C	769	4.0(10)-75	Saccharomyces cerevisiae	[ui:yd1140cl] [pn: dna-directed dna polymerase ii, 215 kd subunit:dna-directed dna polymerase ii largest subunit:b220] [gn:rbp1:rpo21:rpb220:sua8:d2150] [gtcfc:4.1:4.2:10.1:10.2] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.8.1:9.5.0] [db:gtc]
CONTIG4028	2347026_f1_1	3895	17998	2163	721	YDL102W	2301	8.8(10)-239	Saccharomyces cerevisiae	[ui:yd1102w] [pn: dna-directed dna polymerase delta, catalytic 125 kd subunit:dna polymerase delta large chain:dna polymerase iii] [gn:pol3.cdc2:tex1:d2366] [gtcfc:4.1:4.2:10.1:10.10:10.2:10.8: 12.8] [ec:2.7.7.7] [keggfc:4.1:4.2:13.3] [
CONTIG5053	33787811_f2_4	3896	17999	480	160	YDR156W	90	0.003	Saccharomyces cerevisiae	[ui:ydrl56w] [pn: dna-directed dna polymerase i, a14 subunit:dna-directed dna polymerase i 14 kd polypeptide14] [gn:tpa14:yd8558] [gtcfc:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.1.0:9.5.0] [db:gtc-saccharomyces]
CONTIG3853	1214525_c3_7	3897	18000	675	225	YDR226W	826	1.8(10)-82	Saccharomyces cerevisiae	[ui:ydr226w] [pn: adenylylate kinase, cytosolic:adenylate kinase transphosphorylase] [gn:adk1:aky1:aky2:yd9934] [gtcfc:4.1:12.13] [ec:2.7.4.3] [keggfc:4.1.1] [sgdfc:1.3.8:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2602	24792827_c1_4	3898	18001	819	273	YDR408C	483	3.8(10)-46	Saccharomyces cerevisiae	[ui:ydr408c] [pn:phosphoribosylglycinamide formyltransferase;gar:gar transformylase;5'-phosphoribosylglycinamide transformylase][gn:ades8:d9509][gicfc:4:1:9:6][ec:2.1.2.2][keggfc:4:1:9:8][sgdgc:1:3.1:9:2.0][db:gtc-saccharomyces]
CONTIG2638	33204635_c2_5	3899	18002	411	137	YDR454C	495	2.1(10)-47	Saccharomyces cerevisiae	[ui:ydr454c] [pn:guanylylate kinase:gmp kinase][gn:gukl1:d9461][gicfc:4:1:12:13][ec:2.7.4.8][keggfc:4:1][sgdgc:1:3:8][db:gtc-saccharomyces cerevisiae]
CONTIG1452	16302268_f1_1	3900	18003	948	316	YDR530C	266	4.9(10)-31	Saccharomyces cerevisiae	[ui:ydr530c] [pn:atp adenylyltransferase ii;5'''',5'''-p-1,p-4-tetraphosphate phosphotyrosine ii:atp ii:ap-4-a phosphotyrosine ii:atp adenylyltransferase:ap:a phosphorylase ii][gn:apa2:d9719][gicfc:4:1][ec:2.7.7.53][keggfc:4:1][sgdgc:1:3:4][d]
CONTIG5136	78130_c2_7	3901	18004	2661	887	YER070W	3253	0	Saccharomyces cerevisiae	[ui:yer070w] [pn:ribonucleoside-diphosphate reductase, large subunit:ribonucleoside-diphosphate reductase large chain 1:ribonucleotide reductase][gn:mr1][gicfc:4:1:4:2:10:8:12:8][ec:1:17:4:1][keggfc:4:1:4:2:13:2][sgdgc:1:3:3:3:6]

CONTIG5807	10548267_f2_2	3902	18005	2253	751	YER070W	2376	2.6(10)-252	Saccharomyces cerevisiae	[ui:yer070w] [pn:ribonucleoside-diphosphate reductase, large subunit:ribonucleoside-diphosphate reductase large chain 1:ribonucleotide reductase] [gn:mrl][gicfc:4.1:4.2:[0.8:12.8]] [ec:1.17.4.1] [keggfc:4.1:4.2:13.2] [sgdfc:1.3.3:3.6]
CONTIG5743	2148252_f1_6	3903	18006	2493	831	YGL234W	2569	3.5(10)-267	Saccharomyces cerevisiae	[ui:yg1234w] [pn:phosphoribosylformylglycine-glycine ligase and phosphoribosylformylglycineamidine cyclo-ligase] [gn:ade5:7][gicfc:4.1] [keggfc:4.1] [sgdfc:1.3.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4022	10193966_c3_4	3904	18007	432	144	YGL070C	383	1.5(10)-35	Saccharomyces cerevisiae	[ui:yg070c] [pn:dnad-directed dna polymerase ii, 14.2 kd subunit:dna-directed dna polymerase ii 14.2 kd polypeptide:b12.6][gn:rbp9] [gicfc:4.1:4.2:10.1:10.2] [ec:2.7.7.6][keggfc:4.1:4.2] [sgdfc:4.8.1:9.5.0] [db:gtc-saccharomyces cer]
CONTIG2815	21876_c3_1	3905	18008	1512	504	YGR061C	1316	2.1(10)-134	Saccharomyces cerevisiae	[ui:ygr061c] [pn:5'-phosphoribosylformylglycineamidine synthase:formylglycineamidine synthetase;phosphoribosylformylglycineamidine synthase:formylglycineamidine ribotide amidotransferase:figarat] [gn:ade6][gicfc:4.1][ec:6.3.5.3] [keggfc:4.1][sgdfc:1.3]

CONTIG5777	12947078_cl_18	3906	18009	618	206	YGR061C	552	3.5(10)-52	Saccharomyces cerevisiae	[ui;ygr061c] [pn:5"-phosphoribosylformylglycinamide synthetase;phosphoribosylformylglycinamide synthetase:formylglycineamidate ribotide amidotransferase;fgat] [gn:ade6] [gicfc:4.1] [ec:6.3.5.3] [keggfc:4.1] [sgdfc:1.3]
CONTIG5777	16672192_s3_25	3907	18010	660	220	YGR061C	712	2.5(10)-69	Saccharomyces cerevisiae	[ui;ygr061c] [pn:5"-phosphoribosylformylglycinamide synthetase;phosphoribosylformylglycinamide synthetase:formylglycineamidate ribotide amidotransferase;fgat] [gn:ade6] [gicfc:4.1] [ec:6.3.5.3] [keggfc:4.1] [sgdfc:1.3]
CONTIG5777	17087514_cl_16	3908	18011	1155	385	YGR061C	1294	4.5(10)-132	Saccharomyces cerevisiae	[ui;ygr061c] [pn:5"-phosphoribosylformylglycinamide synthetase;phosphoribosylformylglycinamide synthetase:formylglycineamidate ribotide amidotransferase;fgat] [gn:ade6] [gicfc:4.1] [ec:6.3.5.3] [keggfc:4.1] [sgdfc:1.3]
CONTIG2819	7120275_c2_2	3909	18012	897	299	YHR201C	293	2.3(10)-31	Saccharomyces cerevisiae	[ui;yhr201c] [pn:exopolyphosphatase;metaphosphatase][gn:ppx1][gicfc:4.1:13.10][ec:3.6.1.1][keggfc:4.1][sgdc:1.4.1:9.2.0][db:gicsaccharomycescerevisiae]

CONTIG5807	5078401_f3_6	3910	18013	285	95	YIL066C	95	0.00119	Saccharomyces cerevisiae	[ui:yi 066cl] [pn:ribonucleotide reductase, repair inducible large subunit:ribonucleoside-diphosphate reductase large chain 2:ribonucleotide reductase:ribonucleotide reductase dna damage-inducible regulatory subunit] [gr:rnr3:din1] [gt]
CONTIG1887	14648437_f1_2	3911	18014	456	152	YIL021W	343	2.7(10)-31	Saccharomyces cerevisiae	[ui:yi 021w] [pn: dna-directed rna polymerase ii, 45 kda: dna-directed rna polymerase ii 45 kd polypeptide:b44.5] [gn:rpb3] [gicfc:4.1:4.2:10.1:10.2] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.8.1:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5137	24414062_c1_9	3912	18015	1074	358	YIL021W	896	6.7(10)-90	Saccharomyces cerevisiae	[ui:yi 021w] [pn: dna-directed rna polymerase ii, 45 kda: dna-directed rna polymerase ii 45 kd polypeptide:b44.5] [gn:rpb3] [gicfc:4.1:4.2:10.1:10.2] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.8.1:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2481	36111703_f3_3	3913	18016	549	183	YIL140W	194	1.6(10)-15	Saccharomyces cerevisiae	[ui:yi 140w] [pn: dna-directed rna polymerase ii, 32 kda subunit: dna-directed rna polymerase ii 32 kd polypeptide:b52] [gn:rpb4:j0654] [gicfc:4.1:4.2:10.1:10.2] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.8.1:9.5.0] [db:gtc-saccharomyces ce]

CONTIG5239	14640628_f1_1	3914	18017	1236	412	YJL026W	1401	2.1(10)-143	Saccharomyces cerevisiae	[ui:yj 026w] [pn:ribonucleoside-diphosphate reductase, small subunit:ribonucleoside-diphosphate reductase small chain 1:ribonucleotide reductase] [gn:mr2:j1271] [gtcfc:4.1:4.2:10.8] [ec:1.17.4.1] [keggfc:4.1:4.2] [sgdgc: 1.3.3:3.6.0]
CONTIG5714	22381317_c2_20	3915	18018	1083	361	YJL026W	1149	1.0(10)-116	Saccharomyces cerevisiae	[ui:yj 026w] [pn:ribonucleoside-diphosphate reductase, small subunit:ribonucleoside-diphosphate reductase small chain 1:ribonucleotide reductase] [gn:mr2:j1271] [gtcfc:4.1:4.2:10.8] [ec:1.17.4.1] [keggfc:4.1:4.2] [sgdgc: 1.3.3:3.6.0]
CONTIG2234	21678181_c2_6	3916	18019	1059	353	YJL005W	97	0.20999	Saccharomyces cerevisiae	[ui:yj 005w] [pn:adenylate cyclase:atp pyrophosphatolyase:adenylyl cyclase] [gn:cyr1:cdc35:hsr1:sra4:j1401] [gtcfc:4.1:11.1:12.13:12.8] [ec:4.6.1.1] [keggfc:4.1:13.1] [sgdgc: 1.3.4:3.8:0.9:1.0:10.4.3] [db:gic-saccharomyces cerevisiae]
CONTIG3421	24323555_c1_7	3917	18020	2085	695	YJL005W	1216	9.4(10)-123	Saccharomyces cerevisiae	[ui:yj 005w] [pn:adenylate cyclase:atp pyrophosphatolyase:adenylyl cyclase] [gn:cyr1:cdc35:hsr1:sra4:j1401] [gtcfc:4.1:11.1:12.13:12.8] [ec:4.6.1.1] [keggfc:4.1:13.1] [sgdgc: 1.3.4:3.8:0.9:1.0:10.4.3] [db:gic-saccharomyces cerevisiae]

CONTIG3985	14117003_f3_7	3918	18021	705	235	YJL005W	377	3.0(10)-33	Saccharomyces cerevisiae	[ui:ylj005w] [pn:adenylate cyclase:atp pyrophosphate-lyase:adenylyl cyclase] [gn:cyr1:cdc35:hsl1:sra4:j1401] [gicfc:4.:1:1.1:12.13:12.8] [ec:4.6.1.1] [keggfc:4.1:13.1] [sgdfc:1.3.4;3.8;0.9.1.0;10.4.3] [db:gic-saccharomyces cerevisiae]
CONTIG4866	23531307_f2_3	3919	18022	1272	424	YJL005W	146	2.2(10)-6	Saccharomyces cerevisiae	[ui:ylj005w] [pn:adenylate cyclase:atp pyrophosphate-lyase:adenylyl cyclase] [gn:cyr1:cdc35:hsl1:sra4:j1401] [gicfc:4.:1:1.1:12.13:12.8] [ec:4.6.1.1] [keggfc:4.1:13.1] [sgdfc:1.3.4;3.8;0.9.1.0;10.4.3] [db:gic-saccharomyces cerevisiae]
CONTIG5507	3960080_f2_5	3920	18023	1902	634	YJL005W	127	0.00044	Saccharomyces cerevisiae	[ui:ylj005w] [pn:adenylate cyclase:atp pyrophosphate-lyase:adenylyl cyclase] [gn:cyr1:cdc35:hsl1:sra4:j1401] [gicfc:4.:1:1.1:12.13:12.8] [ec:4.6.1.1] [keggfc:4.1:13.1] [sgdfc:1.3.4;3.8;0.9.1.0;10.4.3] [db:gic-saccharomyces cerevisiae]
CONTIG5692	21650260_f1_1	3921	18024	777	259	YJL005W	102	0.042	Saccharomyces cerevisiae	[ui:ylj005w] [pn:adenylate cyclase:atp pyrophosphate-lyase:adenylyl cyclase] [gn:cyr1:cdc35:hsl1:sra4:j1401] [gicfc:4.:1:1.1:12.13:12.8] [ec:4.6.1.1] [keggfc:4.1:13.1] [sgdfc:1.3.4;3.8;0.9.1.0;10.4.3] [db:gic-saccharomyces cerevisiae]

CONTIG88	26690930_f3_2	3922	18025	609	203	YJL005W	188	3.7(10)-13	Saccharomyces cerevisiae	[ui:yrj005w] [pn:adenylate cyclase;atp pyrophosphate-lyase;adenylyl cyclase] [gn:cyr1:cdc35:hsrl:sra4:j1401] [gicfc:4.1:1.1:12.13:12.8] [ec:4.6.1.1] [keggfc:4.1:13.1] [sgdfc:1.3.4.3.8.0.9.1.0:10.4.3] [db:gic-saccharomyces cerevisiae]
CONTIG5230	4490806_f2_11	3923	18026	381	127	YJR063W	481	6.4(10)-46	Saccharomyces cerevisiae	[ui:yrj063w] [pn: dna-directed rna polymerase i, 13.7 kd subunit: dna-directed rna polymerase i 13.7 kd polypeptide:a12.2] [gn:rpa12:rnp4:j1747] [gicfc:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.1.0:9.5.0] [db:gic-sa]
CONTIG5131	31447187_c1_4	3924	18027	1098	366	YJR105W	735	7.7(10)-73	Saccharomyces cerevisiae	[ui:yrj105w] [pn:strong similarity to human adenosine kinase;putative adenosine kinase][gn:j1973] [gicfc:4.1] [ec:2.7.1.20] [keggfc:4.1] [sgdfc:1.3.1] [db:gic-saccharomyces cerevisiae]
CONTIG3012	5863775_f1_1	3925	18028	519	173	YKL144C	476	2.2(10)-45	Saccharomyces cerevisiae	[ui:yrk144c] [pn: dna-directed rna polymerase iii, 25 kd subunit: dna-directed rna polymerase iii 25 kd polypeptide:c25] [gn:rpc25:ykl1:unfl] [gicfc:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.1.0:4.4.0:9.5.0] [db:gic]

CONTIG5212	10975300_c3_18	3926	18029	462	154	YKL067W	571	1.8(10)-55	Saccharomyces cerevisiae	[ui:yl067w] [pn:strong similarity to imp dehydrogenases, pur5p and yml056c:probable inosine-5"-monophosphate dehydrogenase:impdh:impd]
CONTIG2321	20709436_c3_9	3927	18030	516	172	YLR432W	585	6.0(10)-57	Saccharomyces cerevisiae	[gn:19753][gicfc:4.1][ec:1.1.1.205][keggfc:4.1][sgdfc:1.3.1][db:gtc-sacchar
CONTIG2321	35189768_c2_7	3928	18031	195	65	YLR432W	238	2.2(10)-19	Saccharomyces cerevisiae	[ui:ylr432w] [pn:strong similarity to imp dehydrogenases, pur5p and yml056c:probable inosine-5"-monophosphate dehydrogenase:impdh:impd]
CONTIG2321	10553150_c2_6	3929	18032	348	116	YML056C	264	3.1(10)-22	Saccharomyces cerevisiae	[ui:yml056c] [pn:strong similarity to imp dehydrogenases; probable inosine-5"-monophosphate dehydrogenase:impdh:impd]

CONTIG5734	21879412_f2_3	3930	18033	600	200	YML022W	616	3.2(10)-60	Saccharomyces cerevisiae	[ui:yml022w] [pn:adenine phosphoribosyltransferase;adenine phosphoribosyltransferase 1:apr1] [gn:apr1] [gtcfc:4.1] [ec:2.4.2.7] [keggfc:4.1] [sgdfc:1.3.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2652	24220307_f2_3	3931	18034	252	84	YMR120C	342	1.3(10)-30	Saccharomyces cerevisiae	[ui:ymr120c] [pn:strong similarity to chicken purh bifunctional enzyme:phosphoribosylaminoimidazolecarboxamide formyltransferase 2:acar transformylase / imp cyclohydrolase:inosinicase:imp synthetase:atric] [gn:ade17:ym8564] [gtcfc:4.1:
CONTIG5413	5292599_c1_13	3932	18035	1314	438	YMR120C	1757	3.8(10)-181	Saccharomyces cerevisiae	[ui:ymr120c] [pn:strong similarity to chicken purh bifunctional enzyme:phosphoribosylaminoimidazolecarboxamide formyltransferase 2:acar transformylase / imp cyclohydrolase:inosinicase:imp synthetase:atric] [gn:ade17:ym8564] [gtcfc:4.1:
CONTIG3970	29961567_c3_13	3933	18036	633	211	YMR217W	860	4.4(10)-86	Saccharomyces cerevisiae	[ui:ymr217w] [pn:glutamine-synthase:glutamine-hydrolyzing:gmp amidotransferase:gmp synthetase] [gn:gual:ym8261] [keggfc:4.1:5.1] [ec:6.3.5.2] [kgggfc:4.1:5.1] [sgdfc:1.3.] [db:gtc-saccharomyces cerevisiae]

CONTIG3970	4725875_c1_10	3934	18037	987	329	YMR217W	1214	1.3(10)-123	Saccharomyces cerevisiae	[ui:ymr217w] [pn:glutamine-hydrolyzing;gmp-synthase;glutamine-amidotransferase:gmp synthetase] [gn:gual1ym8261] [gtcfc:4.1:5.1] [ec:6.3.5.2] [keggfc:4.1:5.1] [sgdfc:1.3.1] [db:gic-saccharomyces cerevisiae]
CONTIG4054	19534511_f3_2	3935	18038	1629	543	YMR300C	1726	7.2(10)-182	Saccharomyces cerevisiae	[ui:ymr300c] [pn:amidophosphoribosyltransferase:glutamine-phosphoribosylpyrophosphate amidotransferase;atase] [gn:ade4ym9952] [gtcfc:4.1:5.1] [ec:2.4.2.14] [keggfc:4.1:5.1] [sgdfc:1.3.1] [db:gic-saccharomyces cerevisiae]
CONTIG1807	23945782_c1_1	3936	18039	576	192	YNL262W	179	2.0(10)-15	Saccharomyces cerevisiae	[ui:ynl262w] [pn:dna-directed dna polymerase epsilon, catalytic subunit a:dna polymerase epsilon ii subunit a] [gn:pol2:dun2:n0825] [gtcfc:4.1:4.2:10.1:10.1:10.2:10.8: 12.8] [ec:2.7.7.7] [keggfc:4.1]
CONTIG3404	10198957_f2_1	3937	18040	18339	613	YNL262W	1408	3.5(10)-143	Saccharomyces cerevisiae	[ui:ynl262w] [pn:dna-directed dna polymerase epsilon, catalytic subunit a:dna polymerase epsilon, catalytic subunit a:dna polymerase epsilon ii subunit a] [gn:pol2:dun2:n0825] [gtcfc:4.1:4.2:10.1:10.1:10.2:10.8: 12.8] [ec:2.7.7.7] [keggfc:4.1]

CONTIG650	255192_f1_1	3938	18041	699	233	YNL262W	1076	1.3(10)-107	Saccharomyces cerevisiae	[ui:ynl262w] [pn: dna-directed dna polymerase epsilon, catalytic subunit a: dna polymerase epsilon, catalytic subunit a: dna polymerase ii subunit a] [gn:pol2:dun2:n0825] [gtcfc:4.1:4.2:10.1:10.10.2:10.8:12.8] [ec:2.7.7.7] [keggfc:4.1]
CONTIG650	781538_f1_2	3939	18042	459	153	YNL262W	539	2.0(10)-50	Saccharomyces cerevisiae	[ui:ynl262w] [pn: dna-directed dna polymerase epsilon, catalytic subunit a: dna polymerase epsilon, catalytic subunit a: dna polymerase ii subunit a] [gn:pol2:dun2:n0825] [gtcfc:4.1:4.2:10.1:10.10.2:10.8:12.8] [ec:2.7.7.7] [keggfc:4.1]
b1x18543_y	21519057_c3_2	3940	18043	525	175	YNL262W	701	1.2(10)-67	Saccharomyces cerevisiae	[ui:ynl262w] [pn: dna-directed dna polymerase epsilon, catalytic subunit a: dna polymerase epsilon, catalytic subunit a: dna polymerase ii subunit a] [gn:pol2:dun2:n0825] [gtcfc:4.1:4.2:10.1:10.10.2:10.8:12.8] [ec:2.7.7.7] [keggfc:4.1]
b1x18984_y	19689090_c1_2	3941	18044	522	174	YNL262W	355	7.5(10)-31	Saccharomyces cerevisiae	[ui:ynl262w] [pn: dna-directed dna polymerase epsilon, catalytic subunit a: dna polymerase epsilon, catalytic subunit a: dna polymerase ii subunit a] [gn:pol2:dun2:n0825] [gtcfc:4.1:4.2:10.1:10.10.2:10.8:12.8] [ec:2.7.7.7] [keggfc:4.1]

CONTIG5289	33618885_c3_14	3942	18045	1197	399	YNL248C	1049	4.0(10)-106	Saccharomyces cerevisiae	[ui:ynl248c] [pn: dna-directed dna polymerase a:i chain, 46 kda:dna-directed dna polymerase i 49 kd polypeptide:a49] [gn:ipa49;rn13;n0880] [gicfc:4.:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.1.0:9.5.0] [db:gic-saccha
CONTIG5615	34064057_f2_9	3943	18046	1302	434	YNL220W	1553	1.6(10)-159	Saccharomyces cerevisiae	[ui:ynl220w] [pn: adenylosuccinate synthetase:imp--aspartate ligase] [gn:ade12;rn1290] [gicfc:4.1.5.2:10.1:10.2] [ec:6.3.4.4] [keggfc:4.1:5.2] [sgdfc:1.3.1:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4968	21619037_c2_3	3944	18047	1074	358	YNL141W	1117	2.6(10)-113	Saccharomyces cerevisiae	[ui:ynl141w] [pn: similarity to adenosine deaminase; probable adenosine deaminase:adenosine aminohydrolase] [gn:n1208;n1825] [gicfc:4.1] [ec:3.5.4.4] [keggfc:4.1] [sgdfc:1.3.1] [db:gic-saccharomyces cerevisiae]
CONTIG4701	815686_c2_11	3945	18048	195	65	YNL113W	116	3.0(10)-7	Saccharomyces cerevisiae	[ui:ynl113w] [pn: dna-directed dna polymerase i,iii 16 kd subunit:dna-directed dna polymerases i and iii 16 kd polypeptide:ac19] [gn:rpc19;n1937] [gicfc:4.1.4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.1.0:4.4.0:9.5.0] [d]

CONTIG320	6835817_f2_1	3946	18049	711	237	YNL102W	626	5.0(10)-60	Saccharomyces cerevisiae	[ui:ynl102w] [pn:DNA-directed DNA polymerase alpha, 180 kd subunit:DNA polymerase alpha:DNA polymerase I] [gn:polI:cdcl7:n2181] [gtcfc:4.1:4.2:10.1:10.2:10.8] [ec:2.7.7.7] [keggfc:4.1:4.2] [sgdgc:3.6:0.9:5.0] [db:gtc-saccharomyces cer]
CONTIG3485	10962757_c2_4	3947	18050	417	139	YNL102W	216	2.7(10)-16	Saccharomyces cerevisiae	[ui:ynl102w] [pn:DNA-directed DNA polymerase alpha, 180 kd subunit:DNA polymerase alpha:DNA polymerase I] [gn:polI:cdcl7:n2181] [gtcfc:4.1:4.2:10.1:10.2:10.8] [ec:2.7.7.7] [keggfc:4.1:4.2] [sgdgc:3.6:0.9:5.0] [db:gtc-saccharomyces cer]
CONTIG4421	11737878_c2_2	3948	18051	1956	652	YNL102W	1983	4.4(10)-205	Saccharomyces cerevisiae	[ui:ynl102w] [pn:DNA-directed DNA polymerase alpha, 180 kd subunit:DNA polymerase alpha:DNA polymerase I] [gn:polI:cdcl7:n2181] [gtcfc:4.1:4.2:10.1:10.2:10.8] [ec:2.7.7.7] [keggfc:4.1:4.2] [sgdgc:3.6:0.9:5.0] [db:gtc-saccharomyces cer]

CONTIG921	5110343_f2_2	3949	18052	759	253	YNL102W	298	5.0(10)-25	Saccharomyces cerevisiae	[ui:ynl102w] [pn: dna-directed dna polymerase alpha, 180 kd subunit:dna polymerase alpha:dna polymerase i] [gn:rpl1:cdc17:n2181] [gicfc:4.1:4.2:10.1:10.2:10.8] [ec:2.7.7.7] [keggfc:4.1:4.2] [sgdfc:3.6.0:9.5.0] [db:gic-saccharomyces cer]
b3x16086.y	6301575_c3_4	3950	18053	756	252	YNL102W	456	7.2(10)-42	Saccharomyces cerevisiae	[ui:ynl102w] [pn: dna-directed dna polymerase alpha, 180 kd subunit:dna polymerase alpha:dna polymerase i] [gn:rpl1:cdc17:n2181] [gicfc:4.1:4.2:10.1:10.2:10.8] [ec:2.7.7.7] [keggfc:4.1:4.2] [sgdfc:3.6.0:9.5.0] [db:gic-saccharomyces cer]
CONTIG5595	85067_f2_3	3951	18054	1080	360	YNR003C	618	1.8(10)-60	Saccharomyces cerevisiae	[ui:ynr003c] [pn: dna-directed rna polymerase iii, 34 kd subunit:dna-directed rna polymerase iii 36 kd polypeptide:c34] [gn:rpc34:n2031] [gicfc:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.1:0:4:0:9.5.0] [db:gic-saccharomyces ce]
CONTIG4369	4881567_f2_5	3952	18055	324	108	YOL005C	316	1.8(10)-28	Saccharomyces cerevisiae	[ui:yol005c] [pn: dna-directed rna polymerase ii subunit, 13.6 kd:dnadirected rna polymerase ii 13.6 kd polypeptide:b13.6] [gn:rpb11] [gicfc:4.1:4.2:10.1:10.2] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.8.1:9.5.0] [db:gic-saccharomyces ce]

CONTIG3996	16663306_f3_5	3953	18056	531	177	YOR116C	653	6.5(10)-63	Saccharomyces cerevisiae	[ui:yor116c] [pn: dna-directed rna polymerase iii, 160 kd subunit:dna-directed rna polymerase iii largest subunit:c160]
										[gn:rpc1:rp031:rpc160:o3254:yor3254c] [grfc:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.1:0:4.4]
CONTIG5508	4507817_c1_20	3954	18057	3771	1257	YOR116C	4914	0	Saccharomyces cerevisiae	[ui:yor116c] [pn: dna-directed rna polymerase iii, 160 kd subunit:dna-directed rna polymerase iii largest subunit:c160]
										[gn:rpc1:rp031:rpc160:o3254:yor3254c] [gtfc:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.1:0:4.4]
CONTIG3224	22158568_c1_5	3955	18058	1680	560	YCR128C	2004	2.6(10)-207	Saccharomyces cerevisiae	[ui:yor128c]
										[pn:phosphoribosylaminoimidazole carboxylase:air carboxylase:air] [gn:ade2:03293:yor3293c] [grfc:4.1] [ec:4.1.1.21] [keggfc:4.1] [sgdfc:1.3.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2733	20585037_c3_4	3956	18059	1230	410	YOR151C	1658	1.2(10)-170	Saccharomyces cerevisiae	[ui:yor151c] [pn: dna-directed rna polymerase ii, 140 kda chain:dna-directed rna polymerase ii 140 kd polypeptide:b150:ma polymerase ii subunit 2] [gn:rbp2:rp022:rbp150] [grfc:4.1:4.2:10.1:10.2] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4]

CONTIG425	21564188_c3_4	3957	18060	993	331	YOR151C	1180	5.4(10)-120	Saccharomyces cerevisiae	[ui:yor151c] [pn: dna-directed rna polymerase ii, 140 kda chain:dna-directed polypeptide:b150:rna polymerase ii 140 kd subunit 2] [gn:rpb2:rp022:rpbl50] [gtcfc:4.1:4.2:10.1:10.2] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4]
CONTIG5807	14500763_f2_3	3958	18061	198	66	YCR207C	137	5.2(10)-8	Saccharomyces cerevisiae	[ui:yor207c] [pn: dna-directed rna polymerase iii, 130 kd subunit:dna-directed rna polymerase iii 130 kd polypeptide:c128:rna polymerase iii subunit 2] [gn:rpcl28:rpcl28:ret1] [gtcfc:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2]
CONTIG5807	10738878_f3_8	3959	18062	3183	1061	YCR207C	4483	0	Saccharomyces cerevisiae	[ui:yor207c] [pn: dna-directed rna polymerase iii, 130 kd subunit:dna-directed rna polymerase iii 130 kd polypeptide:c128:rna polymerase iii subunit 2] [gn:rpcl28:rpcl28:ret1] [gtcfc:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2]
CONTIG1069	2751432_f2_1	3960	18063	375	125	YOR224C	322	4.5(10)-29	Saccharomyces cerevisiae	[ui:yor224c] [pn: dna-directed rna polymerase i, ii, iii 16 kd subunit:dna-directed rna polymerases i, ii, and iii 14.5 kd polypeptide:abc14.4] [gn:rpb8:yor50-14] [gtcfc:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.1]

CONTIG5560	24251575_33_21	3961	18064	942	314	YOR340C	400	3.7(10)-52	Saccharomyces cerevisiae	[ui;yor340c] [pn: dna-directed dna polymerase i, 36 kd subunit: dna-dependent dna polymerase 36 kd polypeptide:a43] [gn:rpa43;rm12;06271] [gtcfc:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdgc:4.1.0:9.5.0] [db:gic-saccharo
CONTIG4460	6344192_f1_1	3962	18065	1389	463	YOR341W	1367	8.0(10)-144	Saccharomyces cerevisiae	[ui;yor341w] [pn: dna-directed dna polymerase i, 190 kd alpha subunit: dna-directed dna polymerase i 190 kd polypeptide:a190] [gn:rpa1;rm1;06276] [gtcfc:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdgc:4.1.0:9.5.0] [
CONTIG4563	15126942_f2_1	3963	18066	2337	779	YOR341W	2455	4.2(10)-255	Saccharomyces cerevisiae	[ui;yor341w] [pn: dna-directed dna polymerase i, 190 kd alpha subunit: dna-directed dna polymerase i 190 kd polypeptide:a190] [gn:rpa1;rm1;06276] [gtcfc:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdgc:4.1.0:9.5.0] [

CONTIG4776	33854637_c2_7	3964	18067	477	159	YOR341W	583	2.6(10)-55	Saccharomyces cerevisiae	[ui:yor341w] [pn: dna-directed dna polymerase i, 190 kd alpha subunit: dna-directed dna polymerase i, 190 kd polypeptide: a190] [gn:rpai:rpai190:rm1:06276] [gicfc:4.1:4.2:10.1:10.2:0.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.1:0:9.5:0] [db:gic-saccharomyces cerevisiae]
CONTIG4468	25587567_f3_4	3965	18068	963	321	YCR360C	325	3.0(10)-37	Saccharomyces cerevisiae	[ui:yor360c] [pn: high affinity 3'-5' -cyclic-nucleotide phosphodiesterase: 3'-5' -cyclic-nucleotide phosphodiesterase 2: pdease 2: high-affinity camp phosphodiesterase] [gn:pde2:str5] [gicfc:4.1] [ec:3.1.4.17] [keggfc:4.1] [sgdfc:1.3:4.9.2] [db:gic-saccharomyces cerevisiae]
CONTIG1317	14652037_f2_2	3966	18069	825	275	YPL167C	304	1.2(10)-25	Saccharomyces cerevisiae	[ui:yp1167c] [pn: dna-directed dna polymerase zeta: probable dna polymerase] [gn:rev3:psol: p2335] [gicfc:4.1:4.2:10.1:10.1:10.2:10.8] [ec:2.7.7.7] [keggfc:4.1:4.2] [sgdfc:3.6.0:3.7.0:9.5.0:11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG3778	11047833_f3_4	3967	18070	1380	460	YPL167C	1047	1.7(10)-105	Saccharomyces cerevisiae	[ui:yp1167c] [pn: dna-directed dna polymerase zeta: probable dna polymerase] [gn:rev3:psol: p2335] [gicfc:4.1:4.2:10.1:10.1:10.2:10.8] [ec:2.7.7.7] [keggfc:4.1:4.2] [sgdfc:3.6.0:3.7.0:9.5.0:11.2.1] [db:gic-saccharomyces cerevisiae]

CONTIG4564	11893778_f1_1	3968	18071	2013	671	YPR010C	2859	6.5(10)-298	Saccharomyces cerevisiae	[ui:yp010c] [pn: dna-directed rna polymerase i, 135 kd subunit:dna-directed rna polymerase i135:ma polymerase i 135 kd polypeptide:al135:ma polymerase i subunit 2] [gn:rpa2:rpa135:srp3:rnm2:yp9531] [gicfc:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1]
CONTIG4759	35830216_c3_15	3969	18072	1029	343	YPR010C	1479	1.1(10)-151	Saccharomyces cerevisiae	[ui:yp010c] [pn: dna-directed rna polymerase i, 135 kd subunit:dna-directed rna polymerase i135:ma polymerase i subunit 2] [gn:rpa2:rpa135:srp3:rnm2:yp9531] [gicfc:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1]
CONTIG2746	26854067_f2_3	3970	18073	291	97	YPR110C	379	4.0(10)-35	Saccharomyces cerevisiae	[ui:yp110c] [pn: dna-directed rna polymerase i, iii 40 kd subunit:dna-directed rna polymerases i and iii 40 kd polypeptide:ac40] [gn:rpc5:rpc40:p8283] [gicfc:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.1:0:4.4:0:9.5]
b2x18990_y	29332812_c3_2	3971	18074	780	260	YPR110C	772	9.3(10)-77	Saccharomyces cerevisiae	[ui:yp110c] [pn: dna-directed rna polymerase i, iii 40 kd subunit:dna-directed rna polymerases i and iii 40 kd polypeptide:ac40] [gn:rpc5:rpc40:p8283] [gicfc:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.1:0:4.4:0:9.5]

CONTIG3261	16226437_f1_2	3972	18075	2196	732	YPR175W	613	3.1(10)-112	Saccharomyces cerevisiae	[ui:yp175w] [pn: dna-directed dna polymerase epsilon, subunit b: dna polymerase epsilon ii subunit b] [gn:dpb2:p9705] [gicfc:4.1:4.2:10.1:10.2:10.8] [ec:2.7.7.7] [keggfc:4.1:4.2] [sgdfc:3.6.0:9.5.0] [db:gic-sa]
b3x16016.y	24120192_f1_1	3973	18076	744	248	YPR175W	170	8.0(10)-12	Saccharomyces cerevisiae	[ui:yp175w] [pn: dna-directed dna polymerase epsilon, subunit b: dna polymerase epsilon ii subunit b] [gn:dpb2:p9705] [gicfc:4.1:4.2:10.1:10.2:10.8] [ec:2.7.7.7] [keggfc:4.1:4.2] [sgdfc:3.6.0:9.5.0] [db:gic-sa]
CONTIG3838	23992000_c3_5	3974	18077	414	138	YPR187W	375	1.1(10)-34	Saccharomyces cerevisiae	[ui:yp187w] [pn: dna-directed dna polymerase i, ii, iii 18 kd subunit: dna-directed rna polymerases i, ii, and iii 23 kd polypeptide: abc23] [gn:rpb6:rpo26:p9677] [gicfc:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.1.0]
CONTIG2927	11933333_c2_3	3975	18078	435	145	YPR190C	190	5.2(10)-14	Saccharomyces cerevisiae	[ui:yp190c] [pn: dna-directed dna polymerase iii, 82 kd subunit: dna-directed rna polymerase iii 74 kd polypeptide: c74] [gn: rpc3:rpc82] [gicfc:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.1.0:4.4.0:9.5.0] [db:gic-sacc]

b3x16424.x	26256451_f3_1	3976	18079	501	167	YPR190C	217	6.5(10)-17	Saccharomyces cerevisiae	[ui:ypf190c] [pn: dna-directed rna polymerase iii, 82 kd subunit:dna-directed rna polymerase iii 74 kd polypeptide:c74] [gn:rpc3.rpc82] [gtfc:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.1.0:4.4.0:9.5.0] [db:gtc-sacc]
b3x10245.x	36613775_f3_1	3977	18080	528	176	YPR190C	170	7.2(10)-12	Saccharomyces cerevisiae	[ui:ypf190c] [pn: dna-directed rna polymerase iii, 82 kd subunit:dna-directed rna polymerase iii 74 kd polypeptide:c74] [gn:rpc3.rpc82] [gtfc:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.1.0:4.4.0:9.5.0] [db:gtc-sacc]
CONTIG5421	10722537_f1_3	3978	18081	807	269	YDR020C	227	5.2(10)-19	Saccharomyces cerevisiae	[ui:ydr020c] [pn:weak similarity to uridine kinases and phosphoribulokinases] [gtfc:4.1] [keggfc:14.2] [sgdfc:1.3.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4793	34063317_c3_12	3979	18082	738	246	YLR017W	598	2.5(10)-58	Saccharomyces cerevisiae	[ui:yh017w] [pn:multiple enhancer of uas2] [gtfc:4.1] [keggfc:14.2] [sgdfc:1.3.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5059	11719632_c2_12	3980	18083	600	200	YLR209C	573	1.1(10)-55	Saccharomyces cerevisiae	[ui:yh1209c] [pn:strong similarity to purine-nucleoside phosphorylases] [gtfc:4.1] [keggfc:14.2] [sgdfc:1.3.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4096	13173265_f1_1	3981	18084	1200	400	YLR359W	1657	1.5(10)-170	Saccharomyces cerevisiae	[ui:yh359w] [pn:strong similarity to adenylosuccinate lyase] [gtfc:4.1] [keggfc:14.2] [sgdfc:1.3.1] [db:gtc-saccharomyces cerevisiae]

CONTIG4096	5191511_f2_2	3982	18085	297	99	YLR359W	344	2.1(10)-31	Saccharomyces cerevisiae	[ui:ylr359w] [pn:strong similarity to adenylosuccinate lyase] [gtcfc:4.1] [keggfc:14.2] [sgdfc:1.3.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5658	24413962_f3_10	3983	18086	1419	473	YOL061W	746	7.7(10)-118	Saccharomyces cerevisiae	[ui:yo061w] [pn:similarity to ribose-phosphate pyrophosphokinases] [gtcfc:4.1:4.2] [keggfc:14.2] [sgdfc:1.3.1:1.3.2] [db:gtc-saccharomyces cerevisiae]
CONTIG1898	25600913_c3_6	3984	18087	636	212	YOR280C	223	1.3(10)-18	Saccharomyces cerevisiae	[ui:yor280c] [pn:similarity to s.pombe dihydrofolate reductase] [gtcfc:10.7:9.6] [keggfc:14.2] [sgdfc:1.1.1:1.3.1:1.3.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5650	9773432_c2_20	3985	18088	822	274	YCR280C	199	4.9(10)-16	Saccharomyces cerevisiae	[ui:yor280c] [pn:similarity to s.pombe dihydrofolate reductase] [gtcfc:10.7:9.6] [keggfc:14.2] [sgdfc:1.1.1:1.3.1:1.3.2] [db:gtc-saccharomyces cerevisiae]
CONTIG2843	24228192_c1_4	3986	18089	1200	400	YCL081W	478	9.6(10)-44	Saccharomyces cerevisiae	[ui:yo081w] [pn:gtpase-activating protein for ras proteins;inhibitory regulator protein ira2] [gn:ira2:glc4:ccs1:60985] [gtcfc:4.1:10.2:11.1] [keggfc:14.2] [sgdfc:1.3.4:1.3.5:9.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4914	35369027_c3_10	3987	18090	2235	745	YOL081W	468	4.7(10)-41	Saccharomyces cerevisiae	[ui:yo 081w] [pn:gtpase-activating protein for ras proteins:inhibitory regulator protein ira2] [gn:ira2;gic4:ccs1:00985] [gtcfc:4.1:10.2:11.1] [keggfc:14.2] [sgdfc:1.3.4:1.3.5:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5564	4696963_f2_5	3988	18091	3849	1283	YOL081W	287	3.0(10)-25	Saccharomyces cerevisiae	[ui:yo 081w] [pn:gtpase-activating protein for ras proteins:inhibitory regulator protein ira2] [gn:ira2;gic4:ccs1:00985] [gtcfc:4.1:10.2:11.1] [keggfc:14.2] [sgdfc:1.3.4:1.3.5:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3161	33204375_c1_2	3989	18092	1236	412	YPL212C	960	1.1(10)-96	Saccharomyces cerevisiae	[ui:yp 212c] [pn:pseudouridine synthase 1] [gn:pus1] [gtcfc:4.1:10.1:10.2:10.6] [keggfc:14.2] [sgdfc:1.3.4:4.6:0.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5516	563187_c3_22	3990	18093	519	173	YDL125C	412	1.3(10)-38	Saccharomyces cerevisiae	[ui:ydl125c] [pn:similarity to protein kinase c inhibitor-j] [gn:hmt1] [gtcfc:4.1:12.13] [keggfc:14.2] [sgdfc:1.3.8] [db:gtc-saccharomyces cerevisiae]

CONTIG5744	9817542_f3_12	3991	18094	654	218	YDR305C	374	1..3(10)..34	Saccharomyces cerevisiae	[ui:ydr305c] [pn:similarity to s.pombe diadenosine 5',5'''-p1,p4-tetraphosphate asymmetric tetraphosphate hydrolase;hypothetical 24.8 kd hit-like protein] [gn:int2:d9740] [gicfc:4..1..12..13] [keggfc:14..2] [sgdfc:1..3..8] [db:gic-saccharomyces cerevisiae]
CONTIG5324	4334811_f1_1	3992	18095	981	327	YBL039C	1161	5..5(10)..118	Saccharomyces cerevisiae	[ui:ybl039c] [pn:ctp synthase 1:utp-ammonia ligase 1:ctp synthetase 1] [gn:ura7:ybl0410] [gicfc:4..2] [ec:6..3..4..2] [keggfc:4..2] [sgdfc:1..3..2] [db:gic-saccharomyces cerevisiae]
CONTIG5324	20095662_f3_7	3993	18096	822	274	YBL039C	865	1..3(10)..86	Saccharomyces cerevisiae	[ui:ybl039c] [pn:ctp synthase 1:utp-ammonia ligase 1:ctp synthetase 1] [gn:ura7:ybl0410] [gicfc:4..2] [ec:6..3..4..2] [keggfc:4..2] [sgdfc:1..3..2] [db:gic-saccharomyces cerevisiae]
CONTIG1971	26366561_c2_7	3994	18097	267	89	YEL021W	256	4..4(10)..22	Saccharomyces cerevisiae	[ui:yel021w] [pn:orotidine-5'-phosphate decarboxylase;orotidine 5'-phosphate decarboxylase;omp decarboxylase] [gn:ura3] [gicfc:4..2] [ec:4..1..1..23] [keggfc:4..2] [sgdfc:1..3..2] [db:gic-saccharomyces cerevisiae]

CONTIG698	25681512_f3_1	3995	18098	243	81	YEL021W	267	3.0(10)-23	Saccharomyces cerevisiae	[ui:yel021w] [pn:orotidine-5"-phosphate decarboxylase;orotidine 5"-phosphate decarboxylase;omp decarboxylase] [gn:ura3] [gtcfc:4.2] [ec:4.1.1.23] [keggfc:4.2] [sgdfc:1.3.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5721	15672577_f2_9	3996	18099	657	219	YHR128W	833	3.2(10)-83	Saccharomyces cerevisiae	[ui:yhr128w] [pn:uracil phosphoribosyltransferase;ump pyrophosphorylase;uridylate kinase] [gn:fur1] [gtcfc:4.2] [ec:2.4.2.9] [keggfc:4.2] [sgdfc:1.3.2.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5552	26370762_c2_14	3997	18100	1074	358	YHR144C	701	3.1(10)-69	Saccharomyces cerevisiae	[ui:yhr144c] [pn:deoxyxurydylate deaminase;cdmp deaminase] [gn:dcd1] [gtcfc:4.2] [ec:3.5.4.12] [keggfc:4.2] [sgdfc:1.3.2] [db:gtc-saccharomyces cerevisiae]
CONTIG3304	402082_f2_1	3998	18101	1587	529	YJL130C	1122	1.6(10)-112	Saccharomyces cerevisiae	[ui:yjl130c] [pn:multifunctional pyrimidine biosynthesis protein ura2] [protein:contains:glutamine-dependent carbamoyl- phosphate synthase , aspartate carbamoyltransferase] [gn:ura2,j0686] [gtcfc:4.2;5.1;5.2;10.1;10.2] [keggfc:4.2;5.1;5

CONTIG3364	550776_c3_5	3999	18102	1026	342	YJL130C	1199	9.1(10)-121	Saccharomyces cerevisiae	[ui:y][130c] [prn:multifunctional pyrimidine biosynthesis protein:ura2 protein:contains:glutamine-dependent carbamoyl- phosphate synthase , aspartate carbamoyltransferase] [gn:ura2;j:0686] [gtcfc:4.2:5.1:5.2:10.1:10.2] [keggfc:4.2:5.1:5]
CONTIG4851	24620282_f3_7	4000	18103	4215	1405	YJL130C	5189	0	Saccharomyces cerevisiae	[ui:y][130c] [prn:multifunctional pyrimidine biosynthesis protein:ura2 protein:contains:glutamine-dependent carbamoyl- phosphate synthase , aspartate carbamoyltransferase] [gn:ura2;j:0686] [gtcfc:4.2:5.1:5.2:10.1:10.2] [keggfc:4.2:5.1:5]
CONTIG4854	24031654_c2_5	4001	18104	183	61	YJL130C	249	1.3(10)-19	Saccharomyces cerevisiae	[ui:y][130c] [prn:multifunctional pyrimidine biosynthesis protein:ura2 protein:contains:glutamine-dependent carbamoyl- phosphate synthase , aspartate carbamoyltransferase] [gn:ura2;j:0686] [gtcfc:4.2:5.1:5.2:10.1:10.2] [keggfc:4.2:5.1:5]

CONTIG5482	29303127_f1_4	40002	18105	756	252	YJR057W	471	7.2(10)-45	Saccharomyces cerevisiae	[ui:yjr057w] [pn:thymidylate kinase:dtmp kinase] [gn:cdc8;j1715] [gicfc:4.2] [ec:2.7.4.9] [keggfc:4.2] [sgdfc:1.3.2.9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG4597	14551501_I2_4	40003	18106	1098	366	YLR420W	1186	1.3(10)-120	Saccharomyces cerevisiae	[ui:ylr420w] [pn:dihydroorotate:dhoase] [gn:ura4;J9931] [gicfc:4.2] [ec:3.5.2.3] [keggfc:4.2] [sgdfc:1.3.2] [db:gic-saccharomyces cerevisiae]
b9x10d12.y	20100776_E2_1	40004	18107	636	212	YML106W	538	5.7(10)-52	Saccharomyces cerevisiae	[ui:yml106w] [pn:orotate phosphoribosyltransferase:orotate phosphoribosyltransferase 1:opr1] [gn:ura5;pyr5;ym8339] [gicfc:4.2] [ec:2.4.2.10] [keggfc:4.2] [sgdfc:1.3.2] [db:gic-saccharomyces cerevisiae]
CONTIG5672	21953277_E2_7	40005	18108	1734	578	YNR012W	1128	1.8(10)-114	Saccharomyces cerevisiae	[ui:ynr012w] [pn:uridine kinase:uridine monophosphokinase] [gn:urk1;n2050] [gicfc:4.2] [ec:2.7.1.48] [keggfc:4.2] [sgdfc:1.3.2] [db:gic-saccharomyces cerevisiae]
CONTIG2626	4297525_f3_2	40006	18109	870	290	YOR074C	768	5.0(10)-87	Saccharomyces cerevisiae	[ui:yor074c] [pn:thymidylate synthase:tsl] [gn:tmp1;cdc21] [gicfc:4.2;9.6:10.1:10.2] [ec:2.1.1.45] [keggfc:4.2;9.7:9.8] [sgdfc:1.3.3.9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG2698	21675305_f3_2	4007	18110	1044	348	YDL244W	1391	2.3(10)-142	Saccharomyces cerevisiae	[ui:yd1244w] [pn:strong similarity to thi5p, ylr136c, ynl332w and a.parasiticus, s.pombe nmt1 protein] [gtfc:4.2] [keggfc:4.2] [sgdfc:1.3.2] [db:gic-saccharomyces cerevisiae]
CONTIG4457	24276687_c2_8	4008	18111	198	66	YKL024C	142	5.2(10)-10	Saccharomyces cerevisiae	[ui:yk024c] [pn:uridine-monophosphate kinase:uridylylate kinase:uk:uridine monophosphate kinase:ump kinase] [gn:nura6:soc8] [gtfc:4.2:10.1:10.2:14.1] [ec:2.7.4.-] [keggfc:14.1] [sgdfc:1.3.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5694	9775308_c2_22	4009	18112	558	186	YKL024C	350	4.9(10)-32	Saccharomyces cerevisiae	[ui:yk024c] [pn:uridine-monophosphate kinase:uridylylate kinase:uk:uridine monophosphate kinase:ump kinase] [gn:nura6:soc8] [gtfc:4.2:10.1:10.2:14.1] [ec:2.7.4.-] [keggfc:14.1] [sgdfc:1.3.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4935	29922786_c3_7	4010	18113	414	138	YPR062W	379	4.0(10)-35	Saccharomyces cerevisiae	[ui:ypr062w] [pn:cytosine deaminase] [gn:fcy1] [gtfc:4.2] [keggfc:14.2] [sgdfc:1.3.2] [db:gic-saccharomyces cerevisiae]
CONTIG3827	1988817_f1_1	4011	18114	183	61	YDR513W	174	2.2(10)-13	Saccharomyces cerevisiae	[ui:yd1513w] [pn:glutaredoxin:thioltransferase] [gn:trr1:trr19719] [gtfc:4.2:12.12] [keggfc:14.2] [sgdfc:1.3.3:9.2:0:11.3.0] [db:gic-saccharomyces cerevisiae]

CONTIG3812	4407680_f2_3	4012	18115	582	194	YDR513W	250	1.8(10)-21	Saccharomyces cerevisiae	[ui:ydr513w] [pn:glutaredoxin:thioltransferase] [gn:trr1:trr:dr9719] [gtcfc:4.2:12.12] [keggfc:14.2] [sgdfc:1.3.3.9.2.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5781	4541257_f1_2	4013	18116	1485	495	YOR269W	363	2.0(10)-33	Saccharomyces cerevisiae	[ui:yor269w] [pn:similarity to human lis-1 protein:protein] [gn:pac1] [gtcfc:4.2] [keggfc:14.2] [sgdfc:1.3.3] [db:gtc-saccharomyces cerevisiae]
CONTIG1871	394062_c2_3	4014	18117	591	197	YPL059W	424	7.0(10)-40	Saccharomyces cerevisiae	[ui:ypl059w] [pn:similarity to glutaredoxins] [gtcfc:4.2] [keggfc:14.2] [sgdfc:1.3.3] [db:gtc-saccharomyces cerevisiae]
b3x15471.y	35806566_f1_1	4015	18118	462	154	YJR062C	96	5.0(10)-10	Saccharomyces cerevisiae	[ui:yjr062c] [pn:amino-terminal amidase:n-terminal amidase] [gn:mtal1:j1742] [gtcfc:4.3;7.1:10.11:10.7] [ec:3.2.1.-] [keggfc:4.3;4.4] [sgdfc:6.3.0:6.5.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5489	24803187_f2_1	4016	18119	3015	1005	YGL173C	1767	3.3(10)-182	Saccharomyces cerevisiae	[ui:ygl173c] [pn:multifunctional nuclease:strand exchange protein 1-kar:- enhancing mutation protein:5"-3" exoribonuclease:dna strand transfer protein beta:stp-beta] [gn:kem1:sep1.xml:dst2:rar5:g1645] [gtcfc:4.4:10.10:10.3:12.8] [keg

CONTIG5671	4881511_f2_8	4017	18120	1206	402	YGL173C	1332	4.2(10)-136	Saccharomyces cerevisiae	[ui:ygl173c] [pn:multifunctional nuclelease:strand exchange protein 1:kar:- enhancing mutation protein:5"-3" exoribonuclease:dna strand transfer protein beta:sip-beta] [gn:kem1:sep1.xml:ds2:rar5g1645] [lgcfc:4.4:10.10.3:12.8] [keg-]
CONTIG2986	994087_f3_3	4018	18121	378	126	YGR195W	328	1.0(10)-29	Saccharomyces cerevisiae	[ui:ygr195w] [pn:weak similarity to p.aeruginosa mase ph:hypothetical 27.6 kd protein in pdx1-sng1 intergenic region] [gn:g7587] [lgcfc:4.4:10.10] [kegfc:14.2] [sgdgc:1.3.6] [db:gtc-saccharomyces cerevisiae]
CONTIG1992	35807777_f1_1	4019	18122	1203	401	YHR077C	516	1.5(10)-48	Saccharomyces cerevisiae	[ui:yhr077c] [pn:nonsense-mediated mrna decay protein 2:up- frameshift suppressor 2] [gn:nmd2:upf2;ifs1: sua1] [lgcfc:4.4:10.10.10.7] [kegfc:14.2] [sgdgc:1.3.6;5.3.0;9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3143	23634465_c1_5	4020	18123	879	293	YHR077C	108	6.4(10)-10	Saccharomyces cerevisiae	[ui:yhr077c] [pn:nonsense-mediated mrna decay protein 2:up- frameshift suppressor 2] [gn:nmd2:upf2;ifs1: sua1] [lgcfc:4.4:10.10.10.7] [kegfc:14.2] [sgdgc:1.3.6;5.3.0;9.2.0] [db:gtc-saccharomyces cerevisiae]

b1x11358.y	915627_c2_4	4021	18124	756	252	YHR077C	92	0.32	Saccharomyces cerevisiae	[ui:yr077cl [pn:nonsense-mediated mrna decay protein 2:up- frameshift suppressor 2] [gn:nmd2:upf2:ifs1: sua1] [gtfc:4.4:10.10.7] [keggfc:14.2] [sgfc:1.3.6.5.3.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2001	235451_c2_2	4022	18125	909	303	YJR132W	289	2.7(10)-24	Saccharomyces cerevisiae	[ui:yr132w] [pn:nam7p/upf1 p-interacting protein:nonsense-mediated mrna decay protein 5] [gn:nmd5:j2112] [gtfc:4.4:10.10] [keggfc:14.2] [sgfc:1.3.6] [db:gtc-saccharomyces cerevisiae]
CONTIG4962	9776538_f1_1	4023	18126	1212	404	YJR132W	344	3.7(10)-30	Saccharomyces cerevisiae	[ui:yr132w] [pn:nam7p/upf1 p-interacting protein:nonsense-mediated mrna decay protein 5] [gn:nmd5:j2112] [gtfc:4.4:10.10] [keggfc:14.2] [sgfc:1.3.6] [db:gtc-saccharomyces cerevisiae]
CONTIG4998	36371075_c2_13	4024	18127	1623	541	YJR132W	848	8.1(10)-85	Saccharomyces cerevisiae	[ui:yr132w] [pn:nam7p/upf1 p-interacting protein:nonsense-mediated mrna decay protein 5] [gn:nmd5:j2112] [gtfc:4.4:10.10] [keggfc:14.2] [sgfc:1.3.6] [db:gtc-saccharomyces cerevisiae]
CONTIG4998	4335001_c3_15	4025	18128	522	174	YJR132W	200	8.9(10)-15	Saccharomyces cerevisiae	[ui:yr132w] [pn:nam7p/upf1 p-interacting protein:nonsense-mediated mrna decay protein 5] [gn:nmd5:j2112] [gtfc:4.4:10.10] [keggfc:14.2] [sgfc:1.3.6] [db:gtc-saccharomyces cerevisiae]

CONTIG5085	23650312_c1_8	4026	18129	1335	445	YJR132W	546	7.5(10)-52	Saccharomyces cerevisiae	[ui:yr132w] [pn:nam7/upf1/p-interacting protein:nonsense-mediated mrna decay protein 5] [gn:nmd5:j2112] [gtcfc:4.4:10.10] [keggfc:1.4.2] [sgdfc:1.3.6] [db:gtc-saccharomyces cerevisiae]
CONTIG5757	4879063_f3_5	4027	18130	1458	486	YKL149C	597	1.8(10)-64	Saccharomyces cerevisiae	[ui:ykl149c] [pn:larat-debranching enzyme:larat debranching enzyme] [gn:dbr1/prp26:ykl604] [gtcfc:4.4:10.1:10.10:10.2:14.1] [ec:3.1.-.-] [keggfc:14.1] [sgdfc:1.3.6:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5776	14241436_f2_12	4028	18131	1242	414	YLR363C	139	9.6(10)-15	Saccharomyces cerevisiae	[ui:ylr363c] [pn:nam7/upf1/p-interacting protein:nam7] [gn:nmd4] [gtcfc:4.4:10.10] [keggfc:14.2] [sgdfc:1.3.6] [db:gtc-saccharomyces cerevisiae]
CONTIG5769	23612501_c3_20	4029	18132	1155	385	YMR080C	1115	4.2(10)-113	Saccharomyces cerevisiae	[ui:ymr080c] [pn:nonsense-mediated mrna decay protein:nonsense-mediated mrna decay protein 1:up-frameshift suppressor 1] [gn:nam7/upf1:fs2:mof4:ym9582] [gtcfc:4.4:10.10:10.7] [keggfc:14.2] [sgdfc:1.3.6:5.3:0:9.2:0] [db:g]

CONTIG628	35937828_f3_1	4030	18133	537	179	YMR080C	196	2.1(10)-14	Saccharomyces cerevisiae	[ui:ymr080c] [pn:nonsense-mediated mrna decay protein:nam7 protein:nonsense-mediated mrna decay protein 1:up-frame shift suppressor 1] [gn:nam7:upf1:ifs2:mof4:ym9582] [gtfc:4.4:10.10:10.7] [keggc:14.2] [sgdc:1.3.6.5.3.0.9.2.0] [db:g]
CONTIG819	15838508_c3_2	4031	18134	321	107	YMR080C	355	2.1(10)-31	Saccharomyces cerevisiae	[ui:ymr080c] [pn:nonsense-mediated mrna decay protein:nam7 protein:nonsense-mediated mrna decay protein 1:up-frame shift suppressor 1] [gn:nam7:upf1:ifs2:mof4:ym9582] [gtfc:4.4:10.10:10.7] [keggc:14.2] [sgdc:1.3.6.5.3.0.9.2.0] [db:g]
CONTIG819	5985882_c3_1	4032	18135	594	198	YMR080C	744	8.5(10)-74	Saccharomyces cerevisiae	[ui:ymr080c] [pn:nonsense-mediated mrna decay protein:nam7 protein:nonsense-mediated mrna decay protein 1:up-frame shift suppressor 1] [gn:nam7:upf1:ifs2:mof4:ym9582] [gtfc:4.4:10.10:10.7] [keggc:14.2] [sgdc:1.3.6.5.3.0.9.2.0] [db:g]
CONTIG3369	15078550_c1_5	4033	18136	288	96	YMR234W	116	4.2(10)-11	Saccharomyces cerevisiae	[ui:ymr234w] [pn:ribonuclease h:rase h] [gn:rnh1:ym959] [gtfc:4.4:10.10] [ec:3.1.26.4] [keggc:14.1] [sgdc:1.3.6] [db:gc-saccharomyces cerevisiae]

CONTIG3369	4103127_c2_6	4034	18137	723	241	YMR234W	151	1.8(10)-17	Saccharomyces cerevisiae	[ui:ymr234w] [pn:ribonuclease h:mase h] [gn:mh1.ymg9959] [gtcfc:4.4;10.10] [ec:3.1.26.4] [keggfc:14.1] [sgdfc:1.3.6] [db:gic-saccharomyces cerevisiae]
CONTIG5034	581250_f3_8	4035	18138	960	320	YMR234W	217	6.0(10)-31	Saccharomyces cerevisiae	[ui:ymr234w] [pn:ribonuclease h:mase h] [gn:mh1.ymg9959] [gtcfc:4.4;10.10] [ec:3.1.26.4] [keggfc:14.1] [sgdfc:1.3.6] [db:gic-saccharomyces cerevisiae]
CONTIG1638	33478461_c3_3	4036	18139	759	253	YOR033C	329	6.2(10)-29	Saccharomyces cerevisiae	[ui:yor033c] [pn:exo1] encodes an exonuclease which interacts with msh2p:dhs1 protein [gr:dhs1.or26] [gtcfc:4.4;10.10;10.8] [keggfc:14.2] [sgdfc:1.3.6;3.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG3402	1375_fl_1	4037	18140	822	274	YPL123C	491	5.5(10)-47	Saccharomyces cerevisiae	[ui:yp1123c] [pn:similarity to ribonucleases] [gtcfc:4.4;10.10] [keggfc:14.2] [sgdfc:1.3.6] [db:gic-saccharomyces cerevisiae]
CONTIG4791	35158411_c3_8	4038	18141	1047	349	YPL123C	546	8.3(10)-53	Saccharomyces cerevisiae	[ui:yp1123c] [pn:similarity to ribonucleases] [gtcfc:4.4;10.10] [keggfc:14.2] [sgdfc:1.3.6] [db:gic-saccharomyces cerevisiae]
CONTIG4791	4490937_c2_6	4039	18142	291	97	YPL123C	92	0.00097	Saccharomyces cerevisiae	[ui:yp1123c] [pn:similarity to ribonucleases] [gtcfc:4.4;10.10] [keggfc:14.2] [sgdfc:1.3.6] [db:gic-saccharomyces cerevisiae]
CONTIG5758	20119703_c3_24	4040	18143	999	333	YPL123C	430	1.6(10)-40	Saccharomyces cerevisiae	[ui:yp1123c] [pn:similarity to ribonucleases] [gtcfc:4.4;10.10] [keggfc:14.2] [sgdfc:1.3.6] [db:gic-saccharomyces cerevisiae]

CONTIG1117	13867916_f3_1	4041	18144	660	220	YGL245W	931	1.3(10)-93	Saccharomyces cerevisiae	[ui:yg][245w] [pn:strong similarity to glutamine--tRNA ligase;glutamyl-tRNA synthetase, cytoplasmic;glutamate--tRNA ligase;glursp85][gn:g0583;hrb724][gtcfc:5.1:9.10:10.6][ec:6.1.1.17][keggfc:5.1:9.10:10.1:10.2][sgdgc:5.4.0][db:]
CONTIG1607	4507691_f1_1	4042	18145	633	211	YGL245W	648	1.3(10)-63	Saccharomyces cerevisiae	[ui:yg][245w] [pn:strong similarity to glutamine--tRNA ligase;glutamyl-tRNA synthetase, cytoplasmic;glutamate--tRNA ligase;glursp85][gn:g0583;hrb724][gtcfc:5.1:9.10:10.6][ec:6.1.1.17][keggfc:5.1:9.10:10.1:10.2][sgdgc:5.4.0][db:]
CONTIG2711	9876292_c2_4	4043	18146	666	222	YGL245W	288	1.8(10)-24	Saccharomyces cerevisiae	[ui:yg][245w] [pn:strong similarity to glutamine--tRNA ligase;glutamyl-tRNA synthetase, cytoplasmic;glutamate--tRNA ligase;glursp85][gn:g0583;hrb724][gtcfc:5.1:9.10:10.6][ec:6.1.1.17][keggfc:5.1:9.10:10.1:10.2][sgdgc:5.4.0][db:]
CONTIG3361	4969505_f2_1	4044	18147	894	298	YJL101C	493	3.3(10)-47	Saccharomyces cerevisiae	[ui:yg][101c] [pn:glutamate--cysteine ligase;gamma-glutamylcysteine synthetase;gamma-ecs;ges][gn:gsh1;j0332][gtcfc:5.1:6.16:12.12][ec:6.3.2.2][keggfc:5.1:16.9][sgdgc:11.3.0][db:gtc-saccharomyces cerevisiae]

CONTIG3361	23944202_f3_2	4045	18148	609	203	YJL101C	200	4.5(10)-15	Saccharomyces cerevisiae	[ui:yl1101c] [pn:glutamate--cysteine ligase;gamma-glutamylcysteine synthetase;gamma-ecs;ges] [gn:ghs1;j0832] [lgicf:5.1:6.16:12.12] [ec:6.3.2.2] [keggf:5.1:6.9] [sgdfc:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG780	34570275_c3_1	4046	18149	528	176	YJL101C	374	7.0(10)-34	Saccharomyces cerevisiae	[ui:yl1101c] [pn:glutamate--cysteine ligase;gamma-glutamylcysteine synthetase;gamma-ecs;ges] [gn:ghs1;j0832] [lgicf:5.1:6.16:12.12] [ec:6.3.2.2] [keggf:5.1:6.9] [sgdfc:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1307	25634793_c3_2	4047	18150	498	166	YJR109C	443	1.1(10)-40	Saccharomyces cerevisiae	[ui:yl109c] [pn:arginine-specific carbamoylphosphate synthase, large chain:carbamoyl-phosphate synthase, arginine-specific, large chain:arginine-specific carbamoyl-phosphate synthetase, ammonia chain] [gn:cpa2;j2002] [lgicf:5.1:6.6]
CONTIG4268	47250_f2_4	4048	18151	1263	421	YJR109C	1449	1.7(10)-148	Saccharomyces cerevisiae	[ui:yl109c] [pn:arginine-specific carbamoylphosphate synthase, large chain:carbamoyl-phosphate synthase, arginine-specific, large chain:arginine-specific carbamoyl-phosphate synthetase, ammonia chain] [gn:cpa2;j2002] [lgicf:5.1:6.6]

CONTIG4268	7032513_f3_5	4049	18152	915	305	YJR109C	1108	2.2(10)-112	Saccharomyces cerevisiae	[ui:yr 109c] [pn:arginine-specific carbamoylphosphate synthase, large chain:carbamoyl-phosphate synthase, arginine-specific, large chain:arginine-specific carbamoyl-phosphate synthetase, ammonia chain] [gn:cpa2;j:2002] [gtcfc:5.1:6.6]
CONTIG4268	25489007_f3_6	4050	18153	567	189	YJR109C	648	9.1(10)-63	Saccharomyces cerevisiae	[ui:yr 109c] [pn:arginine-specific carbamoylphosphate synthase, large chain:carbamoyl-phosphate synthase, arginine-specific, large chain:arginine-specific carbamoyl-phosphate synthetase, ammonia chain] [gn:cpa2;j:2002] [gtcfc:5.1:6.6]
CONTIG2939	24414187_c1_6	4051	18154	1056	352	YOR168W	702	2.3(10)-69	Saccharomyces cerevisiae	[ui:yr 168w] [pn:glutaminyl-tRNA synthetase;glutamine-tRNA ligase;glnrs] [gn:gln4;j:3601] [gtcfc:5.1:10.6] [ec:6.1.1.18] [keggfc:5.1:10.1:10.2] [sgdfc:5.4:0.9:2.0] [db:gic-saccharomyces cerevisiae]
CONTIG3381	16097902_f1_1	4052	18155	1104	368	YOR168W	1165	2.1(10)-118	Saccharomyces cerevisiae	[ui:yr 168w] [pn:glutaminyl-tRNA synthetase;glutamine-tRNA ligase;glnrs] [gn:gln4;j:3601] [gtcfc:5.1:10.6] [ec:6.1.1.18] [keggfc:5.1:10.1:10.2] [sgdfc:5.4:0.9:2.0] [db:gic-saccharomyces cerevisiae]

CONTIG1083	93792_f1_1	4053	18156	417	139	YCR303W	387	5.7(10)-36	Saccharomyces cerevisiae	[ui:yor303w] [pn:arginine-specific carbamoylphosphate synthase, small chain:carbamoyl-phosphate synthase, arginine-specific, small chain:arginine-specific carbamoyl-phosphate synthetase, glutamine chain:cps-a] [gn:cpa1] [gtcfc:5.1:6.6]
CONTIG75	14273513_f3_1	4054	18157	726	242	YOR303W	787	2.3(10)-78	Saccharomyces cerevisiae	[ui:yor303w] [pn:arginine-specific carbamoylphosphate synthase, small chain:carbamoyl-phosphate synthase, arginine-specific, small chain:arginine-specific carbamoyl-phosphate synthetase, glutamine chain:cps-a] [gn:cpa1] [gtcfc:5.1:6.6]
CONTIG4941	26692285_f2_2	4055	18158	1452	484	YP_091W	1521	4.0(10)-156	Saccharomyces cerevisiae	[ui:yp 091w] [pn:nadph:glutathione reductase;gr:grase] [gn:gir1] [pg 17w] [gtcfc:5.1:6.16:12.12] [ec:1.6.4.2] [keggfc:5.1:6.9] [sgdfc:11.3.0] [db:grc-saccharomyces cerevisiae]
CONTIG908	32460831_f2_1	4056	18159	897	299	YGL017W	479	1.0(10)-45	Saccharomyces cerevisiae	[ui:yg 017w] [pn:arginyl tRNA transferase:arginyl-tRNA--protein transferase:arginyltransferase] [gn:ate1] [gtcfc:5.1:10.11:10.7:14.1] [ec:2.3.2.8] [keggfc:14.1] [sgdfc:1.1.5:6.3.0:6.5.1:9.2.0] [db:grc-saccharomyces cerevisiae]

b9x13k22.x	488281_f1_1	4057	18160	729	243	YKL157W	826	1.8(10)-82	Saccharomyces cerevisiae	[ui:ykl157w] [pn:aminopeptidase yscii:aminopeptidase iiysciij] [gn:ape2:lap]:ykl611 [gicfc:5.1:10.7] [ec:3.4.11.-] [keggfc:14.1] [sgdfc:1.1.5:6.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG3633	11760287_f1_1	4058	18161	573	191	YPR069C	699	5.0(10)-69	Saccharomyces cerevisiae	[ui:ypr069c] [pn:putrescine aminopropyltransferase:spermidine synthase] [gn:spc3] [gicfc:5.1] [keggfc:14.2] [sgdfc:1.1.5] [db:gic-saccharomyces cerevisiae]
CONTIG4615	34179753_f3_8	4059	18162	453	151	YPR069C	519	6.0(10)-50	Saccharomyces cerevisiae	[ui:ypr069c] [pn:putrescine aminopropyltransferase:spermidine synthase] [gn:spc3] [gicfc:5.1] [keggfc:14.2] [sgdfc:1.1.5] [db:gic-saccharomyces cerevisiae]
CONTIG5281	4098375_f1_2	4060	18163	1044	348	YPR069C	767	3.1(10)-76	Saccharomyces cerevisiae	[ui:ypr069c] [pn:putrescine aminopropyltransferase:spermidine synthase] [gn:spc3] [gicfc:5.1] [keggfc:14.2] [sgdfc:1.1.5] [db:gic-saccharomyces cerevisiae]
CONTIG5804	3212575_c2_53	4061	18164	996	332	YER023W	580	2.1(10)-56	Saccharomyces cerevisiae	[ui:yer023w] [pn:delta-1-pyrroline-5-carboxylate reductase:pyrrole-5-carboxylate reductase:p5cr:p5c reductase] [gn:pro3:ore2] [gicfc:5.10:5.16:6.6] [ec:1.5.1.2] [keggfc:5.10:5.16] [sgdfc:1.1.1:9:2.0] [db:gic-saccharomyces cerevisiae]

b9x11y87.y	36367205_c2_1	4062	18165	546	182	YER087W	465	3.2(10)-44	Saccharomyces cerevisiae	[ui:yer087w] [pn:similarity to e.coli prolyl-tRNA synthetase;putative prolyl-tRNA synthetase yer087w:proline--tRNA ligase;prors] [gtcfc:5.10:10.6] [ec:6.1.1.15] [keggfc:5.10:10.1:10.2] [sgdgc:5.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG5287	24411686_c1_5	4063	18166	1503	501	YHR018C	1811	7.4(10)-187	Saccharomyces cerevisiae	[ui:yhr018c] [pn:argininosuccinate lyase;argininosuccinase;asal] [gn:arg41] [gtcfc:5.10.5:16.5:2.6.6] [ec:4.3.2.1] [keggfc:5.2.5.10.5:16] [sgdgc:1.1.1.9:2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5186	16836660_c3_18	4064	18167	2082	694	YHR020W	2134	4.4(10)-221	Saccharomyces cerevisiae	[ui:yhr020w] [pn:strong similarity to human glutamyl-prolyl-tRNA synthetase and fruit fly multifunctional aminoacyl-tRNA synthetase;putative prolyl-tRNA synthetase yhr020w:proline--tRNA ligase;prors] [gtcfc:5.10:10.6] [ec:6.1.1.15] [k]
CONTIG5595	4068753_c3_15	4065	18168	1062	354	YJL088W	1062	1.7(10)-107	Saccharomyces cerevisiae	[ui:yj088w] [pn:ornithine carbamoyltransferase;oc1] [gn:arg3:j0924] [gtcfc:5.10.5:16.6:6] [ec:2.1.3.3] [keggfc:5.10:5.1.6] [sgdgc:1.1.1.9:2.0] [db:gic-saccharomyces cerevisiae]

CONTIG5176	12141552_f3_4	4066	18169	1275	425	YOL052C	694	1.7(10)-68	Saccharomyces cerevisiae	[ui:yol052c] [pn:adenosylmethionine decarboxylase precursors-s-adenosylmethionine decarboxylase proenzyme; adometc] [gn:spe2.0 275] [gicfc:5.10-12.12-12.15:12.8] [ec:4.1.1.50] [keggfc:5.10] [sgdfc:3.1.0;3.4.0:11.3.0] [db:gic-saccharomy
CONTIG3628	4961801_c1_2	4067	18170	1017	339	YBR248C	903	1.2(10)-90	Saccharomyces cerevisiae	[ui:ybr248c] [pn:glutamine amidotransferase/cyclase;histidine biosynthesis bifunctional amidotransferase / cyclase] [gn:his7.ybr1640] [gicfc:5.11:6.6] [ec:2.4.2.-] [keggfc:5.11] [sgdfc:1.1.1] [db:gic-saccharomyces cerevisiae]
CONTIG1	14267186_c3_3	4068	18171	645	215	YCL030C	777	2.7(10)-77	Saccharomyces cerevisiae	[ui:ycl030c] [pn:phosphoribosyl-amp cyclohydrolase/phosphoribosyl-atp pyrophosphatase/histidinol dehydrogenase; phosphoribosyl-amp cyclohydrolase / phosphoribosyl-atp pyrophosphohydrolase / histidinol dehydrogenase;hdh] [gn:his4.ycl30c:

CONTIG39	11727013_f1_1	4069	18172	549	183	YCL030C	590	1.8(10)-57	Saccharomyces cerevisiae	[ui:yc1030c] [pn:phosphoribosyl-amp cyclohydrolase/phosphoribosyl-amp pyrophosphatase/histidinol dehydrogenase:phosphoribosyl-amp cyclohydrolase / phosphoribosyl-amp pyrophosphohydrolase / histidinol dehydrogenase:hdh] [gn:his4:yc130c:
CONTIG640	20117067_f2_1	4070	18173	603	201	YCL030C	335	1.8(10)-29	Saccharomyces cerevisiae	[ui:yc1030c] [pn:phosphoribosyl-amp cyclohydrolase/phosphoribosyl-amp pyrophosphatase/histidinol dehydrogenase:phosphoribosyl-amp cyclohydrolase / phosphoribosyl-amp pyrophosphohydrolase / histidinol dehydrogenase:hdh] [gn:his4:yc130c:
CONTIG640	24245950_f3_2	4071	18174	486	162	YCL030C	397	4.0(10)-36	Saccharomyces cerevisiae	[ui:yc1030c] [pn:phosphoribosyl-amp cyclohydrolase/phosphoribosyl-amp pyrophosphatase/histidinol dehydrogenase:phosphoribosyl-amp cyclohydrolase / phosphoribosyl-amp pyrophosphohydrolase / histidinol dehydrogenase:hdh] [gn:his4:yc130c:

CONTIG1055	21603188_f3_3	4072	18175	396	132	YER055C	338	9.0(10)-31	Saccharomyces cerevisiae	[ui:yer055c] [pn:atp phosphoribosyltransferase] [gn:his1] [gicfc:5.11:6.10.2] [ec:2.4.2.17] [keggfc:5.11] [sgdfc: 1.1.1:1.1.2] [db:gic-saccharomyces cerevisiae]
CONTIG5523	26384828_f3_11	4073	18176	471	157	YER055C	427	3.3(10)-40	Saccharomyces cerevisiae	[ui:yer055c] [pn:atp phosphoribosyltransferase] [gn:his1] [gicfc:5.11:6.10.2] [ec:2.4.2.17] [keggfc:5.11] [sgdfc: 1.1.1:1.1.2] [db:gic-saccharomyces cerevisiae]
CONTIG5186	22379577_f2_2	4074	18177	957	319	YFR025C	609	1.7(10)-59	Saccharomyces cerevisiae	[ui:yfr025c] [pn:histidinol phosphatase;histidinol-phosphatase] [gn:his2] [gicfc:5.11:6.6] [ec:3.1.3.15] [keggfc:5.11] [sgdfc: 1.1.1] [db:gic-saccharomyces cerevisiae]
CONTIG3249	21492151_c3_6	4075	18178	474	158	Y1L116W	346	1.3(10)-31	Saccharomyces cerevisiae	[ui:y1l116w] [pn:histidinol-phosphate aminotransferase;imidazole acetol-phosphate transaminase] [gn:his5] [gicfc:5.11:6.6] [ec:2.6.1.9] [keggfc:5.11] [sgdfc: 1.1.1] [db:gic-saccharomyces cerevisiae]
b1x10611_y	3944090_f2_1	4076	18179	324	108	Y1L116W	205	3.6(10)-16	Saccharomyces cerevisiae	[ui:y1l116w] [pn:histidinol-phosphate aminotransferase;imidazole acetol-phosphate transaminase] [gn:his5] [gicfc:5.11:6.6] [ec:2.6.1.9] [keggfc:5.11] [sgdfc: 1.1.1] [db:gic-saccharomyces cerevisiae]

CONTIG691	23831588_02_2	4077	18180	432	144	YMR283C	143	4.0(10)-9	Saccharomyces cerevisiae	[ui:ymr283c] [pn:tma a64-2"-o-ribosylphosphate transferase: initiator tma phosphoribosyl-transferase] [gn:rit1:ymr8021] [gicfc:5.11:10.6] [ec:2.4.2.-] [keggfc:5.11] [sgdgc:4.6.0] [db:gic-saccharomyces cerevisiae]
b3x16442.x	29955088_f2_1	4078	18181	216	72	YMR283C	172	3.0(10)-12	Saccharomyces cerevisiae	[ui:ymr283c] [pn:tma a64-2"-o-ribosylphosphate transferase: initiator tma phosphoribosyl-transferase] [gn:rit1:ymr8021] [gicfc:5.11:10.6] [ec:2.4.2.-] [keggfc:5.11] [sgdgc:4.6.0] [db:gic-saccharomyces cerevisiae]
b3x16442.x	4804701_f2_2	4079	18182	408	136	YMR283C	116	3.2(10)-6	Saccharomyces cerevisiae	[ui:ymr283c] [pn:tma a64-2"-o-ribosylphosphate transferase: initiator tma phosphoribosyl-transferase] [gn:rit1:ymr8021] [gicfc:5.11:10.6] [ec:2.4.2.-] [keggfc:5.11] [sgdgc:4.6.0] [db:gic-saccharomyces cerevisiae]
CONTIG3477	10742187_f3_5	4080	18183	1545	515	YPR033C	1727	5.9(10)-178	Saccharomyces cerevisiae	[ui:ypr033c] [pn:histidine--tma ligase, mitochondrial:histidyl-tma synthetase, mitochondrial precursor:histidine--tma ligase:hisrl] [gn:hts1:yp3367] [gicfc:5.11:10.1:10.2:10.6] [ec:6.1.1.2] [keggfc:5.11:10.1:10.2] [sgdgc:5.4.0:9.2]

CONTIG1853	33383541_f3_1	4081	18184	1074	358	YER125W	387	5.0(10)-35	Saccharomyces cerevisiae	[ui:yer125w] [pn:ubiquitin-protein ligase:rsp5 protein] [gn:rsp5,np11:sgyp-orf41] [gicfc:5.14.5.9:10.11:10.7:11.1:12.1 5:13.2] [ec:6.3.2.-] [keggfc:5.9.5.14] [sgdfc:3.4.0:6.3.0:6.5.1:9.1.0:11.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG3384	11853377_f3_6	4082	18185	702	234	YER125W	373	1.6(10)-33	Saccharomyces cerevisiae	[ui:yer125w] [pn:ubiquitin-protein ligase:rsp5 protein] [gn:rsp5,np11:sgyp-orf41] [gicfc:5.14.5.9:10.11:10.7:11.1:12.1 5:13.2] [ec:6.3.2.-] [keggfc:5.9.5.14] [sgdfc:3.4.0:6.3.0:6.5.1:9.1.0:11.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG3384	14276538_f1_2	4083	18186	267	89	YER125W	272	1.2(10)-22	Saccharomyces cerevisiae	[ui:yer125w] [pn:ubiquitin-protein ligase:rsp5 protein] [gn:rsp5,np11:sgyp-orf41] [gicfc:5.14.5.9:10.11:10.7:11.1:12.1 5:13.2] [ec:6.3.2.-] [keggfc:5.9.5.14] [sgdfc:3.4.0:6.3.0:6.5.1:9.1.0:11.1.0] [db:gic-saccharomyces cerevisiae]

CONTIG4226	20798943_c3_11	4084	18187	1395	465	YER125W	2064	4.9(10)-218	Saccharomyces cerevisiae	[ui:yer125w] [pn:ubiquitin-protein ligase:rsp5 protein] [gn:rsp5,np11:sygp-orf41] [gfcfc:5.14;5.9;10.11;10.7;11.1;12.1 5;13.2] [ec:6.3.2.-] [keggfc:5.9;5.14] [sgdfc:3.4.0;6.3.0;6.5.1;9.1.0;11.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG901	597177_f3_3	4085	18188	333	111	YER125W	207	1.1(10)-15	Saccharomyces cerevisiae	[ui:yer125w] [pn:ubiquitin-protein ligase:rsp5 protein] [gn:rsp5,np11:sygp-orf41] [gfcfc:5.14;5.9;10.11;10.7;11.1;12.1 5;13.2] [ec:6.3.2.-] [keggfc:5.9;5.14] [sgdfc:3.4.0;6.3.0;6.5.1;9.1.0;11.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG3410	21882942_c1_8	4086	18189	465	155	YHR068W	509	6.9(10)-49	Saccharomyces cerevisiae	[ui:yhr068w] [pn:deoxyhypusine synthase] [gn:dys1] [gfcfc:5.14;6.6] [ec:1.5.1.-1[keggfc:5.1.14] [sgdfc:1.1.1] [db:gic-saccharomyces cerevisiae]
CONTIG4466	7073431_f2_3	4087	18190	630	210	YHR068W	662	4.2(10)-65	Saccharomyces cerevisiae	[ui:yhr068w] [pn:deoxyhypusine synthase] [gn:dys1] [gfcfc:5.14;6.6] [ec:1.5.1.-1[keggfc:5.1.14] [sgdfc:1.1.1] [db:gic-saccharomyces cerevisiae]
CONTIG5378	24417330_f1_1	4088	18191	1527	509	YBR166C	1480	8.8(10)-152	Saccharomyces cerevisiae	[ui:ybr166c] [pn:phenylalanine dehydrogenase:nadp+·prdh] [gn:tyr1,ybr1218] [gfcfc:5.1.5;6.6] [ec:1.3.1.13] [keggfc:5.1.15] [sgdfc:1.1.1;9.2.0] [db:gic-saccharomyces cerevisiae]

CONTIG3412	I4642827_c2_4	4089	18192	1113	371	YBR249C	1135	3.2(10)-115	Saccharomyces cerevisiae	[ui:ybr249c] [pn:2-dehydro-3-deoxyphosphoheptonate aldolase, tyrosine-inhibited:phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited:phospho-2-keto-3-deoxyheptonate aldolase:dahp synthetase:3-deoxy-d-arabinohexitulosonate 7-
CONTIG245	867061_f2_1	4090	18193	537	179	YDR035W	694	1.7(10)-68	Saccharomyces cerevisiae	[ui:ydr035w] [pn:2-dehydro-3-deoxyphosphoheptonate aldolase, phenylalanine-inhibited:phospho-2-dehydro-3-deoxyheptonate aldolase, phenylalanine-inhibited:phospho-2-keto-3-deoxyheptonate aldolase:dahp synthetase:3-deoxy-d-arabinohexitulosonate 7-
b9x11u19.y	12324218_c1_3	4091	18194	435	145	YDR035W	156	8.3(10)-11	Saccharomyces cerevisiae	[ui:ydr035w] [pn:2-dehydro-3-deoxyphosphoheptonate aldolase, phenylalanine-inhibited:phospho-2-dehydro-3-deoxyheptonate aldolase, phenylalanine-inhibited:phospho-2-keto-3-deoxyheptonate aldolase:dahp synthetase:3-deoxy-d-arabinohexitulosonate 7-

CONTIG2409	31878755_f1_1	4092	18195	828	276	YDR127W	695	2.6(10)-67	Saccharomyces cerevisiae	[ui:ydr127w] [pn:arom pentafunctional enzyme:pentafunctional arom polypeptide:contains:3- dehydroquinate synthase , 3- dehydroquinate dehydratase:3- dehydroquinase , shikimate 5- dehydrogenase , shikimate kinase , and esp synthase] [gn:ar
CONTIG539	16281957_f3_1	4093	18196	801	267	YDR127W	663	6.7(10)-64	Saccharomyces cerevisiae	[ui:ydr127w] [pn:arom pentafunctional enzyme:pentafunctional arom polypeptide:contains:3- dehydroquinate synthase , 3- dehydroquinate dehydratase:3- dehydroquinase , shikimate 5- dehydrogenase , shikimate kinase , and esp synthase] [gn:ar
CONTIG539	20437904_c2_3	4094	18197	1266	422	YDR127W	1384	1.3(10)-141	Saccharomyces cerevisiae	[ui:ydr127w] [pn:arom pentafunctional enzyme:pentafunctional arom polypeptide:contains:3- dehydroquinate synthase , 3- dehydroquinate dehydratase:3- dehydroquinase , shikimate 5- dehydrogenase , shikimate kinase , and esp synthase] [gn:ar
CONTIG2181	20833425_s2_5	4095	18198	1140	380	YDR354W	539	1.7(10)-61	Saccharomyces cerevisiae	[ui:ydr354w] [pn:anthranilate phosphoribosyltransferase] [gn:trp4-d9476] [gicfc:5.15:6.6] [ec:2.4.2.18] [keggfc:5.15] [sgdc:1.1:9.2.0] [db:gicsaccharomyces cerevisiae]

CONTIG3009	10392192_c3_7	4096	18199	906	302	YER090W	1123	5.9(10)-114	Saccharomyces cerevisiae	[ui:yer090w] [pn:anthranilate synthase component j] [gn:trp2] [gtcfc:5.15:6.6:9.12] [ec:4.1.3.27] [keggfc:5.15:9.13] [sgdic:1.1.1:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5248	14647587_c3_10	4097	18200	651	217	YER090W	471	7.2(10)-45	Saccharomyces cerevisiae	[ui:yer090w] [pn:anthranilate synthase component j] [gn:trp2] [gtcfc:5.15:6.6:9.12] [ec:4.1.3.27] [keggfc:5.15:9.13] [sgdic:1.1.1:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG724	35194191_c2_3	4098	18201	942	314	YFL022C	652	4.7(10)-64	Saccharomyces cerevisiae	[ui:yfl022c] [pn:phenylalanine--tma ligase beta chain, cytosolic:phenylalanyl-tRNA synthetase beta chain cytoplasmic:phenylalanine--tRNA ligase beta chain] [gn:fns2] [gtcfc:5.15:10.6] [ec:6.1.1.20] [keggfc:5.15:10.1:10.2] [sgdfc:5.4.
CONTIG5335	129161_c2_15	4099	18202	1080	360	YGL148W	1135	3.2(10)-115	Saccharomyces cerevisiae	[ui:ygl148w] [pn:chorismate synthase:5-enolpyruvylshikimate-3-phosphate phosphoholayse] [gn:aro2] [gtcfc:5.15:6.6] [ec:4.6.1.4] [keggfc:5.15] [sgdic:1.1.1:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5464	24033510_f2_7	4100	18203	288	96	YGL148W	146	1.1(10)-9	Saccharomyces cerevisiae	[ui:ygl148w] [pn:chorismate synthase:5-enolpyruvylshikimate-3-phosphate phosphoholayse] [gn:aro2] [gtcfc:5.15:6.6] [ec:4.6.1.4] [keggfc:5.15] [sgdic:1.1.1:9.2.0] [db:gic-saccharomyces cerevisiae]

CONTIG5088	14188317_f2_1	4101	18204	1644	548	YGL026C	2224	1.3(10)-230	Saccharomyces cerevisiae	[ui:ygl026c] [pn:tryptophan synthase] [gn:trp5] [gicfc:5.15.6.6] [ec:4.2.1.20] [keggfc:5.15] [sgdgc:1.1.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3493	24331527_f3_2	4102	18205	1038	346	YGR185C	1228	4.4(10)-125	Saccharomyces cerevisiae	[ui:ygr185c] [pn:tyrosyl-tRNA synthetase, cytoplasmic:tyrosyl-tRNA ligase:tyrsl] [gn:tyrl.mgn104:g7522] [gicfc:5.15:10.6] [ec:6.1.1.1] [keggfc:5.15:10.1:10.2] [sgdgc:5.4.0:9.2.0] [db:gtc-saccharomyces cerevisi]
CONTIG712	197291_c3_5	4103	18206	324	108	YGR185C	148	7.2(10)-10	Saccharomyces cerevisiae	[ui:ygr185c] [pn:tyrosyl-tRNA synthetase:tyrosyl-tRNA ligase:tyrsl] [gn:tyrl.mgn104:g7522] [gicfc:5.15:10.6] [ec:6.1.1.1] [keggfc:5.15:10.1:10.2] [sgdgc:5.4.0:9.2.0] [db:gtc-saccharomyces cerevisi]
CONTIG2552	195312_B_4	4104	18207	1050	350	YKL211C	799	1.3(10)-79	Saccharomyces cerevisiae	[ui:ykl211c] [pn:anthranilate synthase component ii:contains:glutamine amidotransferase:indole-3-glycerol phosphate synthase:pral] [gn:trp3] [gicfc:5.15:6.6:9.12] [keggfc:5.15:9.13] [sgdgc:1.1.1:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG735	2914843_c1_3	4105	18208	285	95	YKL211C	203	1.1(10)-15	Saccharomyces cerevisiae	[ui:ykl211c] [pn:anthranilate synthase component ii:contains:glutamine amidotransferase:indole-3-glycerol phosphate synthase:pral] [gn:trp3] [gtcfc:5.15:6.6:9.12] [keggfc:5.15:9.13] [sgdfc:1.1.1:9.2:0] [db:gic-saccharomyces cerevisiae]
CONTIG2916	9877291_f2_1	4106	18209	723	241	YLR060W	781	1.0(10)-77	Saccharomyces cerevisiae	[ui:ylr060w] [pn:phenylalanyl-tRNA synthetase, alpha subunit, cytosolic:phenylalanyl-tRNA synthetase alpha chain cytoplasmic:phenylalanine-tRNA ligase alpha chain:phers] [gn:frs1:121651] [gtcfc:5.15:10.6] [ec:6.1.1.20] [keggfc:5.15:10]
CONTIG2916	22690962_f2_2	4107	18210	258	86	YLR060W	278	1.3(10)-23	Saccharomyces cerevisiae	[ui:ylr060w] [pn:phenylalanyl-tRNA synthetase, alpha subunit, cytosolic:phenylalanyl-tRNA synthetase alpha chain cytoplasmic:phenylalanine-tRNA ligase alpha chain:phers] [gn:frs1:121652] [gtcfc:5.15:10.6] [ec:6.1.1.20] [keggfc:5.15:10]
CONTIG5007	9879376_f3_5	4108	18211	807	269	YLR060W	879	4.2(10)-88	Saccharomyces cerevisiae	[ui:ylr060w] [pn:phenylalanyl-tRNA synthetase, alpha subunit, cytosolic:phenylalanyl-tRNA synthetase alpha chain cytoplasmic:phenylalanine-tRNA ligase alpha chain:phers] [gn:frs1:121653] [gtcfc:5.15:10.6] [ec:6.1.1.20] [keggfc:5.15:10]

CONTIG5142	24398452_f3_3	4109	18212	801	267	YNL316C	237	8.0(10)-30	Saccharomyces cerevisiae	[ui:ynl316c] [pn:prephenate dehydratase;pd1] [gn:pha2;n0351] [gicfc:5.15;6.6] [ec:4.2.1.51] [keggfc:5.15] [sgdfc:1.1.1.9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5677	16582932_c3_27	4110	18213	948	316	YPR060C	807	1.8(10)-80	Saccharomyces cerevisiae	[ui:ypr060c] [pn:chorismate mutase;cm] [gn:aro7;yp4991] [gicfc:5.1;6.6] [ec:5.4.99.5] [keggfc:5.15] [sgdfc:1.1.1.9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5792	4788128_f1_4	4111	18214	1281	427	YDR300C	1190	4.7(10)-121	Saccharomyces cerevisiae	[ui:ydr300c] [pn:glutamate 5-kinase;gamma-glutamyl kinase;gk] [gn:pro1_d9740] [gicfc:5.16;6.6] [ec:2.7.2.11] [keggfc:5.16] [sgdfc:1.1.9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG1365	789078_c3_2	4112	18215	849	283	YOR323C	781	1.0(10)-77	Saccharomyces cerevisiae	[ui:yor323c] [pn:gamma-glutamyl phosphate reductase;grp;glutamate-5-semialdehyde dehydrogenase] [gn:pro2_o6155] [gicfc:5.16;6.6;9.10] [ec:1.2.1.41] [keggfc:5.16;9.10] [sgdfc:1.1.1] [db:gic-sa]

CONTIG3268	21675425_f3_4	4113	18216	327	109	YCR323C	150	5.7(10)-10	Saccharomyces cerevisiae	[uiyot323c] [pn:gamma-glutamyl phosphate reductase;grp:glutamate-5-semialdehyde dehydrogenase] [gn:pro2.06155] [gicfc:5.16:6:6:9.10] [ec:1.2.1.41] [keggfc:5.16:9.10] [sgdfc:1.1.1] [db:gic-sa]
CONTIG4888	36516688_f1_1	4114	18217	963	321	YHR019C	836	9.3(10)-90	Saccharomyces cerevisiae	[uiyhr019c] [pn:asparaginyl-tRNA synthetase;putative asparagine-tRNA synthetase;asparagine--tRNA ligase;asmrsl] [gn:ded81] [gicfc:5.2:10.6] [ec:6.1.1.22] [keggfc:5.2:10.1:10.2] [sgdfc:5.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG4888	2766578_f3_3	4115	18218	654	218	YHR019C	887	6.0(10)-89	Saccharomyces cerevisiae	[uiyhr019c] [pn:asparaginyl-tRNA synthetase;putative asparagine-tRNA synthetase;asparagine--tRNA ligase;asmrsl] [gn:ded81] [gicfc:5.2:10.6] [ec:6.1.1.22] [keggfc:5.2:10.1:10.2] [sgdfc:5.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG4106	53942_c1_5	4116	18219	564	188	YLL018C	741	1.8(10)-73	Saccharomyces cerevisiae	[uiyll018c] [pn:aspartyl-tRNA synthetase, cytosolic;aspartyl-tRNA synthetase, cytoplasmic;aspartate-tRNA ligase;asp1s] [gn:dps1:aps1:11295] [gicfc:5.2:10.6] [ec:6.1.1.12] [keggfc:5.2:10.1:10.2] [sgdfc:5.4.0:9.2.0] [db:gic-saccha

CONTIG4495	21751587_f2_2	4117	18220	1221	407	YLL018C	741	1.8(10)-73	Saccharomyces cerevisiae	[ui:yl 018c] [pn:aspartyl-tRNA synthetase, cytosolic:aspartyl-tRNA synthetase, cytoplasmic:aspartate-tRNA ligase:aspirs] [gn:dps1:aps1:aps1 l1295] [gtcfc:5.2:10.6] [ec:6.1.1.12] [keggfc:5.2:10.1:10.2] [sgdgc:5.4.0:9.2.0] [db:gtc-saccha
CONTIG2325	26172812_c3_4	4118	18221	372	124	YCR335C	327	2.0(10)-28	Saccharomyces cerevisiae	[ui:yor335c] [pn:alanyl-tRNA synthetase, cytosolic:alanyl-tRNA synthetase, cytoplasmic:alanine-tRNA ligase:alars] [gn:ala1] [gtcfc:5.2:10.6:11.1] [ec:6.1.1.7] [keggfc:5.2:10.1:10.2] [sgdgc:5.4.0:9.1.0] [db:gtc-saccharomyces cerevisiae
CONTIG2325	25636942_c3_3	4119	18222	300	100	YCR335C	180	1.1(10)-12	Saccharomyces cerevisiae	[ui:yor335c] [pn:alanyl-tRNA synthetase, cytosolic:alanyl-tRNA synthetase, cytoplasmic:alanine-tRNA ligase:alars] [gn:ala1] [gtcfc:5.2:10.6:11.1] [ec:6.1.1.7] [keggfc:5.2:10.1:10.2] [sgdgc:5.4.0:9.1.0] [db:gtc-saccharomyces cerevisiae
CONTIG4725	25572577_c2_5	4120	18223	1452	484	YCR335C	1566	6.7(10)-161	Saccharomyces cerevisiae	[ui:yor335c] [pn:alanyl-tRNA synthetase, cytosolic:alanyl-tRNA synthetase, cytoplasmic:alanine-tRNA ligase:alars] [gn:ala1] [gtcfc:5.2:10.6:11.1] [ec:6.1.1.7] [keggfc:5.2:10.1:10.2] [sgdgc:5.4.0:9.1.0] [db:gtc-saccharomyces cerevisiae

b9x12989.y	11751013_c3_3	4121	18224	531	177	YOR335C	621	3.2(10)-60	Saccharomyces cerevisiae	[ui:yor335c] [pn:alanyl-tRNA synthetase, cytosolic:alanyl-tRNA synthetase, cytoplasmic:alanine--tRNA ligase:alars] [gn:alal] [gicfc:5.2:10.6:11.1] [ec:6.1.1.7] [keggfc:5.2:10.1:10.2] [sgdic:5.4.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
b2x13837.x	20912902_c3_2	4122	18225	444	148	YBR121C	408	1.2(10)-37	Saccharomyces cerevisiae	[ui:ybr121c] [pn:glycyl-tRNA synthetase;glycine--tRNA ligase:glyrs] [gn:grs1:ybr0917] [gicfc:5.3:10.6] [ec:6.1.1.14] [keggfc:5.3:10.1:10.2] [sgdfc:5.4.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2090	5870969_c1_4	4123	18226	1386	462	YBR121C	1357	9.5(10)-139	Saccharomyces cerevisiae	[ui:ybr121c] [pn:glycyl-tRNA synthetase;glycine--tRNA ligase:glyrs] [gn:grs1:ybr0917] [gicfc:5.3:10.6] [ec:6.1.1.14] [keggfc:5.3:10.1:10.2] [sgdfc:5.4.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4690	34398402_f3_3	4124	18227	1122	374	YCL064C	520	4.7(10)-50	Saccharomyces cerevisiae	[ui:ycl064c] [pn:l-serine/l-threonine deaminase;catabolic l-serine dehydratase;l-serine deaminase / l-threonine dehydratase;l-threonine deaminase] [gn:ch1:ycl64c] [gicfc:5.3.5] [keggfc:5.3.5.5] [sgdfc:1.1.4] [db:gtc-saccharomyces_c]

CONTIG5213	4687875_f2_6	4125	18228	1164	388	YCL064C	435	4.7(10)-41	Saccharomyces cerevisiae	[ui:ycl064c] [pn:l-serine/l-threonine deaminase:catabolic l-serine dehydratase:l-serine deaminase /l-threonine dehydratase:l-serine deaminase:[gn:chal:yel64c] [gicfc:5.3.5.5] [keggfc:5.3.5.5] [sgdfc:1.1.4] [db:gic-saccharomyces cerevisiae]
CONTIG1064	12926676_f2_1	4126	18229	531	177	YCR053W	530	4.0(10)-51	Saccharomyces cerevisiae	[ui:ycr053w] [pn:o-p-homoserine p-lyase:threonine synthase] [gn:thr4.ycr53w] [gicfc:5.3.6.6:9.3] [ec:4.2.99.2] [keggfc:5.3.9.3] [sgdfc:1.1.1:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG3063	12926676_f3_2	4127	18230	303	101	YCR053W	243	5.7(10)-20	Saccharomyces cerevisiae	[ui:ycr053w] [pn:o-p-homoserine p-lyase:threonine synthase] [gn:thr4.ycr53w] [gicfc:5.3.6.6:9.3] [ec:4.2.99.2] [keggfc:5.3.9.3] [sgdfc:1.1.1:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5366	30603762_f1_1	4128	18231	1071	357	YCR053W	1123	5.9(10)-114	Saccharomyces cerevisiae	[ui:ycr053w] [pn:o-p-homoserine p-lyase:threonine synthase] [gn:thr4.ycr53w] [gicfc:5.3.6.6:9.3] [ec:4.2.99.2] [keggfc:5.3.9.3] [sgdfc:1.1.1:9.2.0] [db:gic-saccharomyces cerevisiae]

CONTIG1772	1562_f2_2	4129	18232	1077	359	YDR023W	1242	1.5(10)-126	Saccharomyces cerevisiae	[ui:ydr023w] [pn:seryl-trna synthetase, cytosolic:seryl-trna synthetase, cytoplasmic:serine-- tRNA ligases:seryl [gn:ses1:ser:yd9813] [gicfc:5.3:10.6] [ec:6.1.1.11] [keggc:5.3:10.1:10.2] [sgdfc:5.4:0.9:2.0] [db:gic-saccharomyces cer]
CONTIG4014	34197502_c2_9	4130	18233	774	258	YDR158W	878	5.4(10)-88	Saccharomyces cerevisiae	[ui:ydr158w] [pn:aspartate-semialdehyde dehydrogenase:asa dehydrogenase:asa dh] [gn:hom2:yd8358] [gicfc:5.3:5.8:6.6] [ec:1.2.1.11] [keggfc:5.3:5.8] [sgdfc:1.1.1] [db:gic-saccharomyces cerevisiae]
CONTIG533	859627_f1_1	4131	18234	324	108	YDR158W	295	3.2(10)-26	Saccharomyces cerevisiae	[ui:ydr158w] [pn:aspartate-semialdehyde dehydrogenase:asa dehydrogenase:asa dh] [gn:hom2:yd8358] [gicfc:5.3:5.8:6.6] [ec:1.2.1.11] [keggfc:5.3:5.8] [sgdfc:1.1.1] [db:gic-saccharomyces cerevisiae]
CONTIG4049	10548137_c1_3	4132	18235	1647	549	YER052C	1470	1.0(10)-150	Saccharomyces cerevisiae	[ui:yer052c] [pn:-aspartate-4-p-transf erase:aspartokinase:aspartate kinase] [gn:hom3] [gicfc:5.3:5.8:6.6] [ec:2.7.2.4] [keggfc:5.3:5.8] [sgdfc:1.1.1] [db:gic-saccharomyces cerevisiae]

CONTIG2043	14563786_c2_4	4133	18236	633	211	YER081W	787	2.3(10)-78	Saccharomyces cerevisiae	[ui:yer081w] [pn:strong similarity to phosphoglycerate dehydrogenases;putative d-3-phosphoglycerate dehydrogenase [gicfc:5.3.6.6] [ec:1.1.1.95] [keggfc:5.3] [sgdfc:1.1.1] [db:gic-saccharomyces cerevisiae]
CONTIG4919	2930192_f3_5	4134	18237	183	61	YER081W	119	1.3(10)-6	Saccharomyces cerevisiae	[ui:yer081w] [pn:strong similarity to phosphoglycerate dehydrogenases;putative d-3-phosphoglycerate dehydrogenase [gicfc:5.3.6.6] [ec:1.1.1.95] [keggfc:5.3] [sgdfc:1.1.1] [db:gic-saccharomyces cerevisiae]
CONTIG5749	24414063_c3_24	4135	18238	1557	519	YGR155W	981	6.5(10)-99	Saccharomyces cerevisiae	[ui:ygr155w] [pn:cystathione beta-synthase;serine sulfhydrylase;beta-thionase] [gn:cys4;stu4;g66667] [gicfc:5.3.5.4.6.4.6.6] [ec:4.2.1.22] [keggfc:5.3.5.4.6.4] [sgdfc:1.1.1] [db:gic-saccharomyces cerevisiae]
CONTIG4612	3960825_f1_1	4136	18239	603	201	YGR208W	532	2.5(10)-51	Saccharomyces cerevisiae	[ui:ygr208w] [pn:phosphoserine phosphatase;o-phosphoserine phosphohydrolase;psp] [gn:ser2;g7744] [gicfc:5.3.6.3.6.6] [ec:3.1.3.3] [keggfc:5.3] [sgdfc:1.1.1;16.0.0] [db:gic-saccharomyces cerevisiae]

b3x16033.y	11855379_c2_4	4137	18240	738	246	YGR208W	118	6.4(10)-5	Saccharomyces cerevisiae	[ui:gr208w] [pn:phosphoserine phosphatase:o-phosphoserine phosphohydrolase;psp] [gn:ser2,g7744] [gtcfc:5.3:6.3:6.6] [ec:3.1.3.3] [keggfc:5.3] [sgdgc:1.1.1:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5780	14876562_c3_38	4138	18241	288	96	YHR011W	227	2.2(10)-18	Saccharomyces cerevisiae	[ui:yhr011w] [pn:seryl-tRNA synthetase;putative seryl-tRNA synthetase yhr011 w:serine--tRNA ligase;seryl] [gtcfc:5.3:10.6] [ec:6.1.1.11] [keggfc:5.3:10.1:10.2] [sgdgc:5.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5780	25635056_c2_32	4139	18242	1296	432	YHR011W	768	2.5(10)-76	Saccharomyces cerevisiae	[ui:yhr011w] [pn:seryl-tRNA synthetase;putative seryl-tRNA synthetase yhr011 w:serine--tRNA ligase;seryl] [gtcfc:5.3:10.6] [ec:6.1.1.11] [keggfc:5.3:10.1:10.2] [sgdgc:5.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3817	10937590_f1_1	4140	18243	1194	398	YHR025W	981	6.5(10)-99	Saccharomyces cerevisiae	[ui:yhr025w] [pn:homoserine kinase:hk] [gn:thr1] [gtcfc:5.3:6.6] [ec:2.7.1.39] [keggfc:5.3] [sgdgc:1.1.1] [db:gtc-saccharomyces cerevisiae]

CONTIG1776	4803801_f1_1	4141	18244	312	104	YII078W	219	4.7(10)-17	Saccharomyces cerevisiae	[ui:yi 078w] [pn:threonyl tRNA synthetase, cytosolic:threonyl-tRNA synthetase, cytoplasmic:threonine--tRNA ligase:thrs] [gn:ths1] [gtcfc:5.3:10.6] [ec:6.1.1.3] [keggc:5.3:10.1:10.2] [sgdgc:5.4.0:9.2.0] [db:gtc-saccharomyces cerevisi]
CONTIG3658	16972257_c2_11	4142	18245	813	271	YII078W	865	1.3(10)-86	Saccharomyces cerevisiae	[ui:yi 078w] [pn:threonyl tRNA synthetase, cytosolic:threonyl-tRNA synthetase, cytoplasmic:threonine--tRNA ligase:thrs] [gn:ths1] [gtcfc:5.3:10.6] [ec:6.1.1.3] [keggc:5.3:10.1:10.2] [sgdgc:5.4.0:9.2.0] [db:gtc-saccharomyces cerevisi]
CONTIG3658	35429656_c1_9	4143	18246	1068	356	YII078W	1331	5.4(10)-136	Saccharomyces cerevisiae	[ui:yi 078w] [pn:threonyl tRNA synthetase, cytosolic:threonyl-tRNA synthetase, cytoplasmic:threonine--tRNA ligase:thrs] [gn:ths1] [gtcfc:5.3:10.6] [ec:6.1.1.3] [keggc:5.3:10.1:10.2] [sgdgc:5.4.0:9.2.0] [db:gtc-saccharomyces cerevisi]
CONTIG5160	24306512_f1_2	4144	18247	1083	361	YJR139C	1083	1.0(10)-109	Saccharomyces cerevisiae	[ui:yr 139c] [pn:homoserine dehydrogenase:hdh] [gn:hom6 2132] [gtcfc:5.3:5.8:6.6] [ec:1.1.1.3] [keggc:5.3:5.8] [sgdgc:1.1.1] [db:gtc-saccharomyces cerevisiae]

CONTIG3353	33382660_f2_1	4145	18248	1197	399	YOR184W	1140	9.4(10)-116	Saccharomyces cerevisiae	[ui:yor184w] [pn:phosphoserine transaminase:phosphoserine aminotransferase] [gn:ser1.serc] [gicfc:5.3:6.6.9.10.9.11.9.3] [ec:2.6.1.52] [keggfc:5.3:9.3] [sgdfc:1.1.1.1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3295	782752_f3_4	4146	18249	582	194	YAL044C	351	3.7(10)-32	Saccharomyces cerevisiae	[ui:yal044c] [pn:strong similarity to human glycine cleavage system protein h:glycine cleavage system h protein precursor] [gn:gcv3:fun40] [gicfc:5.3] [keggfc:14.2] [sgdfc:1.1.4] [db:gtc-saccharomyces cerevisiae]
CONTIG2235	16287662_f1_1	4147	18250	1284	428	YBR006W	1007	1.2(10)-101	Saccharomyces cerevisiae	[ui:ybr006w] [pn:strong similarity to e.coli succinate semialdehyde dehydrogenase:hypothetical aldehyde-dehydrogenase like protein in coq1- hhf1 intergenic region] [gn:ybr0112] [gicfc:5.3] [keggfc:14.2] [sgdfc:1.1.4] [db:gtc-saccharom
CONTIG4997	15041078_o3_4	4148	18251	1464	488	YBR006W	1251	1.6(10)-127	Saccharomyces cerevisiae	[ui:ybr006w] [pn:strong similarity to e.coli succinate semialdehyde dehydrogenase:hypothetical aldehyde-dehydrogenase like protein in coq1- hhf1 intergenic region] [gn:ybr0112] [gicfc:5.3] [keggfc:14.2] [sgdfc:1.1.4] [db:gtc-saccharom
CONTIG5770	33985702_f3_12	4149	18252	807	269	YDR272W	665	2.0(10)-65	Saccharomyces cerevisiae	[ui:ydt272w] [pn:glyoxalase ii:hydroxyacylglutathione hydrolase] [gn:glo2] [gicfc:5.3] [keggfc:14.2] [sgdfc:1.1.4] [db:gtc-saccharomyces cerevisiae]

CONTIG4221	16829635_c3_5	4150	18253	579	193	YDR294C	473	4.5(10)-45	Saccharomyces cerevisiae	[ui:yd294c] [pn:similarity to glutamate decarboxylases] [gtfc:5.3] [keggfc:14.2] [sgdfc:1.1.4] [db:gtc-saccharomyces cerevisiae]
CONTIG4387	3937762_f3_3	4151	18254	1263	421	YDR294C	1007	1.2(10)-101	Saccharomyces cerevisiae	[ui:yd294c] [pn:similarity to glutamate decarboxylases] [gtfc:5.3] [keggfc:14.2] [sgdfc:1.1.4] [db:gtc-saccharomyces cerevisiae]
CONTIG5700	9940637_f2_6	4152	18255	1173	391	YDR502C	1390	3.0(10)-142	Saccharomyces cerevisiae	[ui:yd502c] [pn:s-adenosylmethionine synthetase 2:methionine adenosyltransferase 2: 2:admet synthetase 2] [gn:am2.eth2:d9719] [gtfc:5.3:5.4:6.4] [ec:2.5.1.6] [keggfc:5.4:6.4] [sgdfc:1.1.4] [db:gtc-saccharomyces cerevisiae]
CONTIG3645	35156338_f3_2	4153	18256	267	89	YGL202W	100	0.00016	Saccharomyces cerevisiae	[ui:yg]202w] [pn:similarity to rat kynurene/alpha-aminoadipate aminotransferase:hypothetical 56.2 kd protein in kex1-mcm6 intergenic region] [gtfc:5.3] [keggfc:14.2] [sgdfc:1.1.4] [db:gtc-saccharomyces cerevisiae]
CONTIG5645	6250_f3_13	4154	18257	1200	400	YGL202W	1076	5.7(10)-109	Saccharomyces cerevisiae	[ui:yg]202w] [pn:similarity to rat kynurene/alpha-aminoadipate aminotransferase:hypothetical 56.2 kd protein in kex1-mcm6 intergenic region] [gtfc:5.3] [keggfc:14.2] [sgdfc:1.1.4] [db:gtc-saccharomyces cerevisiae]

CONTIG4646	19765817_f1_1	4155	18258	1524	508	YHR137W	758	5.2(10)-81	Saccharomyces cerevisiae	[ui:yr137w] [pn:similarity to rat kynurenine/alpha-amino adipate aminotransferase;hypothetical 58.5 kd protein in yck1-sps100 intergenic region] [gicfc:5.3] [keggfc:14.2] [sgdfc:1.1.4] [db:gic-saccharomyces cerevisiae]
CONTIG5291	24666030_f3_8	4156	18259	624	208	YIL042C	145	4.9(10)-12	Saccharomyces cerevisiae	[ui:yl042c] [pn:similarity to rat branched-chain alpha-ketoacid dehydrogenase kinase;hypothetical 45.4 kd protein in cbz5-not3 intergenic region] [gicfc:5.3] [keggfc:14.2] [sgdfc:1.1.4] [db:gic-saccharomyces cerevisiae]
CONTIG4157	26618825_c3_5	4157	18260	414	138	YJR025C	434	6.0(10)-41	Saccharomyces cerevisiae	[ui:yr025c] [pn:3-hydroxyanthranilic acid dioxygenase;hypothetical 20.2 kd protein in met2-cpi7 intergenic region] [gn:had1;j1550] [gicfc:5.3:9.10:9.11] [keggfc:14.2] [sgdfc:1.1.4:1.7.1] [db:gic-saccharomyces cerevisiae]
CONTIG5793	24068887_c1_16	4158	18261	1470	490	YJR078W	923	9.3(10)-93	Saccharomyces cerevisiae	[ui:yr078w] [pn:similarity to mammalian indoleamine 2,3-dioxygenase;hypothetical 50.8 kd protein in mir1-stc18 intergenic region] [gn:j1840] [gicfc:5.3:9.10:9.11] [keggfc:14.2] [sgdfc:1.1.4:1.7.1] [db:gic-saccharomyces cerevisiae]

CONTIG2892	32657886_f1_1	4159	18262	666	222	YLR231C	570	2.3(10)-55	Saccharomyces cerevisiae	[uii.ylr231c] [pni:strong similarity to rat kynureninase] [gtfc:5.3:9.10:9.11] [keggfc:14.2] [sgdfc:1.1.4:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3178	29503250_f1_1	4160	18263	894	298	YLR231C	575	7.0(10)-56	Saccharomyces cerevisiae	[uii.ylr231c] [pni:strong similarity to rat kynureninase] [gtfc:5.3:9.10:9.11] [keggfc:14.2] [sgdfc:1.1.4:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3512	2197892_f3_6	4161	18264	1548	516	YER043C	1943	7.5(10)-201	Saccharomyces cerevisiae	[uii.yer043c] [pns:s-adenosyl-l-homocysteine hydrolase;adenosylhomocysteinase:s-adenosyl-l- homocysteine hydrolase:adohcyase] [gn:sah1] [gtfc:5.4:6.4:9.10:9.11] [ec:3.3.1.1] [keggfc:5.4:6.4] [sgdfc:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG537	7070306_f2_2	4162	18265	2310	770	YER091C	3015	0	Saccharomyces cerevisiae	[uii.yer091c] [pni:5-methyltetrahydropteroylglutamate--homocysteine methyltransferase:5-methyltetrahydropteroylglutamate--homocysteine s-methyltransferase:methionine synthase, vitamin-b12 independent isozyme:delta-p8 protein] [gn:

CONTIG5637	14954837_c2_22	4163	18266	957	319	YGR264C	1136	2.5(10)-115	Saccharomyces cerevisiae	[ui:ygr264c] [pn:methionyl-tRNA synthetase;methionyl-tRNA synthetase, cytoplasmic;methionine-tRNA ligase;mers] [gn:mes1] [gcfc:5.4:6.4:10.6] [ec:6.1.1.10] [keggc:5.4:6.4:10.1:10.2] [sgdc:5.4.0:9.2:0] [db:gtc-saccharomyces cerevis
CONTIG5637	34189130_c1_17	4164	18267	813	271	YGR264C	1049	4.0(10)-106	Saccharomyces cerevisiae	[ui:ygr264c] [pn:methionyl-tRNA synthetase;methionyl-tRNA synthetase, cytoplasmic;methionine-tRNA ligase;mers] [gn:mes1] [gcfc:5.4:6.4:10.6] [ec:6.1.1.10] [keggc:5.4:6.4:10.1:10.2] [sgdc:5.4.0:9.2:0] [db:gtc-saccharomyces cerevis
CONTIG5637	21991557_c3_27	4165	18268	528	176	YGR264C	90	0.12	Saccharomyces cerevisiae	[ui:ygr264c] [pn:methionyl-tRNA synthetase;methionyl-tRNA synthetase, cytoplasmic;methionine-tRNA ligase;mers] [gn:mes1] [gcfc:5.4:6.4:10.6] [ec:6.1.1.10] [keggc:5.4:6.4:10.1:10.2] [sgdc:5.4.0:9.2:0] [db:gtc-saccharomyces cerevis

CONTIG3549	25507778_f3_4	4166	18269	468	156	YNL247W	319	9.4(10)-28	Saccharomyces cerevisiae	[ui:ynl247w] [pn:similarity to cysteinyl-tRNA synthetases;putative cysteinyl-tRNA synthetase c29e6_06c:cysteine-- tRNA ligase:cysrls [gn:n0885] [grfc:5.5:10.6] [ec:6.1.1.16] [keggc:5.5:10.1:10.2] [sgdfc:5.4.0] [db:gtc-saccharomyces]
CONTIG3792	34195290_c1_9	4167	18270	225	75	YNL247W	137	3.2(10)-8	Saccharomyces cerevisiae	[ui:ynl247w] [pn:similarity to cysteinyl-tRNA synthetases;putative cysteinyl-tRNA synthetase c29e6_06c:cysteine-- tRNA ligase:cysrls [gn:n0885] [grfc:5.5:10.6] [ec:6.1.1.16] [keggc:5.5:10.1:10.2] [sgdfc:5.4.0] [db:gtc-saccharomyces]
CONTIG3792	34616436_c2_12	4168	18271	1152	384	YNL247W	1083	1.0(10)-109	Saccharomyces cerevisiae	[ui:ynl247w] [pn:similarity to cysteinyl-tRNA synthetases;putative cysteinyl-tRNA synthetase c29e6_06c:cysteine-- tRNA ligase:cysrls [gn:n0885] [grfc:5.5:10.6] [ec:6.1.1.16] [keggc:5.5:10.1:10.2] [sgdfc:5.4.0] [db:gtc-saccharomyces]

CONTIG3792	35807828_c2_11	4169	18272	348	116	YNL247W	359	4.5(10)-32	Saccharomyces cerevisiae	[ui:ynl247w] [pn:similarity to cysteinyl-tRNA synthetases;putative cysteinyl-tRNA synthetase c29e6.06c:cysteine--tRNA ligase:cysrl] [gn:n0885] [gicfc:5..5;10.6] [ec:6.1.1.16] [keggfc:5..5;10.1;10.2] [sgdfc:5..4.0] [db:gtc-saccharomyces]
CONTIG5164	14470311_f3_5	4170	18273	1194	398	YJR148W	1260	1.8(10)-128	Saccharomyces cerevisiae	[ui:yjr148w] [pn:branched chain amino acid aminotransferase, cytosolic;putative branched-chain amino acid aminotransferase, cytosolic;boat] [gn:twn2;j2209] [gicfc:5..6;5..7;6;6;9..5] [ec:2.6.1.42] [keggfc:5..6;5..7;9..5] [sgdfc:1..1..9..2..0]
CONTIG3500	22710078_c2_12	4171	18274	648	216	YJR148W	589	2.2(10)-57	Saccharomyces cerevisiae	[ui:yjr148w] [pn:branched chain amino acid aminotransferase, cytosolic;putative branched-chain amino acid aminotransferase, cytosolic;boat] [gn:twn2;j2209] [gicfc:5..6;5..7;6;6;9..5] [ec:2.6.1.42] [keggfc:5..6;5..7;9..5] [sgdfc:1..1..9..2..0]
CONTIG1669	214583_c2_6	4172	18275	1008	336	YBL076C	1222	1.8(10)-124	Saccharomyces cerevisiae	[ui:ybl076c] [pn:isoleucyl-tRNA synthetase;isoleucyl-tRNA synthetase, cytoplasmic:isoleucine--tRNA ligase:ilrs] [gn:ils1;yb0734] [gicfc:5..7;10..6] [ec:6.1.1.5] [keggfc:5..7;10..1..10..2] [sgdfc:5..4..0..9..2..0] [db:gtc-saccharomyces cerevisiae]

b1x15324.x	34179687_c2_2	4173	18276	624	208	YBL076C	615	2.8(10)-59	Saccharomyces cerevisiae	[ui:yb1076c] [pn:isoleucyl-trna synthetase;isoleucyl-trna synthetase;isoleucyl-trna synthetase;cytoplasmic:isoleucine-- trna ligase;ilrs] [gn:ilrs] [yb10734]
										[tgtfc:5.7:10.6] [ec:6.1.1.5]
										[keggc:5.7:10.1:10.2]
										[sgdfc:5.4.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4072	11882662_f2_2	4174	18277	1137	379	YCL018W	1315	2.7(10)-134	Saccharomyces cerevisiae	[ui:ycl018w] [pn:beta-isopropylmalate dehydrogenase;3-isopropylmalate dehydrogenase;beta-ipm dehydrogenase;imdh3-ipm-dh]
										[gn:eu2:ycl18w] [gtcfc:5.7:6.6]
										[ec:1.1.1.85] [keggc:5.7]
										[sgdfc:1.1.1.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3855	19553175_c2_5	4175	18278	879	293	YGL009C	1136	2.5(10)-115	Saccharomyces cerevisiae	[ui:yg1009c] [pn:3-isopropylmalate dehydratase;isopropylmalate isomerase;alpha-ipm isomerase;ipni] [gn:leu1]
										[tgtfc:5.7:6.6] [ec:4.2.1.33]
										[keggc:5.7:1.1.1.9.2.0]
										[db:gtc-saccharomyces cerevisiae]
CONTIG4886	2197192_f1_1	4176	18279	1086	362	YGL009C	1146	2.2(10)-116	Saccharomyces cerevisiae	[ui:yg1009c] [pn:3-isopropylmalate dehydratase;isopropylmalate isomerase;alpha-ipm isomerase;ipni] [gn:leu1]
										[tgtfc:5.7:6.6] [ec:4.2.1.33]
										[keggc:5.7:1.1.1.9.2.0]
										[db:gtc-saccharomyces cerevisiae]

CONTIG5739	33757812_F2_11	4177	18280	705	235	YPL160W	533	2.2(10)-50	Saccharomyces cerevisiae	[ui:yp1160w] [pn:leucine--tma ligase, cytosolic:leucyl-tma synthetase, cytoplasmic:leucine-tma ligase:leurs] [gn:cdc60:p2564] [gtcfc:5.7:10.6] [ec:6.1.1.4] [keggfc:5.7:10.1:10.2] [sgdfc:5.4.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5382	11074_c1_12	4178	18281	2703	901	YPL160W	3034	0	Saccharomyces cerevisiae	[ui:yp1160w] [pn:leucine--tma ligase, cytosolic:leucyl-tma synthetase, cytoplasmic:leucine-tma ligase:leurs] [gn:cdc60:p2564] [gtcfc:5.7:10.6] [ec:6.1.1.4] [keggfc:5.7:10.1:10.2] [sgdfc:5.4.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3798	35203425_f1_1	4179	18282	462	154	YBR115C	375	2.8(10)-33	Saccharomyces cerevisiae	[ui:yp115c] [pn:l-aminoacidate-semialdehyde dehydrogenase, large subunit:aminoacidate-semialdehyde dehydrogenase large subunit:alpha-aminoacidate reductase:alpha-ar] [gn:lys2:ybr0910] [gtcfc:5.8:5.9:6.6] [ec:1.2.1.31] [keggfc:5.8:5.9]
CONTIG5782	898450_c2_23	4180	18283	1524	508	YBR115C	1484	3.2(10)-152	Saccharomyces cerevisiae	[ui:ybr115c] [pn:l-aminoacidate-semialdehyde dehydrogenase, large subunit:aminoacidate-semialdehyde dehydrogenase large subunit:alpha-aminoacidate reductase:alpha-ar] [gn:lys2:ybr0910] [gtcfc:5.8:5.9:6.6] [ec:1.2.1.31] [keggfc:5.8:5.9]

CONTIG5782	34657062_c2_22	4181	18284	270	90	YBR115C	344	5.7(10)-30	Saccharomyces cerevisiae	[ui:ybr115c] [pn:L-aminoacidate-semialdehyde dehydrogenase, large subunit:aminoadipate-semialdehyde dehydrogenase large subunit:alpha-amino adipate reductase:alpha-ar] [gn:lys2:ybr0910] [gtcfc:5.8:5.9:6.6] [ec:1.2.1.31] [keggfc:5.8:5.9]
CONTIG5782	4766436_c3_27	4182	18285	2040	680	YBR115C	2034	1.7(10)-210	Saccharomyces cerevisiae	[ui:ybr115c] [pn:L-aminoacidate-semialdehyde dehydrogenase, large subunit:aminoadipate-semialdehyde dehydrogenase large subunit:alpha-amino adipate reductase:alpha-ar] [gn:lys2:ybr0910] [gtcfc:5.8:5.9:6.6] [ec:1.2.1.31] [keggfc:5.8:5.9]
CONTIG5253	10160038_c3_15	4183	18286	1824	608	YDR037W	2301	8.8(10)-239	Saccharomyces cerevisiae	[ui:ydr037w] [pn:lysyl-tRNA synthetase, cytosolic:lysyl-tRNA synthetase, cytoplasmic:lysine-- tRNA ligase:[gn:krs1:[gn:krs1:ged5:yd9673]]] [gtcfc:5.8:10.6] [ec:6.1.1.6] [keggfc:5.8:10.1:10.2] [sgdgc:5.4:0.9:2.0] [db:gic-saccharomyces cere
CONTIG5512	4079051_c3_13	4184	18287	1167	389	YIR034C	1310	9.0(10)-134	Saccharomyces cerevisiae	[ui:yir034c] [pn:saccharopine dehydrogenase:nad+, L-lysine forming:lysine-- 2-oxoglutarate reductase:scdh] [gn:lys1] [gtcfc:5.8:5.9:6.6] [ec:1.5.1.7] [keggfc:5.8:5.9] [sgdgc:1.1.1:9.2.0] [db:gic-saccharomyces cerevisiae]

CONTIG5497	953431_c2_8	4185	18288	1362	454	YNR050C	1651	6.5(10)-170	Saccharomyces cerevisiae	[ui:ym050cl] [pn:saccharopine dehydrogenase:nad ⁺ , l-glutamate forming] [gr:lys9:lys13;n3461] [gtcfc:5.8;6.6] [ec:1.5.1.10] [keggfc:5.8] [sgdfc:1.1.] [db:gtc-saccharomyces cerevisiae]
CONTIG4907	25_f2_3	4186	18289	1380	460	YER078C	984	3.2(10)-99	Saccharomyces cerevisiae	[ui:yer078cl] [pn:hypothetical 58.0 kd peptidase in arg5,6-iv1 intergenic region] [gtcfc:5.9] [ec:3.4.-.] [keggfc:5.9] [db:gtc-saccharomyces cerevisiae]
CONTIG4907	14880002_f3_6	4187	18290	234	78	YER078C	150	7.0(10)-10	Saccharomyces cerevisiae	[ui:yfr006w] [pn:similarity to x-pro dipeptidases;hypothetical 61.8 kd peptidase in mpr1-gcn20 intergenic region] [gtcfc:5.9;10.11] [ec:3.4.-.] [keggfc:5.9] [sgdfc:6.5.3] [db:gtc-saccharomyces cerevisiae]
CONTIG2338	\$65888_f3_5	4188	18291	495	165	YFR006W	496	1.6(10)-47	Saccharomyces cerevisiae	[ui:yfr006w] [pn:similarity to x-pro dipeptidases;hypothetical 61.8 kd peptidase in mpr1-gcn20 intergenic region] [gtcfc:5.9;10.11] [ec:3.4.-.] [keggfc:5.9] [sgdfc:6.5.3] [db:gtc-saccharomyces cerevisiae]
CONTIG4924	24238407_f3_7	4189	18292	534	178	YIR022W	522	2.8(10)-50	Saccharomyces cerevisiae	[ui:yir022w] [pn:signal sequence processing protein:signal sequence processing protein precursor] [gn:sec11] [gtcfc:11.1;5.9;10.7] [ec:3.4.-.] [keggfc:5.9] [sgdfc:6.3.0;9.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5159	10600952_c3_8	4190	18293	951	317	YIL145C	711	2.7(10)-70	Saccharomyces cerevisiae	[ui:yil145c] [pn:similarity to e.coli pantothenate synthetase:putative pantoate-β-alanine ligase:pantothenate synthetase activating enzyme] [gtcfc:6.1:9.10:9.11:9.5] [ec:6.3.2.1] [keggfc:6.1:9.5] [sgdfc:1.7.1] [db:gtc-sac]
CONTIG4551	19723132_c1_11	4191	18294	540	180	YBR244W	461	8.4(10)-44	Saccharomyces cerevisiae	[ui:ybr244w] [pn:strong similarity to glutathione peroxidases:glutathione peroxidase homolog ybr244w] [gn:ybr1632] [gtcfc:6.16:12.12] [ec:1.11.1.9] [keggfc:6.9] [sgdfc:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3600	1379006_f2_1	4192	18295	282	94	YIR037W	260	1.7(10)-22	Saccharomyces cerevisiae	[ui:yir037w] [pn:glutathione peroxidase] [gn:hyrl] [gtcfc:6.16:13.2] [ec:1.11.1.9] [keggfc:6.9] [sgdfc:11.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5098	4100133_c1_10	4193	18296	699	233	YIR037W	480	8.0(10)-46	Saccharomyces cerevisiae	[ui:yir037w] [pn:glutathione peroxidase] [gn:hyrl] [gtcfc:6.16:13.2] [ec:1.11.1.9] [keggfc:6.9] [sgdfc:11.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5098	1953502_c3_11	4194	18297	579	193	YIR037W	644	3.3(10)-63	Saccharomyces cerevisiae	[ui:yir037w] [pn:glutathione peroxidase] [gn:hyrl] [gtcfc:6.16:13.2] [ec:1.11.1.9] [keggfc:6.9] [sgdfc:11.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5401	812932_c1_11	4195	18298	474	158	YAL016W	197	9.6(10)-19	Saccharomyces cerevisiae	[uii:yal016w] [pn:ser/thr protein phosphatase 2a, regulatory chain a:protein phosphatase pp2a regulatory subunit a:pr65] [gn:tpd3:fun32] [grfc:6.3:10.2:12.8] [keggfc:14.2] [sgdfc:3.1.0.3.2.0.3.8.0.3.9.0:4.12.0: 16.0.0] [db:gtc-saccharo
CONTIG5401	24806578_c1_10	4196	18299	1104	368	YAL016W	965	3.2(10)-97	Saccharomyces cerevisiae	[uii:yal016w] [pn:ser/thr protein phosphatase 2a, regulatory chain a:protein phosphatase pp2a regulatory subunit a:pr65] [gn:tpd3:fun32] [grfc:6.3:10.2:12.8] [keggfc:14.2] [sgdfc:3.1.0.3.2.0.3.8.0.3.9.0:4.12.0: 16.0.0] [db:gtc-saccharo
CONTIG5401	24495287_c3_16	4197	18300	447	149	YAL016W	439	2.1(10)-41	Saccharomyces cerevisiae	[uii:yal016w] [pn:ser/thr protein phosphatase 2a, regulatory chain a:protein phosphatase pp2a regulatory subunit a:pr65] [gn:tpd3:fun32] [grfc:6.3:10.2:12.8] [keggfc:14.2] [sgdfc:3.1.0.3.2.0.3.8.0.3.9.0:4.12.0: 16.0.0] [db:gtc-saccharo
b1x17840_x	25867876_f2_1	4198	18301	753	251	YBL056W	296	5.0(10)-26	Saccharomyces cerevisiae	[uiiyb056w] [pn:ser/thr protein phosphatase pp2c:putative 51.4 kd phosphatase 2c in shp1-sec17 intergenic region] [gn:pic3:ybl0511:ybl0513] [grfc:6.3:14.3] [ec:3.13.16] [keggfc:14.1] [sgdfc:16.0.0:13.0.0] [db:gtc-saccharomyces cere

CONTIG1970	4771931_c1_3	4199	18302	297	99	YBR125C	171	2.2(10)-12	Saccharomyces cerevisiae	[ui:ybr125c] [pn: similarity to protein phosphatase 2c; putative 44.2 kd phosphatase 2c in tfc1-cif1 intergenic region] [gn:ybr0921] [gicfc:6.3:14.3] [ec:3.1.3.16] [keggfc:14.1] [sgdgc:16.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
b3x10869.x	14973516_f3_1	4200	18303	504	168	YBR125C	266	3.8(10)-23	Saccharomyces cerevisiae	[ui:ybr125c] [pn: similarity to protein phosphatase 2c; putative 44.2 kd phosphatase 2c in tfc1-cif1 intergenic region] [gn:ybr0921] [gicfc:6.3:14.3] [ec:3.1.3.16] [keggfc:14.1] [sgdgc:16.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1257	23629675_f1_1	4201	18304	807	269	YBR276C	117	0.00042	Saccharomyces cerevisiae	[ui:ybr276c] [pn: protein tyrosine phosphatase; probable protein-tyrosine phosphatase ybr276c] [gn:pps1:ybr2013] [gicfc:6.3:12.8] [ec:3.1.3.48] [keggfc:14.1] [sgdgc:3.8.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4090	23609443_c2_3	4202	18305	2202	734	YBR276C	326	6.7(10)-44	Saccharomyces cerevisiae	[ui:ybr276c] [pn: protein tyrosine phosphatase; probable protein-tyrosine phosphatase ybr276c] [gn:pps1:ybr2013] [gicfc:6.3:12.8] [ec:3.1.3.48] [keggfc:14.1] [sgdgc:3.8.0:16.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2457	4881312_f3_2	4203	18306	597	199	YBR276C	177	1.8(10)-12	Saccharomyces cerevisiae	[ui:ybr276cl] [pn:protein tyrosine phosphatase;probable protein-tyrosine phosphatase ybr276c] [gn:ppsl:ybr2013] [gtfc:6.3:12.8] [ec:3.1.3.48] [kegg:ic:4.1] [sgd:fc:3.8.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5770	14502005_f1_7	4204	18307	1122	374	YDL230W	432	9.9(10)-41	Saccharomyces cerevisiae	[ui:ydl230w] [pn:protein tyrosine phosphatase;probable protein-tyrosine phosphatase 1:ppase 1] [gn:pp1p] [gtfc:6.3:12.8:14.3] [ec:3.1.3.48] [kegg:ic:13.3] [sgd:fc:9.2.0:16.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2672	29338333_f3_3	4205	18308	324	108	YDL188C	507	1.1(10)-48	Saccharomyces cerevisiae	[ui:ydl188cl] [pn:protein ser/thr phosphatase pp2a-2:serine/threonine protein phosphatase pp2a-2 catalytic subunit] [gn:pph22:ssis4:d1271] [gtfc:6.3:12.13:12.8] [ec:3.1.3.16] [kegg:ic:14.1] [sgd:fc:1.5.2:3.1.0:3.2.0:3.8.0:16.0.0] [db:gtc]
CONTIG108	26600307_f3_1	4206	18309	816	272	YDL134C	978	1.3(10)-98	Saccharomyces cerevisiae	[ui:ydl134cl] [pn:protein ser/thr phosphatase pp2a-1:serine/threonine protein phosphatase pp2a-1 catalytic subunit] [gn:pph21:d21180] [gtfc:6.3:12.13:12.8] [ec:3.1.3.16] [kegg:ic:13.3] [sgd:fc:1.5.2:3.1.0:3.2.0:3.8.0:16.0.0] [db:gtc-sacc]

CONTIG4167	4870177_f3_5	4207	18310	957	319	YDL047W	1415	6.7(10)-145	Saccharomyces cerevisiae	[ui:ydI047w] [pn:ser/thr protein phosphatase;serine/threonine protein phosphatase pp1-1] [gn:pph1;sid4;d2693] [gicfc:6.3;12.8] [ec:3.1.3.16] [keggfc:13.3] [sgdfc:3.2.0;3.8;0.16;0.0] [db:gic-saccharomyces cerevisiae]
CONTIG1118	24110300_c1_5	4208	18311	558	186	YDL006W	263	8.0(10)-23	Saccharomyces cerevisiae	[ui:ydI006w] [pn:protein serine/threonine phosphatase 2c;protein phosphatase 2c homolog;pp2c] [gn:ptc1;ipd1;d2925] [gicfc:6.3;12.13;12.8;13.2] [ec:3.1.3.16] [keggfc:1.4.1] [sgdfc:1.5.2;3.1.0;3.2.0;10.3.4;11.1.0;16.0.0] [db:gic-saccharoarabiose]
CONTIG5206	24110300_c3_14	4209	18312	1161	387	YDL006W	506	1.3(10)-48	Saccharomyces cerevisiae	[ui:ydI006w] [pn:protein serine/threonine phosphatase 2c;protein phosphatase 2c homolog;pp2c] [gn:ptc1;ipd1;d2925] [gicfc:6.3;12.13;12.8;13.2] [ec:3.1.3.16] [keggfc:1.4.1] [sgdfc:1.5.2;3.1.0;3.2.0;10.3.4;11.1.0;16.0.0] [db:gic-saccharoarabiose]
b3x15922.x	25432192_f1_1	4210	18313	552	184	YDR075W	702	2.3(10)-69	Saccharomyces cerevisiae	[ui:ydI075w] [pn:protein ser/thr phosphatases;serine/threonine protein phosphatase ppb3] [gn:pph3;d4421][gicfc:6.3;12.8] [ec:3.1.3.16] [keggfc:1.4.1] [sgdfc:3.1.0;16.0.0] [db:gic-saccharomyces cerevisiae]

CONTIG4514	4784651_f1_1	4211	18314	1257	419	YDR481C	681	4.0(10)-67	Saccharomyces cerevisiae	[ui:yd481c] [pn:repressible alkaline phosphatase vacuolar:repressible alkaline phosphatase precursor] [gn:pho8] [gicfc:6.3:8.1:9.13:9.6:12.16] [ec:3.1.3.1][keggc:8.1:9.7:9.12] [sgdc:9.10.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5768	20288_f3_13	4212	18315	750	250	YDR481C	585	6.0(10)-57	Saccharomyces cerevisiae	[ui:yd481c] [pn:repressible alkaline phosphatase vacuolar:repressible alkaline phosphatase precursor] [gn:pho8] [gicfc:6.3:8.1:9.13:9.6:12.16] [ec:3.1.3.1][keggc:8.1:9.7:9.12] [sgdc:9.10.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5768	33761050_f1_5	4213	18316	951	317	YDR481C	881	2.6(10)-88	Saccharomyces cerevisiae	[ui:yd481c] [pn:repressible alkaline phosphatase vacuolar:repressible alkaline phosphatase precursor] [gn:pho8] [gicfc:6.3:8.1:9.13:9.6:12.16] [ec:3.1.3.1][keggc:8.1:9.7:9.12] [sgdc:9.10.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5657	12303452_c2_17	4214	18317	1800	600	YEL042W	1357	9.5(10)-139	Saccharomyces cerevisiae	[ui:ye042w] [pn:guanosine-diphosphatase:guanosine-diphosphatase:gdpase] [gn:gdal,sypr-orf16] [gicfc:6.3:10.7:12.16] [ec:3.6.1.42] [keggc:14.1] [sgdc:6.3.0:9.4.0:16.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3205	23697252_f2_1	4215	18318	1623	541	YER075C	145	3.1(10)-14	Saccharomyces cerevisiae	[ui:yer075c] [pn:protein tyrosine phosphatase;probable protein-tyrosine phosphatase yer075c] [gn:ptp3] [gtfcfc:6.3:14.3] [ec:3.1.3.48] [keggfc:14.1] [sgdfc:16.0:0:13.0] [db:gtc-saccharomyces cerevisiae]
CONTIG656	859383_f1_2	4216	18319	291	97	YER075C	102	0.00022	Saccharomyces cerevisiae	[ui:yer075c] [pn:protein tyrosine phosphatase;probable protein-tyrosine phosphatase yer075c] [gn:ptp3] [gtfcfc:6.3:14.3] [ec:3.1.3.48] [keggfc:14.1] [sgdfc:16.0:0:13.0] [db:gtc-saccharomyces cerevisiae]
CONTIG656	24095062_f1_3	4217	18320	390	130	YER075C	148	2.7(10)-9	Saccharomyces cerevisiae	[ui:yer075c] [pn:protein tyrosine phosphatase;probable protein-tyrosine phosphatase yer075c] [gn:ptp3] [gtfcfc:6.3:14.3] [ec:3.1.3.48] [keggfc:14.1] [sgdfc:16.0:0:13.0] [db:gtc-saccharomyces cerevisiae]
b9x12x90.x	32527005_f3_2	4218	18321	519	173	YER075C	115	9.0(10)-6	Saccharomyces cerevisiae	[ui:yer075c] [pn:protein tyrosine phosphatase;probable protein-tyrosine phosphatase yer075c] [gn:ptp3] [gtfcfc:6.3:14.3] [ec:3.1.3.48] [keggfc:14.1] [sgdfc:16.0:0:13.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4089	1054750_c2_10	4219	18322	906	302	YER089C	294	3.6(10)-37.	Saccharomyces cerevisiae	[lui:yfr089c] [pn:strong similarity to phosphoprotein phosphatases;putative 51.4 kd phosphatase2c in seb1-trp2 intergenic region] [gn:pic2] [gicfc:6.3:14.3] [ec:3.1.3.16] [keggfc:14.1] [sgdfc:16.0:0.13.0.0] [db:gtc-saccharomyces cerev]
CONTIG5301	21978924_c1_10	4220	18323	960	320	YER133W	1425	5.9(10)-146	Saccharomyces cerevisiae	[lui:yfr133w] [pn:ser/thr phosphoprotein phosphatase 1, catalytic chain,serine/threonine protein phosphatase pp1-2] [gn:glc7.d1s2.cid1] [gicfc:6.3:7.1.7.2:10.7:12.13.12.8] [ec:3.1.3.16] [keggfc:13.3] [sgdfc:1.5.2.2.7.0:3.2.0:3.5.0:3.8.]
CONTIG5806	2766886_c1_26	4221	18324	1302	434	YFR028C	1232	1.7(10)-125	Saccharomyces cerevisiae	[lui:yfr028c] [pn:protein-tyrosine phosphatase;probable protein-tyrosine phosphatase] [gn:cdc14] [gicfc:6.3:10.8:12.8] [ec:3.1.3.48] [keggfc:13.3] [sgdfc:3.6.0:3.8.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
b3x16043_y	10651905_f2_2	4222	18325	396	132	YFR028C	236	4.0(10)-19	Saccharomyces cerevisiae	[lui:yfr028c] [pn:protein-tyrosine phosphatase;probable protein-tyrosine phosphatase] [gn:cdc14] [gicfc:6.3:10.8:12.8] [ec:3.1.3.48] [keggfc:13.3] [sgdfc:3.6.0:3.8.0:16.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1691	1365882_f3_1	4223	18326	1080	360	YGL190C	1034	1.6(10)-104	Saccharomyces cerevisiae	[ui:yg1190c] [pn:ser/thr phosphatase 2a regulatory subunit b/protein phosphatase pp2a regulatory subunit b;pr53;cell division control protein 55] [gn:cdc55;g:1345] [gicfc:6.3:12.8:13.2] [keggfc:14.2] [sgdfc:3.1.0:3.2:0.3.8:0.3.9:0.11.]
CONTIG609	190888_f3_1	4224	18327	1335	445	YGR123C	778	1.8(10)-91	Saccharomyces cerevisiae	[ui:ygr123c] [pn:protein ser/thr phosphatase;serine/threonine protein phosphatase t;ptp] [gn:ptp1;g6347] [gicfc:6.3:14.3] [ec:3.1.3.16] [keggfc:14.1] [sgdfc: 16.0:0:13.0:0] [db:gic-saccharomyces cerevisiae]
CONTIG5670	19720377_c2_30	4225	18328	525	175	YGR203W	245	6.5(10)-21	Saccharomyces cerevisiae	[ui:ygr203w] [pn:weak similarity to x.laevis protein-tyrosin-phosphatase cdc homolog 2 and to hypothetical protein ypr200c;hypothetical 17.2 kd protein in pcl1-ade3 intergenic region] [gn:g7731] [gicfc:6.3:14.3] [keggfc:14.2] [sgdfc: 1
CONTIG2121	22051912_c3_2	4226	18329	807	269	YIL002C	91	0.38	Saccharomyces cerevisiae	[ui:yil002c] [pn:synaptojanin homolog 1;hypothetical 108.4 kd protein in bet1-pal1 intergenic region] [gn:shl1;ya2c] [gicfc:6.3:8.5:10.7] [keggfc:14.2] [sgdfc: 1.6.7:16.0:0] [db:gic-saccharomyces cerevisiae]

CONTIG4602	9806427_f2_3	4227	18330	1053	351	YIL002C	731	2.1(10)-72	Saccharomyces cerevisiae	[ui:yil002c] [pn:synaptojanin homolog 1:hypothetical 108.4 kd protein in bet-1-pal1 intergenic region] [gn:yih1:ya2c]
CONTIG5813	24065877_c3_61	4228	18331	1080	360	YIR026C	587	3.7(10)-57	Saccharomyces cerevisiae	[ui:yir026c] [pn:protein tyrosine phosphatase:protein-tyrosine phosphatase:pipase1] [gn:yvh1]
CONTIG4689	4188540_f2_2	4229	18332	615	205	YKL190W	614	5.0(10)-60	Saccharomyces cerevisiae	[ui:ykl190w] [pn:calcineurin b, regulatory subunit:calcineurin b subunit:protein phosphatase 2b regulatory subunit] [gn:cnb1:ycnb:ycn2]
CONTIG5466	10625676_f2_4	4230	18333	888	296	YML112W	111	0.00064	Saccharomyces cerevisiae	[ui:yml112w] [pn:carboxy-terminal domain:ctd kinase, gamma subunit:ctd kinase gamma subunit:ctdk-i gamma subunit] [gn:ctk3:ym83339]

CONTIG373	1488441_f3_1	4231	18334	801	267	YML016C	709	4.4(10)-70	Saccharomyces cerevisiae	[ui:yml016c] [pn:ser/thr phosphatase required for normal osmoregulation;serine/threonine protein phosphatase pp-z1] [gn:ppz1.ym9571] [gtfc:6.3:13.2] [ec:3.1.3.16] [keggc:14.1] [sgdfc:11.1.0.16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3862	782887_c2_6	4232	18335	357	119	YML016C	543	1.7(10)-52	Saccharomyces cerevisiae	[ui:yml016c] [pn:ser/thr phosphatase required for normal osmoregulation;serine/threonine protein phosphatase pp-z1] [gn:ppz1.ym9571] [gtfc:6.3:13.2] [ec:3.1.3.16] [keggc:14.1] [sgdfc:11.1.0.16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG210	24020939_c2_1	4233	18336	585	195	YML016C	702	2.3(10)-69	Saccharomyces cerevisiae	[ui:yml016c] [pn:ser/thr phosphatase required for normal osmoregulation;serine/threonine protein phosphatase pp-z1] [gn:ppz1.ym9571] [gtfc:6.3:13.2] [ec:3.1.3.16] [keggc:14.1] [sgdfc:11.1.0.16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1341	25635817_f3_1	4234	18337	1107	369	YMR036C	191	9.0(10)-13	Saccharomyces cerevisiae	[ui:ymr036c] [pn:m-phase inducing protein tyrosine phosphatase;m-phase inducer phosphatase:mitosis initiation protein mih1.mitotic inducer homolog] [gn:mih1.ym9332] [gtfc:6.3:12.8] [ec:3.1.3.48] [keggc:13.3] [sgdfc:3.8.0:16.0.0] [db

b1x14347.x	11775417_f3_1	4235	18338	516	172	YNL217W	172	9.8(10)-13	Saccharomyces cerevisiae	[ui:ynl217w] [pn:weak similarity to e.coli bis:5"-nucleosyl-tetraphosphatase:hypothetical 37.2 kd protein in alg9-rap1 intergenic region] [gn:n1306] [gtcfc:6.3:14.3] [keggfc:14.2] [sgdfc: 16.0:0:13.0.0] [db:gtc-saccharomyces cerevisiae]
b2x18173.y	25625781_f3_1	4236	18339	474	158	YNL128W	139	1.3(10)-16	Saccharomyces cerevisiae	[ui:ynl128w] [pn:weak similarity to tensin:hypothetical 50.2 kd protein in cpt1-sp98 intergenic region] [gn:n1220,n1872] [gtcfc:6.3:14.3] [keggfc:14.2] [sgdfc: 16.0:0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1134	3009683_f3_2	4237	18340	1056	352	YNL106C	323	7.9(10)-28	Saccharomyces cerevisiae	[ui:ynl106c] [pn:phosphatidylinositol phosphate phosphatase:hypothetical 133.3 kd protein in cyb5-leu4 intergenic region] [gn:pic3,n2160] [gtcfc:6.3:10.7:11.1] [keggfc:14.2] [sgdfc:6.2:0:16.0:0] [db:gtc-saccharomyces cerevisiae]
CONTIG2301	20441656_c2_5	4238	18341	414	138	YNL106C	262	2.5(10)-21	Saccharomyces cerevisiae	[ui:ynl106c] [pn:phosphatidylinositol phosphate phosphatase:hypothetical 133.3 kd protein in cyb5-leu4 intergenic region] [gn:pic3,n2160] [gtcfc:6.3:10.7:11.1] [keggfc:14.2] [sgdfc:6.2:0:16.0:0] [db:gtc-saccharomyces cerevisiae]

CONTIG3574	25578760_c2_9	4239	18342	2457	819	YNL106C	1651	6.5(10)-170	Saccharomyces cerevisiae	[ui:ynl106c] [pn:phosphatidylinositol phosphate phosphatase:hypothetical 133.3 kd protein in cyb5-leu4 intergenic region] [gn:pie3.n2 60] [gicfc:6.3:10.7:11.1] [keggfc:14.2] [sgdfc:6.2.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4602	25992268_f1_1	4240	18343	921	307	YNL106C	321	1.3(10)-27	Saccharomyces cerevisiae	[ui:ynl106c] [pn:phosphatidylinositol phosphate phosphatase:hypothetical 133.3 kd protein in cyb5-leu4 intergenic region] [gn:pie3.n2 160] [gicfc:6.3:10.7:11.1] [keggfc:14.2] [sgdfc:6.2.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5748	12947827_c3_25	4241	18344	783	261	YNR032W	755	5.9(10)-75	Saccharomyces cerevisiae	[ui:ynr032w] [pn:phosphoprotein phosphatase ppg catalytic chain:serine/threonine protein phosphatase pp2a-like ppg1] [gn:ppg1_ppg:n3281] [gicfc:6.3:7.1:7.2] [ec:3.1.3.16] [keggfc:14.1] [sgdfc:2.7:0.16.0.0] [db:gtc-saccharomyces cerevi
CONTIG229	32615933_c1_2	4242	18345	330	110	YOL064C	179	2.2(10)-13	Saccharomyces cerevisiae	[ui:yol064c] [pn:protein ser/thr phosphatase:halotolerance protein hal2] [gn:hal2:mcl22] [gicfc:6.3:6.6:13.2] [keggfc:14.2] [sgdfc:1.1.11.1.0:16.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4182	901577_c3_8	4243	18346	876	292	YOL064C	473	4.5(10)-45	Saccharomyces cerevisiae	[ui:yo!064c] [pn:protein ser/thr phosphatase:halotolerance protein hal2] [gn:hal2:met22] [gtfc:6.3:6.13.2] [keggfc:14.2] [sgfc:1.1.1.11.1.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4383	901577_c2_11	4244	18347	1200	400	YOL064C	736	6.0(10)-73	Saccharomyces cerevisiae	[ui:yo!064c] [pn:protein ser/thr phosphatase:halotolerance protein hal2] [gn:hal2:met22] [gtfc:6.3:6.13.2] [keggfc:14.2] [sgfc:1.1.11.1.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5094	6120766_f3_7	4245	18348	693	231	YOL064C	383	1.5(10)-35	Saccharomyces cerevisiae	[ui:yo!064c] [pn:protein ser/thr phosphatase:halotolerance protein hal2] [gn:hal2:met22] [gtfc:6.3:6.13.2] [keggfc:14.2] [sgfc:1.1.11.1.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1548	4787511_f1_1	4246	18349	339	113	YOR007C	145	1.1(10)-9	Saccharomyces cerevisiae	[ui:yo!07c] [pn:similarity to protein phosphatases] [gtfc:6.3:14.3] [keggfc:14.2] [sgfc:16.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4573	6913441_c2_12	4247	18350	1167	389	YOR007C	115	0.00042	Saccharomyces cerevisiae	[ui:yo!07c] [pn:similarity to protein phosphatases] [gtfc:6.3:14.3] [keggfc:14.2] [sgfc:16.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5488	24429813_c1_10	4248	18351	1212	404	YOR007C	638	1.5(10)-62	Saccharomyces cerevisiae	[ui:yo!07c] [pn:similarity to protein phosphatases] [gtfc:6.3:14.3] [keggfc:14.2] [sgfc:16.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2168	9867812_c3_4	4249	18352	999	333	YOR014W	444	3.5(10)-58	Saccharomyces cerevisiae	[ui:yor014w] [pn:potential regulatory subunit of protein phosphatase 2a;rtsl protein:ses1 protein] [gntrls1:scs1:0r26] [gtfcfc:6.3:13.2] [keggfc:14.2] [sgdfc:9.2.0:11.1:0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG641	9782594_c2_5	4250	18353	1104	368	YOR014W	978	1.3(10)-98	Saccharomyces cerevisiae	[ui:yor014w] [pn:potential regulatory subunit of protein phosphatase 2a;rtsl protein:ses1 protein] [gntrls1:scs1:0r26] [gtfcfc:6.3:13.2] [keggfc:14.2] [sgdfc:9.2.0:11.1:0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5577	4117153_f3_6	4251	18354	1293	431	YOR090C	697	8.1(10)-69	Saccharomyces cerevisiae	[ui:yor090c] [pn:similarity to ser/thr protein phosphatases] [gtfcfc:6.0:13.0.0] [keggfc:14.3] [sgdfc:16.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3558	3913132_f3_5	4252	18355	1458	486	YOR178C	143	6.5(10)-11	Saccharomyces cerevisiae	[ui:yor178c] [pn:ser/thr phosphoprotein phosphatase 1, regulatory chain:protein phosphatase 1 regulatory subunit] [gngac1] [gtfcfc:6.3:7.1:7.2:12.13] [keggfc:14.2] [sgdfc:1.5.2.2.7.0:9.2.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4310	20034655_c3_9	4253	18356	1299	433	YOR178C	147	1.3(10)-9	Saccharomyces cerevisiae	[ui:yor178c] [pn:ser/thr phosphoprotein phosphatase 1, regulatory chain:protein phosphatase 1 regulatory subunit] [gngac1] [gtfcfc:6.3:7.1:7.2:12.13] [keggfc:4.2] [sgdfc:1.5.2.2.7.0:9.2.0:16.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1104	31542281_f3_4	4254	18357	372	124	YPL152W	111	6.4(10)-6	Saccharomyces cerevisiae	[ui:yp1152w] [pn:strong similarity to human phosphotyrosyl phosphatase activator] [gicfc:6.3:14.3] [keggfc:14.2] [sgdfc:16.0:13.0][db:gtc-saccharomyces cerevisiae]
CONTIG5596	24417532_c2_16	4255	18358	1128	376	YPL152W	931	1.3(10)-93	Saccharomyces cerevisiae	[ui:yp1152w] [pn:strong similarity to human phosphotyrosyl phosphatase activator] [gicfc:6.3:14.3] [keggfc:14.2] [sgdfc:16.0:13.0][db:gtc-saccharomyces cerevisiae]
b9x13g07.x	2162792_f3_1	4256	18359	510	170	YPL152W	113	3.8(10)-6	Saccharomyces cerevisiae	[ui:yp1152w] [pn:strong similarity to human phosphotyrosyl phosphatase activator] [gicfc:6.3:14.3] [keggfc:14.2] [sgdfc:16.0:13.0][db:gtc-saccharomyces cerevisiae]
CONTIG5781	5085142_f1_8	4257	18360	537	179	YPL151C	322	4.5(10)-29	Saccharomyces cerevisiae	[ui:yp1151c] [pn:strong similarity to a.thaliana prl1 and prl2 proteins] [gicfc:6.3:14.3] [keggfc:14.2] [sgdfc:16.0:13.0][db:gtc-saccharomyces cerevisiae]
CONTIG5781	35188125_f3_15	4258	18361	636	212	YPL151C	404	9.1(10)-38	Saccharomyces cerevisiae	[ui:yp1151c] [pn:strong similarity to a.thaliana prl1 and prl2 proteins] [gicfc:6.3:14.3] [keggfc:14.2] [sgdfc:16.0:13.0][db:gtc-saccharomyces cerevisiae]

CONTIG2789	24273425_f3_2	4259	18362	531	177	YPR073C	433	7.7(10)-41	Saccharomyces cerevisiae	[ui:ypr073c] [pn:protein=tyrosine-phosphatase;low molecular weight phosphatase;cytosolic acid phosphatase;ptpase] [gn:yp1;yp9499] [gicfc:6.3:9.13:9.2:14.3] [keggfc:9.2:9.12] [sgdfc:16.0:0:0]
CONTIG3302	23864068_c3_4	4260	18363	267	89	YAL004W	282	7.7(10)-25	Saccharomyces cerevisiae	[ui:yal004w] [pn:strong similarity to a.klebsiana glutamate dehydrogenase;hypothetical 23.8 kd protein in ssa1-efb1 intergenic region] [gicfc:6.6] [keggfc:14.2] [sgdfc:1.1.1] [db:gic-saccharomyces cerevisiae]
CONTIG5775	24115905_f3_15	4261	18364	193	65	YAL004W	164	2.5(10)-12	Saccharomyces cerevisiae	[ui:yal004w] [pn:strong similarity to a.klebsiana glutamate dehydrogenase;hypothetical 23.8 kd protein in ssa1-efb1 intergenic region] [gicfc:6.6] [keggfc:14.2] [sgdfc:1.1.1] [db:gic-saccharomyces cerevisiae]
CONTIG2671	214026_f3_2	4262	18365	1113	371	YEI046C	1051	2.5(10)-106	Saccharomyces cerevisiae	[ui:yei046c] [pn:required for glycine prototrophy in shmt1 and shmt2 double mutant;gly1 protein] [gn:gly1:sygp-orf34] [gicfc:6.6] [keggfc:14.2] [sgdfc:1.1.1] [db:gic-saccharomyces cerevisiae]

CONTIG5415	281258_c1_12	4263	18366	1236	412	YEL046C	1003	3.1(10)-101	Saccharomyces cerevisiae	[ui:ye 046c] [pn:required for glycine prototrophy in shmt1 and shmt2 double mutant;gly1 protein][gn:gly sygp-orf34] [gicfc:6.6][keggfc:14.2] [sgdfc:1..1] [db:gic-saccharomyces cerevisiae]
CONTIG1506	9859833_f1_1	4264	18367	780	260	YEL038W	437	2.8(10)-41	Saccharomyces cerevisiae	[ui:ye 038w] [pn:similarity to k.oxytoca enolase-phosphatase e-utr4 protein:unknown transcript 4 protein][gn:utr4 sygp-orf20] [gicfc:6.6][keggfc:4.2][sgdfc:1..1] [db:gic-saccharomyces cerevisiae]
CONTIG5814	24015936_f2_12	4265	18368	1233	411	YGL184C	936	3.8(10)-94	Saccharomyces cerevisiae	[ui:yg 184c] [pn:similarity to arabiidopsis cystathione beta-lyase:hypothetical 51.8 kd protein in cox4-gts1 intergenic region][gn:g 6011] [gicfc:6.6][keggfc:14.2] [sgdfc:1..1] [db:gic-saccharomyces cerevisiae]
CONTIG376	10830007_f1_1	4266	18369	549	183	YHR070W	246	2.5(10)-20	Saccharomyces cerevisiae	[ui:yhr 070w] [pn:strong similarity to n.crassa met-t-10+ protein:hypothetical 56.5 kd protein in dys1-erg7 intergenic region][gicfc:6.6][keggfc:14.2][sgdfc:1..1] [db:gic-saccharomyces cerevisiae]
CONTIG3966	9821942_c2_3	4267	18370	246	82	YHR112C	195	4.4(10)-15	Saccharomyces cerevisiae	[ui:yhr 112c] [pn:similarity to cystathione gamma-synthases:hypothetical 42.4 kd protein in cdc12-orc6 intergenic region][gicfc:6.6][keggfc:14.2][sgdfc:1..1] [db:gic-saccharomyces cerevisiae]

CONTIG798	2343907_f1_1	4268	18371	621	207	YHR112C	357	8.8(10)-33	Saccharomyces cerevisiae	[ui:yhr112c] [pn:similarity to cystathioneine gamma-synthases:hypothetical 42.4 kd protein in cdc12-orc6 intergenic region] [gicfc:6.6] [keggfc:14.2] [sgdfc:1..1] [db:gic-saccharomyces cerevisiae]
CONTIG3366	5370677_c2_7	4269	18372	423	141	YIL094C	406	5.7(10)-38	Saccharomyces cerevisiae	[ui:yil094c] [pn:similarity to isopropyl malate and tartrate dehydrogenases:hypothetical 40.1 kd protein in sgat-ths1 intergenic region] [gicfc:6.6] [keggfc:14.2] [sgdfc:1..1] [db:gic-saccharomyces cerevisiae]
CONTIG5518	33782842_f2_7	4270	18373	372	124	YIL094C	238	5.2(10)-20	Saccharomyces cerevisiae	[ui:yil094c] [pn:similarity to isopropyl malate and tartrate dehydrogenases:hypothetical 40.1 kd protein in sgat-ths1 intergenic region] [gicfc:6.6] [keggfc:14.2] [sgdfc:1..1] [db:gic-saccharomyces cerevisiae]
CONTIG5609	14625911_c3_10	4271	18374	1776	592	YJL071W	311	1.8(10)-51	Saccharomyces cerevisiae	[ui:yjl071w] [pn:acetylglutamate synthase:hypothetical 65.6 kd protein in scp160-mrp18 intergenic region] [gnarg2-j109] [hrb574] [gicfc:6.6] [keggfc:14.2] [sgdfc:1..1] [db:gic-saccharomyces cerevisiae]
CONTIG5161	15632643_c2_8	4272	18375	2406	802	YKL215C	1691	3.7(10)-174	Saccharomyces cerevisiae	[ui:ykl215c] [pn:similarity to p.aeruginosa hya and hyub:hypothetical 140.4 kd protein in ura1-doa1 intergenic region] [gicfc:6.6] [keggfc:14.2] [sgdfc:1..1] [db:gic-saccharomyces cerevisiae]

CONTIG3518	20089762_c3_5	4273	18376	1212	404	YKL215C	925	5.7(10)-93	Saccharomyces cerevisiae	[uiykl1215c] [pn:similarity to p.aeruginosa hyua and hyub:hypothetical 140.4 kd protein in ura1-doa1 intergenic region] [gicfc:6.6] [keggfc:14.2] [sgdfc:1.1.1] [db:gic-saccharomyces cerevisiae]
CONTIG3518	29476511_c1_4	4274	18377	423	141	YKL215C	291	2.2(10)-24	Saccharomyces cerevisiae	[uiykl1215c] [pn:similarity to p.aeruginosa hyua and hyub:hypothetical 140.4 kd protein in ura1-doa1 intergenic region] [gicfc:6.6] [keggfc:14.2] [sgdfc:1.1.1] [db:gic-saccharomyces cerevisiae]
CONTIG5714	26571932_c3_25	4275	18378	258	86	YKL215C	152	1.5(10)-9	Saccharomyces cerevisiae	[uiykl1215c] [pn:similarity to p.aeruginosa hyua and hyub:hypothetical 140.4 kd protein in ura1-doa1 intergenic region] [gicfc:6.6] [keggfc:14.2] [sgdfc:1.1.1] [db:gic-saccharomyces cerevisiae]
CONTIG5607	16052091_f3_6	4276	18379	1674	558	YKL191W	792	8.0(10)-112	Saccharomyces cerevisiae	[uiykl1191w] [pn:diphtheria toxin resistance protein:diphtheria toxin resistance protein 2] [gn:dph2] [gicfc:6.6] [keggfc:14.2] [sgdfc:1.1.1] [db:gic-saccharomyces cerevisiae]
CONTIG2518	20361312_f1_1	4277	18380	249	83	YLR172C	236	5.7(10)-20	Saccharomyces cerevisiae	[uiykl172c] [pn:diphthamide methyltransferase:diphthidine synthase:diphthamide biosynthesis methyltransferase] [gn:dph5;19470] [gicfc:6.6] [ec:2.1.1.98] [keggfc:14.1] [sgdfc:1.1.1] [db:gic-saccharomyces cerevisiae]

CONTIG4706	6054758_c2_10	4278	18381	987	329	YLR172C	1062	1.7(10)-107	Saccharomyces cerevisiae	[ui:ylr172c] [pn:diphthamide methyltransferase;diphthine synthase;diphthamide biosynthesis methyltransferase] [gn:dph5;19470] [gcfc:6.6] [ec:2.1.1.98] [keggc:14.1] [sgdgc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5730	4376261_f1_3	4279	18382	2046	682	YML096W	493	2.1(10)-61	Saccharomyces cerevisiae	[ui:ymr096w] [pn:weak similarity to asparagine synthases] [gcfc:6.6] [keggc:14.2] [sgdgc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5682	24009687_f2_9	4280	18383	1323	441	YMR062C	1158	1.2(10)-117	Saccharomyces cerevisiae	[ui:ymr062c] [pn:similarity to glutamate n-acetyltransferase] [gcfc:6.6] [keggc:14.2] [sgdgc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2542	23990627_c3_7	4281	18384	561	187	YMR250W	357	2.7(10)-32	Saccharomyces cerevisiae	[ui:ymr250w] [pn:similarity to glutamate decarboxylases] [gcfc:6.6] [keggc:14.2] [sgdgc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2777	9863281_f1_1	4282	18385	1170	390	YMR250W	750	2.0(10)-74	Saccharomyces cerevisiae	[ui:ymr250w] [pn:similarity to glutamate decarboxylases] [gcfc:6.6] [keggc:14.2] [sgdgc:1.1.1] [db:gtc-saccharomyces cerevisiae]

CONTIG1469	12507088_c2_5	4283	18386	540	180	YCL043C	286	1.2(10)-24	Saccharomyces cerevisiae	[ui:ycl043c] [pn:protein disulfide-isomerase precursor;protein disulfide isomerase precursor:pdi / dolichyl-diphosphooligosaccharide-protein glycotransferase;glycosylation site-binding chain:gsbp:thioredoxin-related glycoprotein 1] [gn]
CONTIG2797	878430_c3_2	4284	18387	765	255	YCL043C	401	1.8(10)-37	Saccharomyces cerevisiae	[ui:ycl043c] [pn:protein disulfide-isomerase precursor;protein disulfide isomerase precursor:pdi / dolichyl-diphosphooligosaccharide-protein glycotransferase;glycosylation site-binding chain:gsbp:thioredoxin-related glycoprotein 1] [gn]
CONTIG2580	4085937_c1_5	4285	18388	678	226	YII005W	222	2.1(10)-17	Saccharomyces cerevisiae	[ui:yii005w] [pn:similarity to protein disulfide isomerases:putative disulfide isomerase yil005w precursor] [gn:yia5w] [gicfc:7.1:10.5:10.7:11.3:12.7] [cc:5.3.4.1] [keggfc:7.2] [sgdfc:6.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG3210	10626036_c1_4	4286	18389	1305	435	YII005W	394	5.2(10)-36	Saccharomyces cerevisiae	[ui:yii005w] [pn:similarity to protein disulfide isomerases:putative disulfide isomerase yil005w precursor] [gn:yia5w] [gicfc:7.1:10.5:10.7:11.3:12.7] [ec:5.3.4.1] [keggfc:7.2] [sgdfc:6.1.0] [db:gic-saccharomyces cerevisiae]

CONTIG537	24414028_f3_10	4287	18390	1239	413	YBL058W	642	5.5(10)-63	Saccharomyces cerevisiae	[ui:ybl058w] [pn:potential regulatory subunit for gic7p:shp1 protein] [gn:shp1:ybl0509:ybl0515] [gicfc:7.1:7.2:10.7:12.8] [keggfc:14.2] [sgdfc:2.7:0.3:2.0:3.5:0.3:8.0:5.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4110	7047053_f2_1	4288	18391	189	63	YHR047C	93	0.0018	Saccharomyces cerevisiae	[ui:yhr047c] [pn:alanine/arginine aminopeptidase] [gn:aap1] [gicfc:7.1:7.2:12.13] [ec:3.4.11.-] [keggfc:14.1] [sgdfc:1.5:2.2:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1438	24254651_f3_1	4289	18392	927	309	YKL128C	147	4.9(10)-8	Saccharomyces cerevisiae	[ui:ykl128c] [pn:high copy suppressor of ts tps2 mutant phenotype:hypothetical 33.8 kd protein in myo3-pgm1 intergenic region] [gn:pmu1] [gicfc:7.1:7.2] [keggfc:14.2] [sgdfc:2.7:0] [db:gtc-saccharomyces cerevisiae]
CONTIG5401	6250625_f1_2	4290	18393	975	325	YKL128C	298	1.6(10)-26	Saccharomyces cerevisiae	[ui:ykl128c] [pn:high copy suppressor of ts tps2 mutant phenotype:hypothetical 33.8 kd protein in myo3-pgm1 intergenic region] [gn:pmu1] [gicfc:7.1:7.2] [keggfc:14.2] [sgdfc:2.7:0] [db:gtc-saccharomyces cerevisiae]
CONTIG5330	14649125_f3_7	4291	18394	996	332	YKL128C	200	1.3(10)-14	Saccharomyces cerevisiae	[ui:ykl128c] [pn:high copy suppressor of ts tps2 mutant phenotype:hypothetical 33.8 kd protein in myo3-pgm1 intergenic region] [gn:pmu1] [gicfc:7.1:7.2] [keggfc:14.2] [sgdfc:2.7:0] [db:gtc-saccharomyces cerevisiae]

CONTIG5530	34016500_f3_8	4292	18395	1038	346	YKL128C	185	7.5(10)-21	Saccharomyces cerevisiae	[ui:ykl128c] [pn:high copy suppressor of ts tps2 mutant phenotype:hypothetical 33.8 kd protein in myo3-pgm1 intergenic region] [gn:pmu] [gicfc:7.1:7.2] [keggfc:14.2] [sgdfc:2.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG5661	788437_f1_1	4293	18396	945	315	YKL128C	167	2.2(10)-10	Saccharomyces cerevisiae	[ui:ykl128c] [pn:high copy suppressor of ts tps2 mutant phenotype:hypothetical 33.8 kd protein in myo3-pgm1 intergenic region] [gn:pmu] [gicfc:7.1:7.2] [keggfc:14.2] [sgdfc:2.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG5704	4772502_f3_8	4294	18397	3726	1242	YLR071C	370	2.2(10)-33	Saccharomyces cerevisiae	[ui:yr071c] [pn:dna-directed dna polymerase ii holoenzyme subunit:glucose repression regulatory protein] [gn:rgr1] [gicfc:7.1:7.2:10.1:10.2:12.13:12.8:12.9] [keggfc:14.2] [sgdfc:1.5:2:2.7:0.3:2.0:3.3:0:4.8:1.9:5.0] [db:gic-saccharomyces]
CONTIG5111	16828400_c3_14	4295	18398	1989	663	YPL240C	1621	2.1(10)-261	Saccharomyces cerevisiae	[ui:yp]240c] [pn:heat shock protein:heat shock protein hsp82] [gn:hsp82:hsp90] [gicfc:12.7:7.1:12.8:13.2] [keggfc:14.2] [sgdfc:2.7:0:3.4:0:3.5:0:9:2.0:11.1.0] [db:gic-saccharomyces cerevisiae]

CONTIG3310	31551_f2_2	4296	18399	999	333	YPL031C	1029	5.4(10)-104	Saccharomyces cerevisiae	[ui:yp 031cl] [pn:cyclin-dependent protein kinase:negative regulator of the pho system] [gn:pho85] [gicfc:7.1.7.2.8.5.9.4:10.1:10.2:12.1 3:12.8:13.10] [ec:2.7.1.-] [keggc:8.5:9.4:13.1:13.2:[3.3] [sgdfc:1.4.2.2.7.0.3.8.0.9.5.0:15.0.0]]
CONTIG208	5320387_f1_1	4297	18400	528	176	YFR019W	241	1.0(10)-18	Saccharomyces cerevisiae	[ui:yfr019w] [pn:probable pip 5-kinase:probable phosphatidylinositol-4-phosphate 5-kinase:1- phosphatidylinositol-4-phosphate kinase:PIP5K:pidins:4p-5-kinase:diphosphoinositide kinase] [gn:fab1] [gicfc:8.1:12.16] [ec:2.7.1.68] [keggf
CONTIG1509	26367036_f3_2	4298	18401	99	333	YFR019W	93	0.41999	Saccharomyces cerevisiae	[ui:yfr019w] [pn:probable pip 5-kinase:probable phosphatidylinositol-4-phosphate 5-kinase:1- phosphatidylinositol-4-phosphate kinase:PIP5K:pidins:4p-5-kinase:diphosphoinositide kinase] [gn:fab1] [gicfc:8.1:12.16] [ec:2.7.1.68] [keggf
CONTIG3834	4943878_c2_2	4299	18402	1362	454	YFR019W	345	4.5(10)-58	Saccharomyces cerevisiae	[ui:yfr019w] [pn:probable pip 5-kinase:probable phosphatidylinositol-4-phosphate 5-kinase:1- phosphatidylinositol-4-phosphate kinase:PIP5K:pidins:4p-5-kinase:diphosphoinositide kinase] [gn:fab1] [gicfc:8.1:12.16] [ec:2.7.1.68] [keggf

CONTIG5376	5861626_f2_3	4300	18403	2544	848	YFR019W	158	3.8(10)-7	Saccharomyces cerevisiae	[ui:yfr019w] [pn:probable pip 5-kinase;probable phosphatidylinositol-4-phosphate 5-kinase;1- phosphatidylinositol-4-phosphate kinase;pip5k;pidins:4p-5-kinase;diphosphoinositide kinase] [gn:fab1] [gcfc:8.1:12.16] [ec:2.7.1.68] [keggf]
CONTIG5617	35347143_f3_4	4301	18404	966	322	YFR019W	941	3.3(10)-93	Saccharomyces cerevisiae	[ui:yfr019w] [pn:probable pip 5-kinase;probable phosphatidylinositol-4-phosphate 5-kinase;1- phosphatidylinositol-4-phosphate kinase;pip5k;pidins:4p-5-kinase;diphosphoinositide kinase] [gn:fab1] [gcfc:8.1:12.16] [ec:2.7.1.68] [keggf]
CONTIG78	433332_f2_1	4302	18405	675	225	YFR019W	253	1.2(10)-22	Saccharomyces cerevisiae	[ui:yfr019w] [pn:probable pip 5-kinase;probable phosphatidylinositol-4-phosphate 5-kinase;1- phosphatidylinositol-4-phosphate kinase;pip5k;pidins:4p-5-kinase;diphosphoinositide kinase] [gn:fab1] [gcfc:8.1:12.16] [ec:2.7.1.68] [keggf]

CONTIG4117	15679688_c1_2	4303	18406	1887	629	YLR305C	805	7.2(10)-79	Saccharomyces cerevisiae	[ui:yr305c] [pn:phosphatidylinositol 4-kinase;phosphatidylinositol 4-kinase stt4;pi4-kinase;ptdins-4-kinase] [gn:stt4;12 42] [gicfc:8.1:12.13:12.8] [ec:2.7.1.67] [keggfc:8.1] [sgdfc:3.8.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4365	956942_f2_1	4304	18407	2136	712	YLR305C	1599	2.2(10)-164	Saccharomyces cerevisiae	[ui:yr305c] [pn:phosphatidylinositol 4-kinase;phosphatidylinositol 4-kinase stt4;pi4-kinase;ptdins-4-kinase] [gn:stt4;12 42] [gicfc:8.1:12.13:12.8] [ec:2.7.1.67] [keggfc:8.1] [sgdfc:3.8.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1188	35792166_f1_1	4305	18408	1059	353	YNL267W	322	8.5(10)-28	Saccharomyces cerevisiae	[ui:yr1267w] [pn:phosphatidylinositol 4-kinase;phosphatidylinositol 4-kinase pik1;pi4-kinase;ptdins-4-kinase] [gn:pik1:n0795] [gicfc:8.1:10.1:10.2:12.13:12.8] [ec:2.7.1.67] [keggfc:8.1] [sgdfc:3.9.0:9.5.0:15.0.0] [db:gtc-saccharomyces]

CONTIG2802	15712757_f3_4	4306	18409	522	174	YNL267W	294	8.4(10)-25	Saccharomyces cerevisiae	[ui:ynl267w] [pn:phosphatidylinositol 4-kinase;phosphatidylinositol 4-kinase:pik1:p14-kinase:ptdins4-kinase] [gn:pik1:n0795] [gicfc:8.1:10.1:10.2:12.13:12.8] [ec:2.7.1.67][keggfc:8.1] [sgdfc:3.9.09.5.0:15.0.0][db:gtc-saccharomyces]
CONTIG2673	25407718_f2_1	4307	18410	852	284	YNL267W	936	2.0(10)-99	Saccharomyces cerevisiae	[ui:ynl267w] [pn:phosphatidylinositol 4-kinase;phosphatidylinositol 4-kinase:pik1:p14-kinase:ptdins4-kinase] [gn:pik1:n0795] [gicfc:8.1:10.1:10.2:12.13:12.8] [ec:2.7.1.67][keggfc:8.1] [sgdfc:3.9.09.5.0:15.0.0][db:gtc-saccharomyces]
CONTIG2911	33254626_f1_1	4308	18411	939	313	YNL267W	991	5.7(10)-100	Saccharomyces cerevisiae	[ui:ynl267w] [pn:phosphatidylinositol 4-kinase;phosphatidylinositol 4-kinase:pik1:p14-kinase:ptdins4-kinase] [gn:pik1:n0795] [gicfc:8.1:10.1:10.2:12.13:12.8] [ec:2.7.1.67][keggfc:8.1] [sgdfc:3.9.09.5.0:15.0.0][db:gtc-saccharomyces]

b1x18076.x	5322766_f1_1	4309	18412	516	172	YNL267W	385	1.5(10)-34	Saccharomyces cerevisiae	[ui:ynl267w] [pn:phosphatidylinositol 4-kinase:phosphatidylinositol 4-kinase pik1:pi4-kinase:pidins-4-kinase] [gn:pik1:n0795] [gicfc:8.1:10.1:10.2:12.13:12.8] [ec:2.7.1.67] [keggfc:8.1] [sgdgc:3.9.0:9.5.0:15.0.0] [db:gtc-saccharomyces]
b9x12s75.y	25969f62_c1_2	4310	18413	558	186	YNL267W	156	4.5(10)-10	Saccharomyces cerevisiae	[ui:ynl267w] [pn:phosphatidylinositol 4-kinase:phosphatidylinositol 4-kinase pik1:pi4-kinase:pidins-4-kinase] [gn:pik1:n0795] [gicfc:8.1:10.1:10.2:12.13:12.8] [ec:2.7.1.67] [keggfc:8.1] [sgdgc:3.9.0:9.5.0:15.0.0] [db:gtc-saccharomyces]
CONTIG5297	22460307_c1_12	4311	18414	1356	452	YAR018C	397	2.6(10)-71	Saccharomyces cerevisiae	[ui:yar018c] [pn:ser/thr protein kinase:serine/threonine-protein kinase kin3][gn:kin3.mpk1:fun52] [gicfc:8.5.9:4:12.13:14.3] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdgc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5233	34251566_c3_14	4312	18415	1206	402	YAR019C	605	2.1(10)-58	Saccharomyces cerevisiae	[ui:yar019c] [pn:protein kinase of the map kinase kinase kinase family:cell division control protein 15][gn:cdc15] [gicfc:8.5.9:4:12.13:12.8] [ec:2.7.1.-] [keggfc:8.5:9.4:13.3] [sgdgc:3.8.0:15.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3766	33990918_c3_6	4313	18416	576	192	YBL105C	647	1.3(10)-62	Saccharomyces cerevisiae	[ui:yb105c] [pn:ser/thr-specific protein kinase;protein kinase c-like 1;pkc 1] [gn:pkcl1;stl1;hp02;yb10807] [gicfc:8.5:9.4:12.13:12.8:13.2] [ec:2.7.1.-1][keggfc:8.5:9.4] [sgdfc:3.2.0:3.8.0:10.2.5:11.1:0:15.0] [db:gtc-saccharomyces c 0]
CONTIG3284	24806563_c1_3	4314	18417	1122	374	YBL016W	974	3.7(10)-98	Saccharomyces cerevisiae	[ui:yb1016w] [pn:mitogen-activated protein kinase;map kinase:mitogen-activated protein kinase fus3:map kinase fus3] [gn:fus3:dac2;yb10303;yb103] [gicfc:8.5:9.4:12.13:12.8:12.9] [ec:2.7.1.-1][keggfc:8.5:9.4:13.1] [sgdfc:3.3.0:3.8.0:9.2]
b1x18255.x	6814506_c2_1	4315	18418	468	156	YBL016W	517	9.8(10)-50	Saccharomyces cerevisiae	[ui:yb1016w] [pn:mitogen-activated protein kinase;map kinase:mitogen-activated protein kinase fus3:map kinase fus3] [gn:fus3:dac2;yb10303;yb103] [gicfc:8.5:9.4:12.13:12.8:12.9] [ec:2.7.1.-1][keggfc:8.5:9.4:13.1] [sgdfc:3.3.0:3.8.0:9.2]
CONTIG5604	10553135_f3_5	4316	18419	897	299	YBR028C	287	9.3(10)-25	Saccharomyces cerevisiae	[ui:ybr028c] [pn:similarity to ribosomal protein kinases;probable serine/threonine-protein kinase ybr028c][gn:ybrd312] [gicfc:8.5:9.4:12.13:14.3] [ec:2.7.1.-1][keggfc:8.5:9.4] [sgdfc:15.0:13.0:0][db:gtc-saccharomyces cerevisiae]

CONTIG5604	34070937_f2_4	4317	18420	870	290	YBR028C	343	1.3(10)-40	Saccharomyces cerevisiae	[ui:ybr028c] [pn:similarity to ribosomal protein kinases;probable serine/threonine-protein kinase ybr028c] [gn:ybr0312]
										[gicfc:8.5:9.4:12.13:14.3]
										[ec:2.7.1.-] [keggfc:8.5:9.4]
										[sgdfc:15.0.0:13.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG3320	9772750_f2_2	4318	18421	627	209	YBR059C	485	3.2(10)-45	Saccharomyces cerevisiae	[ui:ybr059c] [pn:similarity to ser/thr-specific protein kinase pak1p;probable serine/threonine-protein kinase ybr059c]
										[gn:ybr0519]
										[gicfc:8.5:9.4:12.13:14.3]
										[ec:2.7.1.-] [keggfc:8.5:9.4]
										[sgdfc:15.0.0:13.0.0] [db:gic-saccharomyces c]
CONTIG5051	3957063_f1_1	4319	18422	1608	536	YBR059C	352	3.2(10)-29	Saccharomyces cerevisiae	[ui:ybr059c] [pn:similarity to ser/thr-specific protein kinase pak1p;probable serine/threonine-protein kinase ybr059c]
										[gn:ybr0519]
										[gicfc:8.5:9.4:12.13:14.3]
										[ec:2.7.1.-] [keggfc:8.5:9.4]
										[sgdfc:15.0.0:13.0.0] [db:gic-saccharomyces c]
CONTIG1377	29567590_c2_3	4320	18423	1146	382	YBR097W	538	1.3(10)-50	Saccharomyces cerevisiae	[ui:ybr097w] [pn:ser/thr protein kinase;protein kinase vps15]
										[gn:vps15:ybr0825]
										[gicfc:8.5:9.4:10.7:11.1:12.10:12.13]
										[ec:2.7.1.-] [keggfc:8.5:9.4]
										[sgdfc:6.2.0:8.3.0:8.5.0:15.0.0]
										[db:gic-saccharomyces cerevisiae]

CONTIG1705	33635052_f2_1	4321	18424	1377	459	YBR097W	173	1.0(10)-10	Saccharomyces cerevisiae	[ui:ybr097w] [pn:ser/hr protein kinase:protein kinase yps15] [gn:yps15:ybr0825] [gicfc:8.5:9.4:0.7:11.1:12.10:12.13] [ec:2.7.1.-][keggfc:8.5:9.4] [sgdgc:6.2.0:8.3.0:8.5.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5403	24789827_f1_4	4322	18425	1056	352	YBR097W	700	6.0(10)-68	Saccharomyces cerevisiae	[ui:ybr097w] [pn:ser/hr protein kinase:protein kinase yps15] [gn:yps15:ybr0825] [gicfc:8.5:9.4:0.7:11.1:12.10:12.13] [ec:2.7.1.-][keggfc:8.5:9.4] [sgdgc:6.2.0:8.3.0:8.5.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4705	4475912_f2_3	4323	18426	993	331	YBR160W	1202	2.5(10)-122	Saccharomyces cerevisiae	[ui:ybr160w] [pn:cyclin-dependent protein kinase:cell division control protein 28] [gn:cdc28:srm5:ybr1211] [gicfc:8.5:9.4:10.8:12.13:12.8] [ec:2.7.1.-] [keggfc:8.5:9.4:13.1:13.2:13.3] [sgdgc:3.2.0:3.6.0:3.8.0:15.0.0] [db:gtc-saccharom
CONTIG5495	803161_c2_16	4324	18427	1932	644	YCR008W	1313	4.4(10)-134	Saccharomyces cerevisiae	[ui:ycr008w] [pn:similarity to npr1p and hal5p protein kinases:probable serine/threonine-protein kinase ycr8w] [gn:sat4.ycr8w:ycr101:ycr046] [gicfc:8.5:9.4:12.13.13.2] [ec:2.7.1.-][keggfc:8.5:9.4] [sgdgc: 11.1.0:15.0.0] [db:gtc-saccha

CONTIG4031	4772782_f1_1	4325	18428	1044	348	YDL108W	1142	5.7(10)-116	Saccharomyces cerevisiae	[ui:yd1108w] [pn:cyclin-dependent ser/thr protein kinase:serine/threonine-protein kinase:kin28] [gn:kin28:d2330] [gicfc:8.5:9.4:10.1:10.10.2:12.13 :12.8] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:3.8.0:4.8.1:9.5.0:11.2.1:15.0.0] [db:gic-0]
b9x11x80.x	24227342_c2_2	4326	18429	309	103	YDL101C	219	2.3(10)-17	Saccharomyces cerevisiae	[ui:yd1101c] [pn:protein kinase:dna damage response protein kinase dun1] [gn:dun1:d2370] [gicfc:8.5:9.4:10.1:10.10.2:12.13 :12.8] [ec:2.7.1.-] [keggfc:8.5:9.4:13.3] [sgdfc:9.5.0:11.2.1:15.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG1961	14569708_c3_4	4327	18430	1143	381	YDL028C	411	1.0(10)-37	Saccharomyces cerevisiae	[ui:yd1028c] [pn:serine/threonine/tyrosine protein kinase:serine/threonine/protein kinase mpst1:regulatory cell proliferation kinase 1] [gn:mpst1:rpk1:d22785] [gicfc:8.5:9.4:12.13:12.8] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:3.5.0:3.8.0:15]

CONTIG2279	1269534_c1_4	4328	18431	636	212	YDL028C	536	1.1(10)-51	Saccharomyces cerevisiae	[ui:yd1028c] [pn:serine/threonine/tyrosine protein kinase;serine/threonine protein kinase mpsi:regulatory cell proliferation kinase 1] [gn:mps1:rpk1:d2785] [gicfc:8.5:9.4:[12.13:12.8]] [ec:2.7.1.-][keggc:8.5:9.4] [sgdgc:3.5.0:3.8:0:15]
CONTIG2710	34182902_f3_2	4329	18432	1380	460	YDL017W	525	6.9(10)-75	Saccharomyces cerevisiae	[ui:yd1017w][pn:protein kinase:cell division control protein 7] [gn:cdc7:oaf2:d2855] [gicfc:8.5:9.4:[10.1:10.2:10.8:12.13:12.8]] [ec:2.7.1.-] [keggfc:8.5:9.4:13.2] [sgdgc:3.5.0:3.6:0:3.8:0:9.5:0:15.0] [db:gic-saccharomyces cerevisiae]
CONTIG3789	16432842_f3_3	4330	18433	501	167	YDL017W	94	0.00073	Saccharomyces cerevisiae	[ui:yd1017w][pn:protein kinase:cell division control protein 7] [gn:cdc7:oaf2:d2855] [gicfc:8.5:9.4:[10.1:10.2:10.8:12.13:12.8]] [ec:2.7.1.-] [keggfc:8.5:9.4:13.2] [sgdgc:3.5.0:3.6:0:3.8:0:9.5:0:15.0] [db:gic-saccharomyces cerevisiae]

CONTIG433	36351637_f2_1	43331	18434	318	106	YDL017W	103	8.0(10)-5	Saccharomyces cerevisiae	[ui:yd 017w] [pn:protein kinase:cell division control protein 7] [gn:cdc7:oaf2:db:2855] [gtfc:8.5:9.4:10.1:10.2:10.8:12.13: 12.8] [ec:2.7.1.-] [kegg:fc:8.5:9.4:13.2] [sgdfc:3.5.0:3.6.0:3.8.0:9.5:0:15.0:0] [db:gtc-saccharomyces cerevisiae]
CONTIG2631	29495912_c1_5	43332	18435	1173	391	YDR122W	1051	2.5(10)-106	Saccharomyces cerevisiae	[ui:yd 122w] [pn:ser/thr protein kinase:protein kinase] [gn:kin1] [gtfc:8.5:9.4:11.1:12.13: ec:2.7.1.-] [kegg:fc:8.5:9.4] [sgdfc:9.1.0:15.0:0] [db:gtc-saccharomyces cerevisiae]
b3x13461.x	16064567_f2_2	43333	18436	612	204	YDR122W	92	0.069	Saccharomyces cerevisiae	[ui:yd 122w] [pn:ser/thr protein kinase:protein kinase] [gn:kin1] [gtfc:8.5:9.4:11.1:12.13: ec:2.7.1.-] [kegg:fc:8.5:9.4] [sgdfc:9.1.0:15.0:0] [db:gtc-saccharomyces cerevisiae]
CONTIG2765	6852175_f3_2	43334	18437	1233	411	YDR283C	286	6.0(10)-48	Saccharomyces cerevisiae	[ui:yd 283c] [pn:ser/thr protein kinase:protein kinase gen2] [gn:gen2:aas1] [gtfc:8.5:9.4:10.7:12.13: ec:2.7.1.-] [kegg:fc:8.5:9.4] [sgdfc:5.3.0:9.2:0:15.0:0] [db:gtc-saccharomyces cerevisiae]
CONTIG3593	19532525_c3_4	43335	18438	1053	351	YDR283C	400	9.6(10)-58	Saccharomyces cerevisiae	[ui:yd 283c] [pn:ser/thr protein kinase:protein kinase gen2] [gn:gen2:aas1] [gtfc:8.5:9.4:10.7:12.13: ec:2.7.1.-] [kegg:fc:8.5:9.4] [sgdfc:5.3.0:9.2:0:15.0:0] [db:gtc-saccharomyces cerevisiae]

CONTIG4328	4797160_f1_1	4336	18439	792	264	YDR283C	160	2.8(10)-10	Saccharomyces cerevisiae	[ui:ydr283c] [pn:ser/thr protein kinase:protein kinase gen2] [gn:gcn2:aas] [gtcfc:8.5:9.4:10.7:12.13] [ec:2.7.1.-][keggfc:8.5:9.4] [sgdgc:5.3.0:9.2:0.15:0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG443	2384652_c3_1	4337	18440	645	215	YDR283C	334	8.6(10)-29	Saccharomyces cerevisiae	[ui:ydr283c] [pn:ser/thr protein kinase:protein kinase gen2] [gn:gcn2:aas] [gtcfc:8.5:9.4:10.7:12.13] [ec:2.7.1.-][keggfc:8.5:9.4] [sgdgc:5.3.0:9.2:0.15:0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2526	4492135_f1_1	4338	18441	1254	418	YDR477W	1345	1.8(10)-137	Saccharomyces cerevisiae	[ui:ydr477w] [pn:carbon catabolite derepressing ser/thr protein kinase:carbon catabolite derepressing protein kinase] [gn:snf1:ccr1:pas14:glc2:d8035] [gtcfc:8.5:9.4:12.13:13.2] [ec:2.7.1.-][keggfc:8.5:9.4] [sgdgc:1.5:2:9.2:0:11]
CONTIG369	11813561_f2_1	4339	18442	438	146	YDR477W	500	6.2(10)-48	Saccharomyces cerevisiae	[ui:ydr477w] [pn:carbon catabolite derepressing ser/thr protein kinase:carbon catabolite derepressing protein kinase] [gn:snf1:ccr1:pas14:glc2:d8035] [gtcfc:8.5:9.4:12.13:13.2] [ec:2.7.1.-][keggfc:8.5:9.4] [sgdgc:1.5:2:9.2:0:11]

CONTIG5005	820385_f3_3	4340	18443	1293	431	YDR523C	311	1.3(10)-27	Saccharomyces cerevisiae	[ui:ydr523c] [pn:ser/thr protein kinase:sporulation-specific protein 1] [gn:spsl:d9719]
CONTIG5636	35164093_f3_4	4341	18444	1095	365	YDR523C	237	4.2(10)-34	Saccharomyces cerevisiae	[ui:ydr523c] [pn:ser/thr protein kinase:sporulation-specific protein 1] [gn:spsl:d9719]
CONTIG1559	24707588_c2_5	4342	18445	903	301	YER123W	95	0.05099	Saccharomyces cerevisiae	[ui:yck3:cki3] [gn:yck3:cki3]
CONTIG2252	20133502_c3_2	4343	18446	912	304	YER129W	448	3.2(10)-41	Saccharomyces cerevisiae	[ui:yer129w] [pn:casein kinase, isoform 3.casein kinase i homolog 3] [gn:yck3:cki3]
CONTIG5646	23648375_c2_16	4344	18447	4278	1426	YER129W	575	1.1(10)-91	Saccharomyces cerevisiae	[ui:yer129w] [pn:protein kinase:serine/threonine-protein kinase pak1] [gn:pak1:sygp-orf45]

b3x13076.x	24820337_c1_1	4345	18448	288	96	YER129W	127	6.0(10)-7	Saccharomyces cerevisiae	[uri:yer129w] [pn:protein kinase;serine/threonine-protein kinase pak1] [gn:pak1;sgp:orf45] [gicfc:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2770	35829017_c2_2	4346	18449	909	303	YFL033C	550	9.5(10)-52	Saccharomyces cerevisiae	[uri:yfl033c] [pn:similarity to s.pombe cek1 serine/threonine protein kinase;probable serine/threonine-protein kinase yfl033c] [gicfc:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4635	14178450_f3_6	4347	18450	858	286	YFL033C	97	0.17	Saccharomyces cerevisiae	[uri:yfl033c] [pn:similarity to s.pombe cek1 serine/threonine protein kinase;probable serine/threonine-protein kinase yfl033c] [gicfc:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4951	196890_f2_3	4348	18451	1158	386	YFL033C	290	3.5(10)-33	Saccharomyces cerevisiae	[uri:yfl033c] [pn:similarity to s.pombe cek1 serine/threonine protein kinase;probable serine/threonine-protein kinase yfl033c] [gicfc:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4951	4164136_f2_4	4349	18452	732	244	YFL033C	179	2.8(10)-12	Saccharomyces cerevisiae	[ui:yfl033c] [pn: similarity to s.pombe cek1 serine/threonine protein kinase; probable yfl033c] [gicfc:8.5.9.4:12.13:14.3] [ec:2.7.1.-] [keggfc:8.5.9.4] [sgdfc:15.0:0:13.0.0] [db:gic-saccharomyces cerevis]
CONTIG879	1464010_c1_2	4350	18453	570	190	YFL033C	92	0.01	Saccharomyces cerevisiae	[ui:yfl033c] [pn: similarity to s.pombe cek1 serine/threonine protein kinase; probable yfl033c] [gicfc:8.5.9.4:12.13:14.3] [ec:2.7.1.-] [keggfc:8.5.9.4] [sgdfc:15.0:0:13.0.0] [db:gic-saccharomyces cerevis]
CONTIG2080	20114042_f1_2	4351	18454	1038	346	YFL029C	239	5.2(10)-19	Saccharomyces cerevisiae	[ui:yfl029c] [pn: cdk-activating protein kinase; serine/threonine-protein kinase cak1 : cdk-activating kinase] [gn:cak1 : civ1] [gicfc:8.5.9.4:12.13:12.8] [ec:2.7.1.-] [keggfc:8.5.9.4:13.3] [sgdfc:3.8.0:15.0.0] [db:gic-saccharomyces cerevis]
CONTIG3639	25398512_c1_4	4352	18455	786	262	YGL180W	187	1.6(10)-17	Saccharomyces cerevisiae	[ui:ygl180w] [pn: weak similarity to ser/hr protein kinases; probable ygl180w] [gn:g1615] [gicfc:8.5.9.4:12.13:14.3] [ec:2.7.1.-] [keggfc:8.5.9.4] [sgdfc:15.0:0:13.0.0] [db:gic-saccharomyces cerevisiae]

CONTIG5646	2191277_c3_20	4353	18456	1233	411	YGL180W	874	1.3(10)-87	Saccharomyces cerevisiae	[ui:yg1180w] [pn:weak similarity to ser/thr protein kinases;probable serine/threonine-protein kinase ygl1180w] [gn:g1615] [gtcfc:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdgc:15.0:13.0] [db:gtc-saccharomyces cerevisiae]
CONTIG607	9814063_f2_1	4354	18457	792	264	YCR092W	352	8.4(10)-32	Saccharomyces cerevisiae	[ui:yg092w] [pn:ser/hr protein kinase related to dbf20p;cell cycle protein kinase] [gn:dbf2] [gtcfc:8.5:9.4:12.13:12.8] [ec:2.7.1.-] [keggfc:8.5:9.4:13.3] [sgdgc:3.8.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
b3x16309_x	23437827_c2_3	4355	18458	879	293	YCR092W	509	5.5(10)-59	Saccharomyces cerevisiae	[ui:yg092w] [pn:ser/hr protein kinase related to dbf20p;cell cycle protein kinase] [gn:dbf2] [gtcfc:8.5:9.4:12.13:12.8] [ec:2.7.1.-] [keggfc:8.5:9.4:13.3] [sgdgc:3.8.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3029	13835130_c1_4	4356	18459	1443	481	YCR188C	661	2.0(10)-64	Saccharomyces cerevisiae	[ui:yg188c] [pn:ser/thr protein kinase:checkpoint serine/threonine-protein kinase bub1] [gn:bub1:g7542] [gtcfc:8.5:9.4:10.1:10.2:12.13:12.8] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdgc:3.8.0:9.5.0:15.0.0] [db:gtc-saccharomyces cerevisiae]

b1x17652.y	16287538_f3_1	4357	18460	807	269	YGR188C	194	8.5(10)-17	Saccharomyces cerevisiae	[ui:ygr188c] [pn:ser/thr protein kinase;checkpoint serine/threonine-protein kinase bub1] [gn:bub1:g7542] [gicfc:8.5:9.4:10.1:10.2:12.13:12.8] [ec:2.7.1.-][keggfc:8.5:9.4] [sgdfc:3.8.0:9.5:0:15.0:0][db:gic-saccharomyces cerevisiae]
CONTIG4932	15745328_f2_3	4358	18461	1233	411	YHL007C	1209	4.5(10)-123	Saccharomyces cerevisiae	[ui:yhl007c] [pn:ser/thr protein kinase of the pheromone pathway;serine/threonine-protein kinase][gn:ste20] [gicfc:8.5:9.4:12.13:12.8:12.9] [ec:2.7.1.-] [keggfc:8.5:9.4:13.1:13.3] [sgdfc:3.2.0:3.3.0:9.2:0:10.1:4:15.0] [db:gic-sacch0]
CONTIG5773	24413287_c3_31	4359	18462	1623	541	YHR030C	1348	8.5(10)-138	Saccharomyces cerevisiae	[ui:yhr030c] [pn:ser/thr protein kinase of map kinase family;mitogen-activated protein kinase sl12/mpk1;map kinase mpk1] [gn:sl12:mpk1] [gicfc:8.5:9.4:12.11:12.13:12.8:13.2] [ec:2.7.1.-][keggfc:8.5:9.4] [sgdfc:3.1.0:3.2:0:3.8:0:1:0.2.]
CONTIG2779	181557_c2_3	4360	18463	1161	387	YHR079C	445	6.2(10)-41	Saccharomyces cerevisiae	[ui:yhr079c] [pn:protein kinase;probable protein kinase ire1 precursor][gn:ire1:erm1] [gicfc:8.5:9.4:12.13:12.16:13.2] [ec:2.7.1.-][keggfc:8.5:9.4] [sgdfc:9.4.0:11.1.0:15.0:0][db:gic-saccharomyces cerevisiae]

CONTIG652	4772567_f2_1	4361	18464	804	268	YHR079C	643	3.1(10)-62	Saccharomyces cerevisiae	[ui:yrh079c] [pn:protein kinase;probable protein kinase ire1 precursor] [gn:ire1;ern1] [gicfc:8.5:9.4:12.13:12.16:13.2] [ec:2.7.1.-] [keggc:8.5:9.4] [sgdic:9.4:0.11.1.0:15.0.0] [db:gic-saccharomyces cerevisiae]
b2x14728.x	11173962_f2_1	4362	18465	528	176	YHR079C	385	1.7(10)-34	Saccharomyces cerevisiae	[ui:yrh079c] [pn:protein kinase;probable protein kinase ire1 precursor] [gn:ire1;ern1] [gicfc:8.5:9.4:12.13:12.16:13.2] [ec:2.7.1.-] [keggc:8.5:9.4] [sgdic:9.4:0.11.1.0:15.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG4004	15829380_c2_7	4363	18466	1914	638	YHR082C	301	1.3(10)-25	Saccharomyces cerevisiae	[ui:yrh082c] [pn:ser/thr protein kinase;serine/threonine-protein kinase] [gn:ksp] [gicfc:8.5:9.4:10.1:10.2:12.13] [ec:2.7.1.-] [keggc:8.5:9.4] [sgdic:9.5:0.15.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG4754	787550_f1_6	4364	18467	315	105	YHR082C	133	1.2(10)-7	Saccharomyces cerevisiae	[ui:yrh082c] [pn:ser/thr protein kinase;serine/threonine-protein kinase] [gn:ksp] [gicfc:8.5:9.4:10.1:10.2:12.13] [ec:2.7.1.-] [keggc:8.5:9.4] [sgdic:9.5:0.15.0.0] [db:gic-saccharomyces cerevisiae]

CONTIG4227	10985682_c3_8	4365	18468	2061	687	YHR102W	1093	9.0(t10)-111	Saccharomyces cerevisiae	[ui:yr102w] [pn:ser/thr protein kinase that interacts with cdc31p;serine/threonine-protein kinase:n-rich kinase 1] [gn:nrk1] [gicfc:8.5:9.4:12.13:12.8] [ec:2.7.1.-][keggfc:8.5:9.4] [sgdfc:3.8:0:15.0:0] [db:gtc-saccharomyces cerevisi]
CONTIG5005	1175001_f3_2	4366	18469	396	132	YHR102W	197	1.8(t10)-14	Saccharomyces cerevisiae	[ui:yr102w] [pn:ser/thr protein kinase that interacts with cdc31p;serine/threonine-protein kinase:n-rich kinase 1] [gn:nrk1] [gicfc:8.5:9.4:12.13:12.8] [ec:2.7.1.-][keggfc:8.5:9.4] [sgdfc:3.8:0:15.0:0] [db:gtc-saccharomyces cerevisi]
CONTIG5332	31652083_f2_3	4367	18470	570	190	YHR102W	109	4.7(t10)-5	Saccharomyces cerevisiae	[ui:yr102w] [pn:ser/thr protein kinase that interacts with cdc31p;serine/threonine-protein kinase:n-rich kinase 1] [gn:nrk1] [gicfc:8.5:9.4:12.13:12.8] [ec:2.7.1.-][keggfc:8.5:9.4] [sgdfc:3.8:0:15.0:0] [db:gtc-saccharomyces cerevisi]
CONTIG3439	23869215_c3_8	4368	18471	1833	611	YJL187C	566	2.2(t10)-69	Saccharomyces cerevisiae	[ui:yj187c] [pn:ser/tyr dual-specificity protein kinase:mitosis inhibitor protein kinase swe1] [gnswe1:j0406] [gicfc:8.5:9.4:12.13:12.8] [ec:2.7.1.-][keggfc:8.5:9.4:13.3] [sgdfc:3.8:0:15.0:0] [db:gtc-saccharomyces cerevisiae]

CONTIG3751	21681527_f3_1	4369	18472	1791	597	YJL141C	517	3.1(10)-49	Saccharomyces cerevisiae	[uiyj1141c] [pn:ser/thr protein kinase;protein kinase yak1] [gn:yak1_j0652] [gtfc:8.5:9.4:12.13:12.8] [ec:2.7.1.-] [keggc:8.5:9.4] [sgd:3.8.0:15.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG3091	97531_f1_1	4370	18473	1455	485	YJL141C	1074	9.1(10)-109	Saccharomyces cerevisiae	[uiyj1141c] [pn:ser/thr protein kinase;protein kinase yak1] [gn:yak1_j0652] [gtfc:8.5:9.4:12.13:12.8] [ec:2.7.1.-] [keggc:8.5:9.4] [sgd:3.8.0:15.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG3112	12695187_f3_2	4371	18474	996	332	YJL128C	562	1.7(10)-54	Saccharomyces cerevisiae	[uiyj1128c] [pn:tyrosine protein kinase of the map kinase kinase family;polymyxin b resistance protein kinase] [gn:pbs2:hog4:sfs4:ssk4:j0699] [gtfc:8.5:9.4:12.11:12.13:13.2] [ec:2.7.1.-] [keggc:8.5:9.4] [sgd:1.5.2:10.3.3:11.1:0.1]
CONTIG5493	7267961_f3_7	4372	18475	1581	527	YJL106W	933	8.0(10)-94	Saccharomyces cerevisiae	[uiyj1106w] [pn:ser/thr protein kinase;meiosis induction protein kinase smf1/lime2] [gn:smf1:jme2:j0817] [gtfc:8.5:9.4:12.13:12.15:12.8] [ec:2.7.1.-] [keggc:8.5:9.4] [sgd:3.4.0:3.5.0:3.8.0:15.0.0] [db:gic-saccharomyces cerevisiae]

CONTIG4749	4881586_c2_9	4373	18476	1860	620	YJL057C	337	9.8(10)-28	Saccharomyces cerevisiae	[ui:yi 057c] [pn:weak similarity to human p1/eif-2a protein kinase;probable serine/threonine-protein kinase yi 057c] [gn:j1143] [gtfc:8.5:9.4:14.3] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:13.0.0] [db:gtc-saccharomyces cerevisiae]
b2x11515.x	43754438_f3_3	4374	18477	561	187	YJL006C	147	5.7(10)-10	Saccharomyces cerevisiae	[ui:yi 006c] [pn:carboxy-terminal domain:ctd kinase, beta subunit:ctd kinase beta subunit:ctd kinase 38 kd subunit:ctdk-i beta subunit] [gn:ctk2 j1390] [gtfc:8.5:9.4:10.1:10.2] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:4.8:2.9.5.0] [db:gt]
CONTIG3458	22071000_c3_12	4375	18478	801	267	YJR059W	401	1.6(10)-36	Saccharomyces cerevisiae	[ui:yr059w] [pn:involved in polyamine uptake;probable serine/threonine-protein kinase yr059w] [gn:plk2 j1725] [gtfc:8.5:9.4:12.13:12.16] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:8.8.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3458	31899812_c1_5	4376	18479	978	326	YJR059W	469	6.5(10)-44	Saccharomyces cerevisiae	[ui:yr059w] [pn:involved in polyamine uptake;probable serine/threonine-protein kinase yr059w] [gn:plk2 j1725] [gtfc:8.5:9.4:12.13:12.16] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:8.8.0:15.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2622	26048442_f3_2	4377	18480	1986	662	YKL171W	235	1.8(10)-29	Saccharomyces cerevisiae	[ui:ykl171w] [pn:ser/thr protein kinase;probable serine/threonine-protein kinase ykl171w] [gn:ykl635] [gtfc:12.13:8.5:9.4] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:15.0.0:13.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG3900	24039516_f3_4	4378	18481	1680	560	YKL139W	874	1.3(10)-87	Saccharomyces cerevisiae	[ui:ykl139w] [pn:carboxy-terminal domain:ctd kinase, alpha subunit:ctd kinase alpha subunit:ctd kinase 58 kd subunit:ctdk-1 alpha subunit] [gn:ctk1] [gtfc:8.5:9.4:10.1:10.2:12.13] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:4.8.2:9.5:0:15.0]
CONTIG3582	24005340_c3_5	4379	18482	1413	471	YKL126W	1386	8.0(10)-142	Saccharomyces cerevisiae	[ui:ykl126w] [pn:ser/thr-specific protein kinase;serine/threonine-protein kinase] [gn:ypk1] [gtfc:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:15.0.0:13.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG4716	15120377_f3_7	4380	18483	1476	492	YKL116C	139	2.0(10)-6	Saccharomyces cerevisiae	[ui:ykl116c] [pn:ser/thr protein kinase with similarity to rat snf1, <i>celegans unc-51</i> , <i>dun1p</i> probable serine/threonine-protein kinase ykl116c] [gn:ykl516] [gtfc:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:15.0.0:13.0.0] [

CONTIGS282	33222062_f1_1	4381	18484	1320	440	YKL101W	112	0.0077	Saccharomyces cerevisiae	[ui:ykl101w] [pn:ser/thr protein kinase that interacts genetically with histone mutations:probable serine/threonine-protein kinase ykl101w] [gn:hs11:ykl453] [gtfc:8.5:9.4:12.13:12.8] [ec:2.7.1.-][keggfc:8.5:9.4:13.3] [sgdfc:3.8.0:15]
CONTIGS594	4885787_f3_7	4382	18485	1164	388	YKL101W	438	6.4(10)-40	Saccharomyces cerevisiae	[ui:ykl101w] [pn:ser/thr protein kinase that interacts genetically with histone mutations:probable serine/threonine-protein kinase ykl101w] [gn:hs11:ykl453] [gtfc:8.5:9.4:12.13:12.8] [ec:2.7.1.-][keggfc:8.5:9.4:13.3] [sgdfc:3.8.0:15]
b2x12381.y	14540930_f3_1	4383	18486	351	117	YKL101W	198	2.2(10)-14	Saccharomyces cerevisiae	[ui:ykl101w] [pn:ser/thr protein kinase that interacts genetically with histone mutations:probable serine/threonine-protein kinase ykl101w] [gn:hs11:ykl453] [gtfc:8.5:9.4:12.13:12.8] [ec:2.7.1.-][keggfc:8.5:9.4:13.3] [sgdfc:3.8.0:15]
CONTIG3954	4393910_c2_4	4384	18487	996	332	YLL019C	117	0.00027	Saccharomyces cerevisiae	[ui:yll019c] [pn:ser/thr protein kinase:probable serine/threonine-protein kinase] [gn:kns1] [gtfc:8.5:9.4:12.13:14.3] [ec:2.7.1.-][keggfc:8.5:9.4] [sgdfc:15.0:13.0:0] [db:gtc-saccharomyces cerevisiae]

b9x13q33.x	21766543_f1_1	4385	18488	621	207	YLL019C	499	1.3(10)-47	Saccharomyces cerevisiae	[uri:y1019c] [pn:ser/thr protein kinase;probable serine/threonine-protein kinase] [gn:kins1] [gicfc:8.5:9.4:12.13:14:3] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:15.0:0:13.0:0] [db:gic-saccharomyces cerevisiae]
CONTIG2037	13869203_f1_1	4386	18489	708	236	YLR096W	270	3.3(10)-22	Saccharomyces cerevisiae	[uri:y1r096w] [pn:ser/thr protein kinase;protein kinase] [gn:kin2] [gicfc:8.5:9.4:11.1:12.13] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:9.1.0:15.0:0] [db:gic-saccharomyces cerevisiae]
CONTIG2037	12617180_f1_2	4387	18490	555	185	YLR096W	167	3.2(10)-11	Saccharomyces cerevisiae	[uri:y1r096w] [pn:ser/thr protein kinase;protein kinase] [gn:kin2] [gicfc:8.5:9.4:11.1:12.13] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:9.1.0:15.0:0] [db:gic-saccharomyces cerevisiae]
CONTIG3656	195437_f1_3	4388	18491	240	80	YLR113W	253	2.5(10)-21	Saccharomyces cerevisiae	[uri:y1r113w] [pn:ser/thr protein kinase of map kinase.mapk family.mitogen-activated protein kinase hog1.map kinase hog:osmosensing protein hog1] [gn:hog1:ss3:19354] [gicfc:8.5:9.4:12.11:12.13:13.2] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdf
b9x12d90.y	11737841_f2_1	4389	18492	666	222	YLR113W	826	1.8(10)-82	Saccharomyces cerevisiae	[uri:y1r113w] [pn:ser/thr protein kinase of map kinase.mapk family.mitogen-activated protein kinase hog1.map kinase hog:osmosensing protein hog1] [gn:hog1:ss3:19354] [gicfc:8.5:9.4:12.11:12.13:13.2] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdf

CONTIG3789	24495715_c2_1	4390	18493	1182	394	YLR248W	325	1.3(10)-55	Saccharomyces cerevisiae	[ui:ylr248w] [pn:ca/calmodulin-dependent ser/thr protein kinase rck2:cam kinase-like protein kinase clk1] [gn:rck2:clk1:cmk3:19672] [gicfc:8.5:9.4:12.13:12.8] [ec:2.7.1.-1][keggfc:8.5:9.4] [sgdfc:3.8.0].
CONTIG4245	203175_c2_14	4391	18494	1803	601	YLR248W	892	3.5(10)-94	Saccharomyces cerevisiae	[ui:ylr248w] [pn:ca/calmodulin-dependent ser/thr protein kinase:serine/threonine-protein kinase rck2:cam kinase-like protein kinase clk1] [gn:rck2:clk1:cmk3:19672] [gicfc:8.5:9.4:12.13:12.8] [ec:2.7.1.-1][keggfc:8.5:9.4] [sgdfc:3.8.0].
CONTIG4407	787812_c2_6	4392	18495	1791	597	YLR362W	759	2.2(10)-109	Saccharomyces cerevisiae	[ui:ylr362w] [pn:ser/thr protein kinase of the mekk family:serine/threonine-protein kinase ste11] [gn:ste11:18039] [gicfc:8.5:9.4:12.13:12.8:12.9] [ec:2.7.1.-1][keggfc:8.5:9.4:13.1] [sgdfc:3.2.0:3.3.0:10.1.4:10.4.6:15.0] [0] [db:gic-sac]
CONTIG3441	25947075_c3_6	4393	18496	1005	335	YMR001C	467	9.4(10)-53	Saccharomyces cerevisiae	[ui:ymr001c] [pn:involved in regulation of dna replication:cell cycle protein kinase cdc5/msd2] [gn:cdc5:pkx2-msd2:ym8270] [gicfc:8.5:9.4:0.8:12.13:12.8] [ec:2.7.1.-1][keggfc:8.5:9.4:13.3] [sgdfc:3.6.0:3.8.0:15.0.0] [db:gic-saccharom

CONTIG3441	31510455_c2_5	4394	18497	993	331	YMR001C	1104	6.0(10)-112	Saccharomyces cerevisiae	[ui:ymr001c] [pn:involved in regulation of dna replication:cell cycle protein kinase cdd5/msd2] [gn:edc5:pkx2:msd2:ymr8270] [gicfc:8.5:9.4:10.8:12.13:12.8] [ec:2.7.1.-1][keggfc:8.5:9.4:13.3] [sgdfc:3.6.0:3.8.0:15.0:0] [db:gtc-saccharom
CONTIG153	34568942_f1_1	4395	18498	228	76	YMR104C	276	3.1(10)-23	Saccharomyces cerevisiae	[ui:ymr104c] [pn:ser/thr protein kinases:serine/threonine-protein kinase ypk2/ykr2] [gn:ypk2:ykr2:ym9718] [gicfc:8.5:9.4:12.13:12.8] [ec:2.7.1.-1][keggfc:8.5:9.4] [sgdfc:3.8.0:15.0:0] [db:gtc-saccharomyces cerevisiae]
CONTIG3395	34073402_f3_6	4396	18499	1185	395	YMR139W	1047	6.7(10)-106	Saccharomyces cerevisiae	[ui:ymr139w] [pn:ser/thr protein kinases:serine/threonine-protein kinase mds1/rim11] [gn:mds1:rim11:gsk3:ym9375] [gicfc:8.5:9.4:10.1:10.2:12.13:12.8] [ec:2.7.1.-1][keggfc:8.5:9.4] [sgdfc:3.5.0:9.5.0:15.0:0] [db:gtc-saccharomyces cerevi
CONTIG2534	2454007_f3_2	4397	18500	1236	412	YNL307C	944	1.2(10)-104	Saccharomyces cerevisiae	[ui:ynl307c] [pn:ser/thr/tyr protein kinase:protein kinase mck1:meiosis and centromere regulatory kinase] [gn:mck1:ypk1:n0392] [gicfc:8.5:9.4:12.13:12.15:12.8] [ec:2.7.1.-1][keggfc:8.5:9.4] [sgdfc:3.4.0:3.5.0:3.8.0:15.0:0] [db:gic-sac

CONTIG5640	1417062_f3_5	4398	18501	915	305	YNL298W	948	2.(10)-95	Saccharomyces cerevisiae	[ui:ynl298w] [pn:ser/thr protein kinase;serine/threonine-protein kinase cla4] [gn:cla4;nt0450] [gicfc:8.5;9.4:12.13:12.8] [ec:2.7.1.-] [keggfc:8.5;9.4:13.3] [sgdgc:3.9.0:15.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG4277	26178451_c3_5	4399	18502	192	64	YNL161W	160	1.(10)-10	Saccharomyces cerevisiae	[ui:ynl161w] [pn:similarity to ser/thr protein kinase;probable serine/threonine-protein kinase ynl161w] [gn:n1727] [gicfc:8.5;9.4:12.13:14.3] [ec:2.7.1.-] [keggfc:8.5;9.4] [sgdgc:15.0.0:13.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG4277	24428261_c2_4	4400	18503	1251	417	YNL161W	1705	1.3(10)-175	Saccharomyces cerevisiae	[ui:ynl161w] [pn:similarity to ser/thr protein kinase;probable serine/threonine-protein kinase ynl161w] [gn:n1727] [gicfc:8.5;9.4:12.13:14.3] [ec:2.7.1.-] [keggfc:8.5;9.4] [sgdgc:15.0.0:13.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG2988	14572163_c2_11	4401	18504	1509	503	YNL154C	1392	1.8(10)-142	Saccharomyces cerevisiae	[ui:ynl154c] [pn:casein kinase i isoform:casein kinase i homolog 2] [gn:yck2:ck11_n1755] [gicfc:8.5;9.4:12.13:12.8:13.2] [ec:2.7.1.-] [keggfc:8.5;9.4] [sgdgc:3.1.0:3.2.0:11.1:0:5.0.0] [db:gic-saccharomyces cerevisiae]

CONTIG3895	19926302_f1_1	4402	18505	1419	473	YNL154C	1282	8.4(10)-131	Saccharomyces cerevisiae	[ui:ynl154c] [pn:casein kinase i isoform;casein kinase i homolog 2] [gn:ycck2_ck1 :n1755] [gicfc:8.5:9.4:12.13:12.8:13.2] [ec:2.7.1.-][keggfc:8.5:9.4] [sgdfc:3.1.0;3.2.0;11.1.0;15.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG4709	12922175_c2_15	4403	18506	1035	345	YNL020C	842	3.5(10)-84	Saccharomyces cerevisiae	[ui:ynl020c] [pn:strong similarity to protein kinase pak1:probable serine/threonine-protein kinase ynl020c] [gn:n2823] [gicfc:8.5:9.4:12.13:14.3] [ec:2.7.1.-][keggfc:8.5:9.4] [sgdfc:15.0.0;13.0.0][db:gic-saccharomyces cerevisiae]
CONTIG815	32814_c1_2	4404	18507	777	259	YNR047W	549	1.8(10)-52	Saccharomyces cerevisiae	[ui:ynr047w] [pn:similarity to microtubule-associated ser/thr protein kinases;probable serine/threonine-protein kinase ynr047w] [gn:n3449] [gicfc:8.5:9.4:12.13:14.3] [ec:2.7.1.-][keggfc:8.5:9.4] [sgdfc:15.0.0;13.0.0][db:gic-saccharomyces cerevisiae]
CONTIG702	11932293_c3_4	4405	18508	945	315	YCR231W	714	1.3(10)-70	Saccharomyces cerevisiae	[ui:yor231w] [pn:ser/hr protein kinase;protein kinase mkk1(ssp32)] [gn:mkk1_sspp32_o:050951] [gicfc:8.5:9.4:12.13:12.8:13.2] [ec:2.7.1.-][keggfc:8.5:9.4] [sgdfc:3.1.0;3.2.0;3.8.0;10.2.5;11.1.0;15.0.0][db:gic-saccharomyces cerevisiae]

CONTIG3739	22861312_c3_2	4406	18509	951	317	YOR233W	220	4.4(10)-17	Saccharomyces cerevisiae	[ui:yor233w] [pn:ser/thr protein kinase;serine/threonine-protein kinase kin4] [gn:kin4:kin31:kin3:o5220] [gicfc:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5788	20348300_c2_22	4407	18510	294	98	YOR351C	97	0.00034	Saccharomyces cerevisiae	[ui:yor351c] [pn:ser/thr protein kinase;protein kinase mek1/mre4] [gn:mek1:mre4:06357] [gicfc:8.5:9.4:10.1:10.2:10.8:12.13: 12.8] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:3.5.0:3.7.0:9.5:0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5788	24882806_c1_14	4408	18511	489	163	YOR351C	412	1.3(10)-38	Saccharomyces cerevisiae	[ui:yor351c] [pn:ser/thr protein kinase;protein kinase mek1/mre4] [gn:mek1:mre4:06357] [gicfc:8.5:9.4:10.1:10.2:10.8:12.13: 12.8] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:3.5.0:3.7.0:9.5:0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5788	6734387_c3_26	4409	18512	807	269	YOR351C	169	2.0(10)-10	Saccharomyces cerevisiae	[ui:yor351c] [pn:ser/thr protein kinase;protein kinase mek1/mre4] [gn:mek1:mre4:06357] [gicfc:8.5:9.4:10.1:10.2:10.8:12.13: 12.8] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:3.5.0:3.7.0:9.5:0:15.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5171	23884758_f1_1	4410	18513	1533	511	YPL209C	447	1.3(10)-69	Saccharomyces cerevisiae	[ui:yp1209c] [pn:ser/thr/protein kinase;serine/threonine-protein kinase] [gn:ip11]
CONTIG2810	897706_c1_3	4411	18514	879	293	YPL204W	1096	4.2(10)-111	Saccharomyces cerevisiae	[ui:yp1204w] [pn:casein kinase, ser/thr/tyr protein kinase;casein kinase i homolog] [gn:hr25]
CONTIG4679	4729067_f3_3	4412	18515	1539	513	YPL153C	933	1.8(10)-114	Saccharomyces cerevisiae	[ui:yp1153c] [pn:ser/thr/tyr protein kinase;protein kinase spk1;serine-protein kinase 1]
CONTIG5596	35551337_c2_15	4413	18516	450	150	YPL153C	172	6.2(10)-12	Saccharomyces cerevisiae	[ui:yp1153c] [pn:ser/thr/tyr protein kinase;protein kinase spk1;serine-protein kinase 1]

CONTIG3883	25995694_c1_1	4414	18517	1380	460	YPL042C	958	1.0(10)-111	Saccharomyces cerevisiae	[ui:yp1042c] [pn:cyclin-dependent ser/thr protein kinase:meiotic mma stability protein kinase ume5] [gn:ume5:ssn3:srb10] [gicfc:8.5.9.4:10.1:10.2:12.13:12.8] [ec:2.7.1.-] [keggfc:8.5.9.4] [sgdfc:1.5.2.3.5.0.4.8.2.9.5.0.15.0.0]] [db:gt]
CONTIG1164	15628182_c3_2	4415	18518	696	232	YPR054W	560	2.7(10)-54	Saccharomyces cerevisiae	[ui:yp054w] [pn:sporulation-specific map kinase:sporulation-specific mitogen-activated protein kinase smk1:map kinase smk1] [gn:smk1:yp9499] [gicfc:8.5.9.4:12.15] [ec:2.7.1.-] [keggfc:8.5.9.4] [sgdfc:3.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG3688	2915632_c3_6	4416	18519	207	69	YPR054W	149	5.4(10)-10	Saccharomyces cerevisiae	[ui:yp054w] [pn:sporulation-specific map kinase:sporulation-specific mitogen-activated protein kinase smk1:map kinase smk1] [gn:smk1:yp9499] [gicfc:8.5.9.4:12.15] [ec:2.7.1.-] [keggfc:8.5.9.4] [sgdfc:3.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG472	1988425_c2_2	4417	18520	771	257	YPR161C	598	2.5(10)-58	Saccharomyces cerevisiae	[ui:yp161c] [pn:ser/thr protein kinase:serine/threonine protein kinase sgv1] [gn:sgv1:burl:p9584] [gicfc:8.5.9.4:12.13:12.8:12.9] [ec:2.7.1.-] [keggfc:8.5.9.4] [sgdfc:3.1.0.3.3.0.3.8.0:15.0.0] [db:gic-saccharomyces cerevisiae]

CONTIG5063	12929650_f3_6	4418	18521	534	178	YMR020W	208	3.7(10)-16	Saccharomyces cerevisiae	[ui:ymr020w] [pn:suppressor of fenpropimorph resistance mutation fen2:fms1 protein] [gn:fms1;ym9711] [gtcfc:8.5] [keggfc:14.2] [sgdfc:1.6.6] [db:gtc-saccharomyces cerevisiae]
CONTIG5063	25947078_f1_2	4419	18322	969	323	YMR020W	278	1.7(10)-43	Saccharomyces cerevisiae	[ui:ymr020w] [pn:suppressor of fenpropimorph resistance mutation fen2:fms1 protein] [gn:fms1;ym9711] [gtcfc:8.5] [keggfc:14.2] [sgdfc:1.6.6] [db:gtc-saccharomyces cerevisiae]
CONTIG2063	4818878_f3_1	4420	18523	795	265	YDR302W	101	0.00119	Saccharomyces cerevisiae	[ui:ydr302w] [pn:weak similarity to human gpi-anchor biosynthesis protein] [gtcfc:8.5;10.7] [keggfc:14.2] [sgdfc:1.6.7] [db:gtc-saccharomyces cerevisiae]
CONTIG5769	5188452_f2_7	4421	18524	882	294	YMR079W	988	1.2(10)-99	Saccharomyces cerevisiae	[ui:ymr079w] [pn:phosphatidylinositol:pi/phosphatidylinoline:pc transfer protein:sec14 cytosolic factor:phosphatidylinositol/phosphatidylcholine transfer protein:pi:pc (p)] [gn:sec14;pit1;ym9582] [gtcfc:8.5;10.7;12.10] [keggfc:14.2] [s]
CONTIG3457	4301301_c3_16	4422	18525	657	219	YNL264C	334	2.3(10)-30	Saccharomyces cerevisiae	[ui:ynl264c] [pn:similarity to sec14p:hypothetical 40.7 kd protein in pik1-poi2 intergenic region] [gn:n0815] [gtcfc:8.5;10.7] [keggfc:14.2] [sgdfc:1.6.7] [db:gtc-saccharomyces cerevisiae]

CONTIG5475	10203282_f3_6	4423	18526	1137	379	YNL264C	725	8.9(10)-72	Saccharomyces cerevisiae	[ui:ynl264c] [pn:similarity to sec14p:hypothetical 40.7 kd protein in pik1-pol2 intergenic region] [gn:n0815] [gtcfc:8.5:10.7] [keggfc:14.2] [sgdfc:1.6.7] [db:gtc-saccharomyces cerevisiae]
CONTIG632	3913312_f1_1	4424	18527	225	75	YNL264C	139	5.4(10)-9	Saccharomyces cerevisiae	[ui:ynl264c] [pn:similarity to sec14p:hypothetical 40.7 kd protein in pik1-pol2 intergenic region] [gn:n0815] [gtcfc:8.5:10.7] [keggfc:14.2] [sgdfc:1.6.7] [db:gtc-saccharomyces cerevisiae]
CONTIG2447	35440936_c1_3	4425	18528	708	236	YDL205C	739	2.8(10)-73	Saccharomyces cerevisiae	[ui:yd205c] [pn:porphobilinogen deaminase;pbg:hydroxymethylbilan synthase;hbms:pre-uroporphyrinogen synthase] [gn:hem3:d1:057] [gtcfc:9.10:9.11] [ec:4.3.1.8] [keggfc:9.10] [sgdfc:1.7.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5411	191311_c2_10	4426	18529	1047	349	YDR044W	1205	1.2(10)-122	Saccharomyces cerevisiae	[ui:yd044w] [pn:coproporphyrinogen iii oxidase;coproporphyrinogenase:coprogen oxidase] [gn:hem13:yd5112] [gtcfc:9.10:9.11] [ec:1.3.3.3] [keggfc:9.10] [sgdfc:1.7.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3839	2556288_f1_1	4427	18530	1059	353	YDR047W	1277	2.7(10)-130	Saccharomyces cerevisiae	[ui:yd047w] [pn:uroporphyrinogen decarboxylase;upd] [gn:hem12:hem6:pop3:yd9609] [gtcfc:9.10:9.11] [ec:4.1.1.37] [keggfc:9.10] [sgdfc:1.7.1:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3082	10995167_c3_11	4428	18531	744	248	YGL040C	793	5.5(10)-79	Saccharomyces cerevisiae	[ui:yg!040c] [pn:delta-aminolevulinic acid dehydratase;porphobilinogen synthase;aladl] [gn:hem2] [gicfc:9.10:9.11] [ec:4.2.1.24] [keggc:9.10] [sgdgc:1.7.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3082	36351513_c2_7	4429	18532	513	171	YGL040C	469	1.2(10)-44	Saccharomyces cerevisiae	[ui:yg!040c] [pn:delta-aminolevulinic acid dehydratase;porphobilinogen synthase;aladl] [gn:hem2] [gicfc:9.10:9.11] [ec:4.2.1.24] [keggc:9.10] [sgdgc:1.7.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5819	163930_c1_35	4430	18533	1839	613	YKR069W	814	1.3(10)-111	Saccharomyces cerevisiae	[ui:ykr069w] [pn:siroheme synthase;probable uroporphyrin-iii c-methyltransferase;urogen iii methylase;sumt;uroporphyrinogen iii methylase;urom] [gn:met1] [gicfc:9.10:9.11] [ec:2.1.1.107] [keggc:9.10] [sgdgc:1.7.1] [db:gtc-saccharomyces]
CONTIG5455	22344025_c1_7	4431	18534	630	210	YOR278W	364	1.6(10)-33	Saccharomyces cerevisiae	[ui:yor278w] [pn:uroporphyrinogen iii synthase;uroporphyrinogen-iii cosynthetase;hydroxymethylbilane hydrolase;cyclizing;uroiiis] [gn:hem4;orf1:o5463] [gicfc:9.10:9.11] [ec:4.2.1.75] [keggc:9.10] [

CONTIG5706	13673313_c2_21	4432	18535	1092	364	YBL033C	619	1.5(10)-60	Saccharomyces cerevisiae	[ui:ybf033c] [pn:nntp cyclohydrolase ii] [gn:rib1:ybf0417] [gcfc:9.10.9.11.9.2] [ec:3.5.4.25] [keggfc:9.2] [sgdfc:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5647	14238805_c2_19	4433	18536	882	294	YBR035C	648	1.3(10)-63	Saccharomyces cerevisiae	[ui:ybf035c] [pn:pyridoxamine-phosphate oxidase;pyridoxamine-5"-phosphate oxidase;pmp/pmp-oxidase] [gn:pdx3:ybf0321] [gcfc:9.10.9.11.9.3] [ec:1.4.3.5] [keggfc:9.3] [sgdfc:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG835	31673938_E2_1	4434	18537	771	257	YBR035C	696	1.1(10)-68	Saccharomyces cerevisiae	[ui:ybf035c] [pn:pyridoxamine-phosphate oxidase;pyridoxamine-5"-phosphate oxidase;pmp/pmp-oxidase] [gn:pdx3:ybf0321] [gcfc:9.10.9.11.9.3] [ec:1.4.3.5] [keggfc:9.3] [sgdfc:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3539	869037_f1_2	4435	18538	309	103	YBR153W	238	3.6(10)-20	Saccharomyces cerevisiae	[ui:ybf153w] [pn:hp reductase] [gn:rib7:ybf1203] [gcfc:9.10.9.11] [keggfc:14.2] [sgdfc:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4859	4973762_f2_4	4436	18539	279	93	YBR176W	163	8.6(10)-12	Saccharomyces cerevisiae	[ui:ybf176w] [pn:strong similarity to e.coli 3-methyl-2-oxobutanoate hydroxymethyltransferase;putative 3-methyl-2-oxobutanoate hydroxymethyltransferase;ketopantone hydroxymethyltransferase] [gn:ybf1238] [gcfc:9.10.9.11.9.5.9.6] [ec:

CONTIG5523	2003502_c1_16	4437	18540	855	285	YBR256C	701	3.1(10)-69	Saccharomyces cerevisiae	[ui:ybr256c] [pn:riboflavin synthase, alpha chain:riboflavin synthase alpha chain] [gn:rib5;ybr1724] [gicfc:9.10:9.11:9.2] [ec:2.5.1.9] [keggic:9.2] [sgdfc:1.7.1] [db:gic-saccharomyces cerevisiae]
CONTIG4978	23486660_c2_10	4438	18541	657	219	YDL045C	363	2.0(10)-33	Saccharomyces cerevisiae	[ui:ydl045c] [pn:flavin adenine dinucleotide:fad synthetase:fmn pyrophosphorylase:flavin adenine dinucleotide synthetase] [gn:fad1;d2702] [gicfc:9.10:9.11:9.2] [ec:2.7.7.2] [keggic:9.2] [sgdfc:1.7.1:9.2.0] [db:saccharomyces cerevisiae]
CONTIG5735	485306_c1_14	4439	18542	360	120	YDR487C	296	2.6(10)-26	Saccharomyces cerevisiae	[ui:ydr487c] [pn:3,4-dihydroxy-2-butaneone 4-phosphate synthase] [gn:rib3] [gicfc:9.10:9.11] [keggic:1.4.2] [sgdfc:1.7.1] [db:gic-saccharomyces cerevisiae]
CONTIG5120	3945937_c1_4	4440	18543	912	304	YFR047C	1008	9.0(10)-102	Saccharomyces cerevisiae	[ui:yfr047c] [pn:similarity to human quinolinate phosphoribosyltransferase:putative nicotinate-nucleotide pyrophosphorylase:carboxylating:quinolinate phosphoribosyltransferase:decarboxylating:quanilate] [gicfc:9.10:9.11:9.4] [ec:2.4.2]

CONTIG5490	6140937_c1_9	4441	18544	1407	469	YGL125W	1322	4.7(10)-135	Saccharomyces cerevisiae	[ui:yg1125w] [pn:similarity to human methylenetetrahydrofolate reductase:hypothetical 68.5 kd protein in ssc3-sup44 intergenic region] [gn:g2882] [gtcfc:10.7] [keggfc:14.2] [sgdfc:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5728	15675637_c2_20	4442	18545	1524	508	YGR255C	792	7.0(10)-79	Saccharomyces cerevisiae	[ui:yg255c] [pn:similarity to e.coli ubih and vic proteins:hypothetical 53.5 kd protein in eno1-gnd2 intergenic region] [gn:g9165] [gtcfc:9.10.9.11] [keggfc:14.2] [sgdfc:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5513	24004557_f3_9	4443	18546	330	110	YGR267C	117	6.0(10)-7	Saccharomyces cerevisiae	[ui:yg267c] [pn:gtp cyclohydrolase i:gtph-ch-i] [gn:fol2,g9349] [gtcfc:9.10.9.11.9.6] [ec:3.5.4.16] [keggfc:9.7] [sgdfc:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5637	1070376_c3_25	4444	18547	498	166	YGR267C	653	3.7(10)-64	Saccharomyces cerevisiae	[ui:yg267c] [pn:gtp cyclohydrolase i:gtph-ch-i] [gn:fol2,g9349] [gtcfc:9.10.9.11.9.6] [ec:3.5.4.16] [keggfc:9.7] [sgdfc:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5560	4415700_f3_6	4445	18548	1263	421	YGR286C	1193	2.2(10)-121	Saccharomyces cerevisiae	[ui:yg286c] [pn:biotin synthetase] [gn:bio2] [gtcfc:9.10.9.11.9.6] [ec:2.8.1.-] [keggfc:9.6] [sgdfc:1.7.1] [db:gtc-saccharomyces cerevisiae]

CONTIG5546	24275077_c2_17	4446	18549	372	124	YHR042W	300	8.1(10)-26	Saccharomyces cerevisiae	[ui:yhr042w] [pn:nadph-cytochrome p450 reductase:cpr] [gn:ncp1:ncpr1:prd1] [gtcfc:9.10.9.11.9.13.12.12.12.16] [ec:1.6.2.4][keggfc:9.12] [sgdgc:1.7.1.9.4.0.11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5546	25782638_c1_14	4447	18550	1713	571	YHR042W	1229	3.5(10)-125	Saccharomyces cerevisiae	[ui:yhr042w] [pn:nadph-cytochrome p450 reductase:cpr] [gn:ncp1:ncpr1:prd1] [gtcfc:9.10.9.11.9.13.12.12.12.16] [ec:1.6.2.4][keggfc:9.12] [sgdgc:1.7.1.9.4.0.11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3135	36057828_f3_3	4448	18551	609	203	YHR111W	435	4.7(10)-41	Saccharomyces cerevisiae	[ui:yhr111w] [pn:similarity to molybdopterin biosynthesis proteins:hypothetical 49.4 kd protein in cdc12-orc6 intergenic region] [gtcfc:9.10.9.11] [keggfc:14.2] [sgdgc:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3468	4335825_f3_5	4449	18552	402	134	YHR111W	282	1.3(10)-24	Saccharomyces cerevisiae	[ui:yhr111w] [pn:similarity to molybdopterin biosynthesis proteins:hypothetical 49.4 kd protein in cdc12-orc6 intergenic region] [gtcfc:9.10.9.11] [keggfc:14.2] [sgdgc:1.7.1] [db:gtc-saccharomyces cerevisiae]

CONTIG4532	4162762_c2_8	4450	18553	255	85	YIR142W	248	3.1(10)-21	Saccharomyces cerevisiae	[ui:yir142w] [pn:similarity to thiamin pyrophosphokinase;hypothetical 39.7 kd protein in hom6-pmt4 intergenic region] [gn:2171] [gtfc:9.10:9.11] [keggc:14.2] [sgfc: 1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2848	29394562_f2_2	4451	18554	894	298	YKL027W	970	9.6(10)-98	Saccharomyces cerevisiae	[ui:ykl027w] [pn:similarity to e.coli molybdopterin-converting factor chlN;hypothetical 50.3 kd protein in tfa1-l-pan3 intergenic region] [gtfc:9.10:9.11] [keggc:14.2] [sgfc: 1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2513	21964455_f3_1	4452	18555	1329	443	YMR113W	669	7.5(10)-66	Saccharomyces cerevisiae	[ui:ymr113w] [pn:similarity to folylpolyglutamate synthetases and strong similarity to hypothetical protein ykl132c] [gtfc:9.10:9.11] [keggc: 14.2] [sgfc: 1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3763	27050781_c3_5	4453	18556	951	317	YNL256W	521	1.7(10)-49	Saccharomyces cerevisiae	[ui:ynl256w] [pn:similarity to bacterial dihydropteroate synthase;probable folic acid synthesis protein;contains:dihydropteroate synthase;dhs:dihydropteroate pyrophosphorylase:2-amino-4-hydroxymethyldihydropteroidine pyropho

CONTIG5793	20098165_c2_23	4454	18557	1752	584	YNL256W	718	4.9(10)-71	Saccharomyces cerevisiae	[ui:ynl256w] [pn:similarity to bacterial dihydropteroate synthase;probable folic acid synthesis protein:contains:dihydropteroate synthase;dhpS:dihydropteroate pyrophosphorylase:2-amino-4-hydroxy-6-hydroxymethyl)dihydropteridine pyropho pyropho
CONTIG4540	4897188_c1_6	4455	18558	648	216	YNR057C	412	1.3(10)-38	Saccharomyces cerevisiae	[ui:ym-057c] [pn:putative dehydrobiotin synthetase;dehydrobiotin synthetase;dhtS:dehydrobiotin synthetase:dbtS] [gn:bio4:n3506] [gtfc:9.10.9.11-9.6] [ec:6.3.3.3] [keggc:9.6] [sgdc:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3721	21881311_f2_2	4456	18559	453	151	YOL151W	317	1.5(10)-28	Saccharomyces cerevisiae	[ui:yol151w] [pn:similarity to plant dihydroflavonol-4-reductases] [gtfc:9.10.9.11] [keggfc:14.2] [sgdfc:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3787	21876287_c2_6	4457	18560	1041	347	YOL151W	549	4.0(10)-53	Saccharomyces cerevisiae	[ui:yol151w] [pn:similarity to plant dihydroflavonol-4-reductases] [gtfc:9.10.9.11] [keggfc:14.2] [sgdfc:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3950	23610936_f3_2	4458	18561	804	268	YOL151W	521	3.7(10)-50	Saccharomyces cerevisiae	[ui:yol151w] [pn:similarity to plant dihydroflavonol-4-reductases] [gtfc:9.10.9.11] [keggfc:14.2] [sgdfc:1.7.1] [db:gtc-saccharomyces cerevisiae]

CONTIG5221	24414136_f2_10	4459	18562	453	151	YOL151W	255	5.7(10)-22	Saccharomyces cerevisiae	[ui:yo1151w] [pn:similarity to plant dihydroflavonol-4-reductases] [gicfc:9.10.9.11] [keggfc:14.2] [sgdfc:1.7.1] [db:gic-saccharomyces cerevisiae]
CONTIG5494	24064437_f3_7	4460	18563	189	63	YOL151W	105	2.7(10)-5	Saccharomyces cerevisiae	[ui:yo1151w] [pn:similarity to plant dihydroflavonol-4-reductases] [gicfc:9.10.9.11] [keggfc:14.2] [sgdfc:1.7.1] [db:gic-saccharomyces cerevisiae]
CONTIG5568	24406555_c1_13	4461	18564	1059	353	YOL151W	806	2.2(10)-80	Saccharomyces cerevisiae	[ui:yo1151w] [pn:similarity to plant dihydroflavonol-4-reductases] [gicfc:9.10.9.11] [keggfc:14.2] [sgdfc:1.7.1] [db:gic-saccharomyces cerevisiae]
CONTIG5664	26250632_c3_22	4462	18565	645	215	YOL151W	385	9.5(10)-36	Saccharomyces cerevisiae	[ui:yo1151w] [pn:similarity to plant dihydroflavonol-4-reductases] [gicfc:9.10.9.11] [keggfc:14.2] [sgdfc:1.7.1] [db:gic-saccharomyces cerevisiae]
CONTIG5708	2525201_c1_18	4463	18566	633	211	YOL151W	301	7.5(10)-27	Saccharomyces cerevisiae	[ui:yo1151w] [pn:similarity to plant dihydroflavonol-4-reductases] [gicfc:9.10.9.11] [keggfc:14.2] [sgdfc:1.7.1] [db:gic-saccharomyces cerevisiae]
CONTIG2992	32070305_c3_6	4464	18567	549	183	YOL143C	581	1.6(10)-56	Saccharomyces cerevisiae	[ui:yo1143c] [pn:6,7-dimethyl-8-ribityllumazine synthase:dmrl synthase:lumazine synthase:riboflavin synthase beta chain] [gn:rib4] [gicfc:9.10.9.11.9.2] [ec:2.5.1.9] [keggfc:9.2] [sgdfc:1.7.1] [db:gic-saccharomyces cerevisiae]

CONTIG1475	20506952_c3_3	4465	18568	663	221	YOL066C	359	1.7(10)-32	Saccharomyces cerevisiae	[ui:yo 066c] [pn:drap deaminase] [gn:rib2] [gctfc:9.10.9.1.1] [keggc:14.2] [sgdfc:1.7.1] [db:gic-saccharomyces cerevisiae]
CONTIG2804	5892535_f3_3	4466	18569	1275	425	YOL066C	1015	1.7(10)-102	Saccharomyces cerevisiae	[ui:yo 066c] [pn:drap deaminase] [gn:rib2] [gctfc:9.10.9.1.1] [keggc:14.2] [sgdfc:1.7.1] [db:gic-saccharomyces cerevisiae]
CONTIG873	20506952_f2_1	4467	18570	624	208	YOL066C	359	1.7(10)-32	Saccharomyces cerevisiae	[ui:yo 066c] [pn:drap deaminase] [gn:rib2] [gctfc:9.10.9.1.1] [keggc:14.2] [sgdfc:1.7.1] [db:gic-saccharomyces cerevisiae]
CONTIG5165	26440792_c1_10	4468	18571	336	112	YOL049W	298	4.0(10)-26	Saccharomyces cerevisiae	[ui:yo 049w] [pn:strong similarity to s.pombe gsa1 protein] [gctfc:9.10.9.1.1] [keggc:14.2] [sgdfc:1.7.1] [db:gic-saccharomyces cerevisiae]
CONTIG5165	11189587_c3_17	4469	18572	441	147	YOL049W	294	1.2(10)-25	Saccharomyces cerevisiae	[ui:yo 049w] [pn:strong similarity to s.pombe gsa1 protein] [gctfc:9.10.9.1.1] [keggc:14.2] [sgdfc:1.7.1] [db:gic-saccharomyces cerevisiae]
CONTIG3711	892056_f1_2	4470	18573	456	152	YOL049W	284	1.5(10)-24	Saccharomyces cerevisiae	[ui:yo 049w] [pn:strong similarity to s.pombe gsa1 protein] [gctfc:9.10.9.1.1] [keggc:14.2] [sgdfc:1.7.1] [db:gic-saccharomyces cerevisiae]
CONTIG2084	12612755_c2_5	4471	18574	717	239	YOR143C	318	1.2(10)-28	Saccharomyces cerevisiae	[ui:yo 143c] [pn:thiamin pyrophosphokinase:tpk:thiamin kinase] [gn:thi80.yor3373c] [gctfc:9.10.9.1.9.1.1] [ec:2.7.6.2] [keggc:9.1] [sgdfc:1.7.1] [db:gic-saccharomyces cerevisiae]

CONTIG3157	21891955_c2_5	4472	18575	300	100	YOR143C	148	4.4(10)-10	Saccharomyces cerevisiae	[ui:yor143c] [pn:thiamin pyrophosphokinase;tpk:thiamin kinase] [gn:thi80;yo3373c]
CONTIG2709	22550026_f1_1	4473	18576	1011	337	YOR209C	946	3.3(10)-95	Saccharomyces cerevisiae	[ui:yor209c] [pn:nicotinate phosphoribosyltransferase;probable nicotinate phosphoribosyltransferase;naprtase]
CONTIG4348	22437775_f1_1	4474	18577	1557	519	YOR241W	1257	3.7(10)-128	Saccharomyces cerevisiae	[ui:yor241w] [pn:similarity to tetrahydrofolylpolyglutamate synthase] [gn:cfc9;10:9.11]
CONTIG1422	119015_f3_1	4475	18578	525	175	YPL214C	390	2.7(10)-36	Saccharomyces cerevisiae	[ui:ypl214c] [pn:thiamin-phosphate pyrophosphorylase and hydroxyethylthiazole kinase:thiamin biosynthetic bifunctional enzyme:contains:thiamin-phosphate pyrophosphorylase;tmp-ppase / hydroxyethylthiazole kinase:4]

CONTIG5317	20601527_c3_15	4476	18579	1095	365	YPL023C	842	3.5(10)-84	Saccharomyces cerevisiae	[ui:yp 023c] [pn:similarity to human methylenetetrahydrofolate reductase;putative methylenetetrahydrofolate reductase] [gn:ipb8c] [gicfc: 10.7] [ec: 1.5.1.20] [keggfc: 14.1] [sgdfc: 1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5798	26689001_f1_1	4477	18580	822	274	YIR008C	732	1.6(10)-72	Saccharomyces cerevisiae	[ui:yir008c] [pn: dna-directed dna polymerase alpha 48kda subunit; dna primase; dna primase small chain:p48] [gn:prl1:yib8c] [gicfc: 9.12:10.1:10.2:10.8] [ec:2.7.7.-] [keggfc: 9.13] [sgdfc: 3.6.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5798	24801275_f2_10	4478	18581	636	212	YIR008C	250	4.0(10)-21	Saccharomyces cerevisiae	[ui:yir008c] [pn: dna-directed dna polymerase alpha 48kda subunit; dna primase; dna primase small chain:p48] [gn:prl1:yib8c] [gicfc: 9.12:10.1:10.2:10.8] [ec:2.7.7.-] [keggfc: 9.13] [sgdfc: 3.6.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1903	31423252_f3_1	4479	18582	1110	370	YKL045W	756	4.5(10)-75	Saccharomyces cerevisiae	[ui:ykl045w] [pn: dna-directed dna polymerase alpha , 58 kd subunit; dna primase; dna primase large chain:p58] [gn:prl2:ykl258] [gicfc: 9.12:10.1:10.2:10.8] [ec:2.7.7.-] [keggfc: 9.13] [sgdfc: 3.6.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4654	978541_c2_9	4480	18583	660	220	YKL045W	373	1.8(10)-34	Saccharomyces cerevisiae	[ui:ycl045w] [pn: dna-directed dna polymerase alpha , 58 kd subunit:dna primase large chain:p58] [gn:priz2.ykl045w] [gtfc:9.12:10.1:10.2:10.8] [ec:2.7.7.-1][keggfc:9.13] [sgdfc:3.6.0.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5809	32680300_c2_24	4481	18584	783	261	YOR346W	107	0.006	Saccharomyces cerevisiae	[ui:yor346w] [pn: dna repair protein:dna repair protein rev1] [gn:rev1.06339] [gtfc:9.12:10.10] [ec:2.7.7.-1][keggfc:9.13] [sgdfc:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5809	2910900_c2_23	4482	18585	2583	861	YOR346W	737	4.2(10)-100	Saccharomyces cerevisiae	[ui:yor346w] [pn: dna repair protein:dna repair protein rev1] [gn:rev1.06339] [gtfc:9.12:10.10] [ec:2.7.7.-1][keggfc:9.13] [sgdfc:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5342	15640660_f3_11	4483	18386	1545	515	YDL141W	712	2.1(10)-70	Saccharomyces cerevisiae	[ui:ydl141w] [pn: biotin holocarboxylase synthetase:biotin--protein ligase:biotin apo-protein ligase:biotin--] [gn:bp11.acc2:d2.40] [gtfc:9.12:9.6:10.7] [keggfc:9.6] [sgdfc:1.7.2:6.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5342	20901412_f2_8	4484	18587	546	182	YDL141W	295	2.7(10)-25	Saccharomyces cerevisiae	[ui:yd1141w] [pn:biotin-holocarboxylase synthetase;biotin--protein ligase;biotin apo-protein ligase;biotin--] [gn:bpl1:acc2:d2140] [gicfc:9.12.9.6:10.7] [keggfc:9.6] [sgdfc:1.7.2.6.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG5148	2145453_c1_5	4485	18588	1329	443	YAR071W	935	5.0(10)-94	Saccharomyces cerevisiae	[ui:yar071w] [pn:secreted acid phosphatase;acid phosphatase precursor:p56] [gn:pho11] [gicfc:9.13.9.2:13.10] [ec:3.1.3.2] [keggfc:9.2.9.12] [sgdfc:1.4.1] [db:gic-saccharomyces cerevisiae]
CONTIG439	20023552_c3_10	4486	18589	1494	498	YAR071W	1016	1.3(10)-102	Saccharomyces cerevisiae	[ui:yar071w] [pn:secreted acid phosphatase;acid phosphatase precursor:p56] [gn:pho11] [gicfc:9.13.9.2:13.10] [ec:3.1.3.2] [keggfc:9.2.9.12] [sgdfc:1.4.1] [db:gic-saccharomyces cerevisiae]
CONTIG4782	29588513_f2_2	4487	18590	1215	405	YAR071W	969	1.2(10)-97	Saccharomyces cerevisiae	[ui:yar071w] [pn:secreted acid phosphatase;acid phosphatase precursor:p56] [gn:pho11] [gicfc:9.13.9.2:13.10] [ec:3.1.3.2] [keggfc:9.2.9.12] [sgdfc:1.4.1] [db:gic-saccharomyces cerevisiae]
CONTIG5080	23626501_c3_16	4488	18591	1065	355	YDR541C	530	4.0(10)-51	Saccharomyces cerevisiae	[ui:yd541c] [pn:similarity to dihydroflavonol-4-reductases] [gicfc:9.13] [keggfc:14.2] [sgdfc:1.7.5] [db:gic-saccharomyces cerevisiae]

CONTIG4287	30476526_f3_7	4489	18592	543	181	YER183C	152	4.7(10)-11	Saccharomyces cerevisiae	[ui:yer183c] [pn:similarity to human 5,10-methenyltetrahydrofolate synthetase:hypothetical 24.1 kd protein in isc10 3"region] [gicfc:10.7] [keggfc:14.2] [sgdfc:1.7.5] [db:gic-saccharomyces cerevisiae]
CONTIG2130	19062_cl_4	4490	18593	621	207	YGL157W	200	5.2(10)-25	Saccharomyces cerevisiae	[ui:ygl157w] [pn:similarity to v.vinifera dihydroflavonol 4-reductase:hypothetical 38.1 kd protein in rck1 -ams1 intergenic region] [gng1857] [gicfc:9.13] [keggfc:14.2] [sgdfc:1.7.5] [db:gic-saccharomyces cerevisiae]
CONTIG5595	4725438_c2_9	4491	18594	375	125	YGL157W	105	2.7(10)-5	Saccharomyces cerevisiae	[ui:ygl157w] [pn:similarity to v.vinifera dihydroflavonol 4-reductase:hypothetical 38.1 kd protein in rck1 -ams1 intergenic region] [gng1857] [gicfc:9.13] [keggfc:14.2] [sgdfc:1.7.5] [db:gic-saccharomyces cerevisiae]
CONTIG3659	20003802_f1_1	4492	18595	252	84	YGL157W	106	2.1(10)-5	Saccharomyces cerevisiae	[ui:ygl157w] [pn:similarity to v.vinifera dihydroflavonol 4-reductase:hypothetical 38.1 kd protein in rck1 -ams1 intergenic region] [gng1857] [gicfc:9.13] [keggfc:14.2] [sgdfc:1.7.5] [db:gic-saccharomyces cerevisiae]
CONTIG5521	10719657_o3_31	4493	18596	1083	361	YGR144W	781	1.0(10)-77	Saccharomyces cerevisiae	[ui:ygr144w] [pn:thiamine-repressed protein:mol1 protein] [gn:mol1:esp35:thi4:g6620] [gicfc:9.13.13.2] [keggfc:14.2] [sgdfc:1.7.5.11.1.0] [db:gic-saccharomyces cerevisiae]

CONTIG078	4885950_c3_3	4494	18597	738	246	YDR039C	873	1.8(10)-87	Saccharomyces cerevisiae	[ui:ydr039c] [pn:p-type aipase involved in na+ efflux:sodium transport aipase 2] [gn:ena2;pmr2b] [gicfc:12.5:9.6] [ec:3.6.1.-] [keggfc:9.7] [sgdfc:1.8.2:7.8.0] [db:gic-saccharomyces cerevisiae]
CONTIG1948	15632052_f1_1	4495	18598	390	130	YDR039C	342	6.4(10)-30	Saccharomyces cerevisiae	[ui:ydr039c] [pn:p-type aipase involved in na+ efflux:sodium transport aipase 2] [gn:ena2;pmr2b] [gicfc:12.5:9.6] [ec:3.6.1.-] [keggfc:9.7] [sgdfc:1.8.2:7.8.0] [db:gic-saccharomyces cerevisiae]
CONTIG4224	5119000_c2_5	4496	18399	927	309	YDR039C	695	6.0(10)-68	Saccharomyces cerevisiae	[ui:ydr039c] [pn:p-type aipase involved in na+ efflux:sodium transport aipase 2] [gn:ena2;pmr2b] [gicfc:12.5:9.6] [ec:3.6.1.-] [keggfc:9.7] [sgdfc:1.8.2:7.8.0] [db:gic-saccharomyces cerevisiae]
CONTIG4224	4884385_c1_4	4497	18600	768	256	YDR039C	437	4.4(10)-40	Saccharomyces cerevisiae	[ui:ydr039c] [pn:p-type aipase involved in na+ efflux:sodium transport aipase 2] [gn:ena2;pmr2b] [gicfc:12.5:9.6] [ec:3.6.1.-] [keggfc:9.7] [sgdfc:1.8.2:7.8.0] [db:gic-saccharomyces cerevisiae]
CONTIG5529	25680192_c2_13	4498	18601	474	158	YDR039C	365	2.2(10)-32	Saccharomyces cerevisiae	[ui:ydr039c] [pn:p-type aipase involved in na+ efflux:sodium transport aipase 2] [gn:ena2;pmr2b] [gicfc:12.5:9.6] [ec:3.6.1.-] [keggfc:9.7] [sgdfc:1.8.2:7.8.0] [db:gic-saccharomyces cerevisiae]

CONTIG2005	16844757_f1_1	4499	18602	777	259	YEL031W	915	6.5(10)-92	Saccharomyces cerevisiae	[ui:yer031w] [pn:p-type atpase;probable cation-transporting atpase_yel031w] [gn:spf1] [gtfc:12.5:9.6] [ec:3.6.1.-] [keggc:9.7] [sgdfc: 1.8.2:7.2:7.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3972	4117930_c3_7	4500	18603	2061	687	YEL031W	2065	8.9(10)-214	Saccharomyces cerevisiae	[ui:yer031w] [pn:p-type atpase;probable cation-transporting atpase_yel031w] [gn:spf1] [gtfc:12.5:9.6] [ec:3.6.1.-] [keggc:9.7] [sgdfc: 1.8.2:7.2:7.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3972	10550012_c3_6	4501	18604	672	224	YEL031W	307	4.2(10)-26	Saccharomyces cerevisiae	[ui:yer031w] [pn:p-type atpase;probable cation-transporting atpase_yel031w] [gn:spf1] [gtfc:12.5:9.6] [ec:3.6.1.-] [keggc:9.7] [sgdfc: 1.8.2:7.2:7.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4721	14270187_f3_1	4502	18605	3039	1013	YER172C	1797	2.2(10)-185	Saccharomyces cerevisiae	[ui:yer172c] [pn:ma helicase-related protein;pre-mrna splicing helicase_brr2] [gn:br2:ss1:sgp-orf66] [gtfc:9.6.10.1:10.2] [ec:3.6.1.-] [keggc:9.7] [sgdfc:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5651	10182681_f3_13	4503	18606	1635	545	YER172C	661	8.5(10)-69	Saccharomyces cerevisiae	[ui:yer172c] [pn:ma helicase-related protein;pre-mrna splicing helicase_brr2] [gn:br2:ss1:sgp-orf66] [gtfc:9.6.10.1:10.2] [ec:3.6.1.-] [keggc:9.7] [sgdfc:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2357	7292217_c1_4	4504	18607	1713	571	YII048W	1688	8.0(10)-174	Saccharomyces cerevisiae	[ui:yii048w] [pn:similarity to amino-phospholipids-atape drs2p;probable cation-transporting atpase yii048w] [gicfc:12.5:9.6] [ec:3.6.1.-1] [keggfc:9.7] [sgdfc:7.8.0] [db:gic-saccharomyces cerevisiae]
CONTIG3255	6285256_f2_2	4505	18608	819	273	YII048W	892	1.8(10)-89	Saccharomyces cerevisiae	[ui:yii048w] [pn:similarity to amino-phospholipids-atape drs2p;probable cation-transporting atpase yii048w] [gicfc:12.5:9.6] [ec:3.6.1.-1] [keggfc:9.7] [sgdfc:7.8.0] [db:gic-saccharomyces cerevisiae]
CONTIG1626	2909662_f2_2	4506	18609	672	224	YJL092W	331	1.1(10)-28	Saccharomyces cerevisiae	[ui:yj092w] [pn:atp-dependent dna helicase:atp-dependent dna helicase srs2] [gn:srs2:radh:hpri5;j0913] [gicfc:9.6:10.1:10.10:10.2] [ec:3.6.1.-1] [keggfc:9.7] [sgdfc:9.5.0:112.1] [db:gic-saccharomyces cerevisiae]
CONTIG3330	21726626_c2_3	4507	18610	1356	452	YJL092W	573	1.3(10)-54	Saccharomyces cerevisiae	[ui:yj092w] [pn:atp-dependent dna helicase:atp-dependent dna helicase srs2] [gn:srs2:radh:hpri5;j0913] [gicfc:9.6:10.1:10.10:10.2] [ec:3.6.1.-1] [keggfc:9.7] [sgdfc:9.5.0:112.1] [db:gic-saccharomyces cerevisiae]

CONTIG3407	21697181_f3_3	4508	18611	3147	1049	YAL051W	157	2.7(10)-7	Saccharomyces cerevisiae	[ui:yal051w] [pn:peroxisome proliferating transcription factor;putative 118.2 kd transcriptional regulatory protein in acs1-gcv3 intergenic region] [gn:oafl.fun43] [gicfc:10.1:10.2] [keggfc: 14.2] [sgdfc: 1.6.4:4.8.2:9.5.0] [db:gic-sacc]
CONTIG4406	4116551_f2_1	4509	18612	2079	693	YAL051W	134	4.5(10)-5	Saccharomyces cerevisiae	[ui:yal051w] [pn:peroxisome proliferating transcription factor;putative 118.2 kd transcriptional regulatory protein in acs1-gcv3 intergenic region] [gn:oafl.fun43] [gicfc:10.1:10.2] [keggfc: 14.2] [sgdfc: 1.6.4:4.8.2:9.5.0] [db:gic-sacc]
CONTIG5212	488430_f3_11	4510	18613	735	245	YAL025C	675	1.8(10)-66	Saccharomyces cerevisiae	[ui:yal025c] [pn:nuclear viral propagation protein;protein] [gn:mak16] [gicfc:10.1:10.2:12.8] [keggfc: 14.2] [sgdfc:3.8.0:9.5.0] [db:gic-saccharomyces_cerevisiae]
CONTIG1717	35439526_f2_2	4511	18614	1155	385	YAL021C	909	2.7(10)-91	Saccharomyces cerevisiae	[ui:yal021c] [pn:transcriptional regulator;glucose-repressible alcohol dehydrogenase transcriptional effector;carbon catabolite repressor protein 4] [gn:ccr4.fun27] [gicfc:10.1:10.2] [keggfc: 14.2] [sgdfc:4.8.2:9.5.0] [db:gic-saccharom

CONTIG620	9848317_f3_3	4512	18615	384	128	YAL021C	398	3.5(10)-36	Saccharomyces cerevisiae	[ui:yal021c] [pn:transcriptional regulator:glucose-repressible alcohol dehydrogenase transcriptional effector:carbon catabolite repressor protein 4] [gn:cer4.fun27] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3958	164002_f3_5	4513	18616	390	130	YAL019W	364	3.0(10)-32	Saccharomyces cerevisiae	[ui:yal019w] [pn:similarity to helicases of the snf2/rad54 family:hypothetical 128.5 kd helicase in ats1-tpd3 intergenic region] [gnyal001.fun30] [gicfc:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4665	117805_c1_10	4514	18617	1326	442	YAL019W	94	0.41999	Saccharomyces cerevisiae	[ui:yal019w] [pn:similarity to helicases of the snf2/rad54 family:hypothetical 128.5 kd helicase in ats1-tpd3 intergenic region] [gnyal001.fun30] [gicfc:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG676	986561_f3_1	4515	18618	1038	346	YAL019W	945	4.2(10)-95	Saccharomyces cerevisiae	[ui:yal019w] [pn:similarity to helicases of the snf2/rad54 family:hypothetical 128.5 kd helicase in ats1-tpd3 intergenic region] [gnyal001.fun30] [gicfc:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]

b3x12445.y	10757692_c3_3	4516	18619	270	90	YAL019W	93	0.0025	Saccharomyces cerevisiae	[ui:yal019w] [pn: similarity to helicases of the snf2/rad54 family:hypothetical 128.5 kd helicase in asl1-pd3 intergenic region] [gn:yal001:fun30] [gtfc:10.1:10.10:10.2] [keggfc:1.4.2] [sgdfc:9.5.0:11.2.1] [db:gtc-saccharomyces cerevi
CONTIG5393	24392825_cl_17	4517	18620	2040	680	YAL001C	316	1.7(10)-26	Saccharomyces cerevisiae	[ui:yal001cl] [pn: tfiic:transcription initiation factor subunit, 138 kd:transcription factor tau 138 kd subunit:tfiic 138 kd subunit] [gn:tfc3:tsv115:fun24] [gtfc:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.1.0:4.4.0:9.5.0] [db:gtc-sacch
CONTIG5393	10657757_c3_19	4518	18621	2232	744	YAL001C	126	3.5(10)-16	Saccharomyces cerevisiae	[ui:yal001cl] [pn: tfiic:transcription initiation factor subunit, 138 kd:transcription factor tau 138 kd subunit:tfiic 138 kd subunit] [gn:tfc3:tsv115:fun24] [gtfc:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.1.0:4.4.0:9.5.0] [db:gtc-sacch

CONTIG5814	29491427_f2_13	4519	18622	1098	366	YAR007C	788	1.8(10)-78	Saccharomyces cerevisiae	[ui:yar007c] [pn: dna replication factor a, 69 kd subunit:replication factor-a protein 1:rfa:single-stranded dna-binding protein:buf2] [gn:rfa1:buf2:rpa1:fun3] [gtfc:10.1:10.2:10.8:12.9] [keggfc:14.2] [sgdfc:3.3.0]
CONTIG5814	4806312_f3_26	4520	18623	303	101	YAR007C	139	1.3(10)-8	Saccharomyces cerevisiae	[ui:yar007c] [pn: dna replication factor a, 69 kd subunit:replication factor-a protein 1:rfa:single-stranded dna-binding protein:buf2] [gn:rfa1:buf2:rpa1:fun3] [gtfc:10.1:10.2:10.8:12.9] [keggfc:14.2] [sgdfc:3.3.0]
CONTIG5814	26737503_f2_14	4521	18624	381	127	YAR007C	303	2.8(10)-26	Saccharomyces cerevisiae	[ui:yar007c] [pn: dna replication factor a, 69 kd subunit:replication factor-a protein 1:rfa:single-stranded dna-binding protein:buf2] [gn:rfa1:buf2:rpa1:fun3] [gtfc:10.1:10.2:10.8:12.9] [keggfc:14.2] [sgdfc:3.3.0]
CONTIG5688	24242181_f3_13	4522	18625	1575	525	YBL103C	134	3.5(10)-6	Saccharomyces cerevisiae	[ui:ybl103c] [pn:bhlh/zip transcription factor that regulates cit2 gene expression:retrograde regulation protein 3] [gn:rtg3:ybl0810] [gtfc:10.1:10.2:12.13] [keggfc:14.2] [sgdfc: 1.5.24.8.29.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3479	4722510_f1_1	4523	18626	513	171	YBL093C	151	5.9(10)-11	Saccharomyces cerevisiae	[ui:ybl093c] [pn:transcription factor:rox3 nuclear protein] [gn:rox3;ybl0837] [gicfc:10.1:10.2:13.2] [keggfc:14.2] [sgdfc:4.8 2:9.5:0.11.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG5561	19565875_c3_16	4524	18627	2646	882	YBL084C	698	6.0(10)-86	Saccharomyces cerevisiae	[ui:ybl084c] [pn:subunit of anaphase-promoting complex:cyclosome:cell division control protein 27] [gn:cdc27;snb1;ybl0718] [gicfc:10.1:10.11:10.2:12.16:12.8] [keggfc:14.2] [sgdfc:3.8:0.6:5.1:9.3:0.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG1136	10962752_c3_3	4525	18628	735	245	YBL079W	227	1.8(10)-17	Saccharomyces cerevisiae	[ui:ybl079w] [pn:nuclear pore protein:nucleoporin nup170;nuclear pore protein nup170] [gn:nup170;ybl0725] [gicfc:10.1:10.2:12.6] [keggfc:14.2] [sgdfc:8.1:0.9:5.0:17.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG2309	2131950_f3_2	4526	18629	609	203	YBL079W	169	2.7(10)-11	Saccharomyces cerevisiae	[ui:ybl079w] [pn:nuclear pore protein:nucleoporin nup170;nuclear pore protein nup170] [gn:nup170;ybl0725] [gicfc:10.1:10.2:12.6] [keggfc:14.2] [sgdfc:8.1:0.9:5.0:17.0.0] [db:gic-saccharomyces cerevisiae]

CONTIG2594	24422162_c1_3	4527	18630	612	204	YBL079W	328	3.2(10)-28	Saccharomyces cerevisiae	[ui:ybl079w] [pn:nuclear pore protein:nucleoporin nup170;nuclear pore protein nup170] [gn:nup170;ybl0725] [gicfc:10.1:10.2:12.6] [keggfc:14.2] [sgdfc:8.1.0:9.5:0:17.0] [db:gic-saccharomyces cerevisiae]
CONTIG2791	23563513_B1_1	4528	18631	1230	410	YBL063W	683	1.3(10)-66	Saccharomyces cerevisiae	[ui:ybl063w] [pn:kinesin-related protein:kinesin-like protein kip1] [gn:kip1:cin9;ybl0504;ybl0521] [gtcfc:10.1:10.2:12.16:12.8] [keggfc:14.2] [sgdfc:3.8:0.9:3.0:9.5:0] [db:gic-saccharomyces cerevisiae]
CONTIG5586	12614033_c1_16	4529	18632	1692	564	YBL063W	402	2.5(10)-36	Saccharomyces cerevisiae	[ui:ybl063w] [pn:kinesin-related protein:kinesin-like protein kip1] [gn:kip1:cin9;ybl0504;ybl0521] [gtcfc:10.1:10.2:12.16:12.8] [keggfc:14.2] [sgdfc:3.8:0.9:3.0:9.5:0] [db:gic-saccharomyces cerevisiae]
CONTIG4385	14876506_f2_4	4530	18633	462	154	YBL035C	110	6.5(10)-5	Saccharomyces cerevisiae	[ui:ybl035c] [pn:subunit of dna polymerase alpha-primase complex:dna polymerase alpha/primase associated subunit:p86 subunit] [gn:pol112;ybl0414] [gtcfc:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.6:0.9:5.0] [db:gic-saccharomyces cerevisiae]

CONTIG4737	203251_c3_5	4531	18634	1131	377	YBL035C	725	8.9(10)-72	Saccharomyces cerevisiae	[ui:tbl035c] [pn:subunit of dna polymerase alpha-primate complex:dna polymerase alpha/primate associated subunit:p86 subunit] [gn:pol12;tbl0414] [gicfc:10.1:10.2:10.8] [keggfc:14.2][sgdfc:3.6:0.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4470	23470317_c3_8	4532	18635	375	125	YBL026W	367	7.7(10)-34	Saccharomyces cerevisiae	[ui:tbl026w] [pn:snmp-related protein:hypothetical 11.2 kd protein in rpl19-mcm2 intergenic region] [gn:snp3;tbl0425] [gicfc:10.1:10.2][keggfc:14.2][sgdfc:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4772	14555312_f2_3	4533	18636	2061	687	YBL024W	1801	8.5(10)-186	Saccharomyces cerevisiae	[ui:tbl024w] [pn:similarity to nucleolar np2p/hypothetical 77.9 kd protein in rml0-mcm2 intergenic region] [gn:tbl0437] [gicfc:10.1:10.2] [keggfc:14.2][sgdfc:9.5.0:13.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG4940	58532_f2_1	4534	18637	1635	545	YBL023C	1691	4.9(10)-218	Saccharomyces cerevisiae	[ui:tbl023c] [pn:member of the mcm2p,mcm3p,cdc46p family:minichromosome maintenance protein 2] [gn:mcm2;tbl0438] [gicfc:10.1:10.2:10.8:12.8] [keggfc:13.2] [sgdfc:3.6:0.9:5.0] [db:gic-saccharomyces cerevisiae]

CONTIG1248	12209752_f2_1	4535	18638	660	220	YBL021C	303	4.5(10)-27	Saccharomyces cerevisiae	[ui:ybl021c] [pn:ccaaat-binding factor subunit:nap3 transcriptional activator:uas2 regulatory protein a] [gn:hap3:ybl0441] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5141	4104637_f2_1	4536	18639	330	110	YBL021C	413	1.0(10)-38	Saccharomyces cerevisiae	[ui:ybl021c] [pn:ccaaat-binding factor subunit:nap3 transcriptional activator:uas2 regulatory protein a] [gn:hap3:ybl0441] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2073	4772630_f2_1	4537	18640	1425	475	YBL020W	422	1.1(10)-39	Saccharomyces cerevisiae	[ui:ybl020w] [pn:nuclear division protein:nuclear division rfl1 protein] [gn:rfl1:ybl0442] [gtcfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5197	10001885_f3_1	4538	18641	2436	812	YBL014C	219	2.8(10)-14	Saccharomyces cerevisiae	[ui:ybl014c] [pn:rna polymerase i specific transcription initiation factor:ma polymerase i specific transcription initiation factor rmf6] [gn:rmf6:ybl0311:ybl0312] [gtcfc:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.1.0:9.5.0] [db:gtc-sacc]

CONTIG3645	4711636_f3_3	4539	18642	1263	421	YBL008W	1125	3.6(10)-114	Saccharomyces cerevisiae	[ui:ylb008w] [pn:histone transcription regulator:histone transcription regulator 1] [gn:hir1.ybl0318] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4343	782806_c3_9	4540	18643	1404	468	YBL008W	101	0.07299	Saccharomyces cerevisiae	[ui:ylb008w] [pn:histone transcription regulator:histone transcription regulator 1] [gn:hir1.ybl0318] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5245	5080340_c3_21	4541	18644	1467	489	YBL008W	189	9.5(10)-15	Saccharomyces cerevisiae	[ui:ylb008w] [pn:histone transcription regulator:histone transcription regulator 1] [gn:hir1.ybl0318] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG2190	10976555_f1_2	4542	18645	324	108	YBR009C	383	1.5(10)-35	Saccharomyces cerevisiae	[ui:ylb009c] [pn:histone h4] [gn:hhf1.ybr0122.hhf2.n2752] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0:9.6.0] [db:gic-saccharomyces cerevisiae]
CONTIG5334	23437687_f2_6	4543	18646	348	116	YBR009C	384	1.2(10)-35	Saccharomyces cerevisiae	[ui:ylb009c] [pn:histone h4] [gn:hhf1.ybr0122.hhf2.n2752] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0:9.6.0] [db:gic-saccharomyces cerevisiae]
CONTIG485	16032090_f2_2	4544	18647	507	169	YBR010W	324	2.7(10)-29	Saccharomyces cerevisiae	[ui:ylb010w] [pn:histone h3] [gn:hhf1.ybr0201.hhf2.sin2.n2749] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0:9.6.0] [db:gic-saccharomyces cerevisiae]

CONTIG2687	34250313_c3_3	4545	18648	261	87	YBR010W	387	5.7(10)-36	Saccharomyces cerevisiae	[ui:ybr010w] [pn:histone h3] [gn:htt1.ybr0201:htt2.sin2.n2749] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5:0.9:6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5534	19531300_c3_18	4546	18649	459	153	YBR010W	647	1.6(10)-63	Saccharomyces cerevisiae	[ui:ybr010w] [pn:histone h3] [gn:htt1.ybr0201:htt2.sin2.n2749] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5:0.9:6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2229	26378503_f1_1	4547	18650	471	157	YBR026C	318	1.2(10)-28	Saccharomyces cerevisiae	[ui:ybr026c] [pn:mitochondrial respiratory function protein:mitochondrial respiratory function protein 1] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG4624	3305317_f3_4	4548	18651	1185	395	YBR026C	507	1.1(10)-48	Saccharomyces cerevisiae	[ui:ybr026c] [pn:mitochondrial respiratory function protein:mitochondrial respiratory function protein 1] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG1160	22695943_c1_4	4549	18652	240	80	YBR049C	113	2.7(10)-14	Saccharomyces cerevisiae	[ui:ybr049c] [pn:transcription factor: dna-binding protein reb1.qbp] [gn:reb1.grf2:ybr0502] [gicfc:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.1.0:4.8.2:9.5:0] [db:gtc-saccharomyces cerevisiae]

CONTIG5208	25476516_02_14	4550	18653	1185	395	YBR055C	462	5.4(10)-43	Saccharomyces cerevisiae	[ui:ybr055c] [pn:snmp:u4/u6-associated splicing factor:pre-mrna splicing factor prp6] [gn:prp6:ma6:ybr0508] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.9:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5208	22854652_02_13	4551	18654	747	249	YBR055C	180	9.9(10)-13	Saccharomyces cerevisiae	[ui:ybr055c] [pn:snmp:u4/u6-associated splicing factor:pre-mrna splicing factor prp6] [gn:prp6:ma6:ybr0508] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.9:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
b2x12464_x	4860050_c3_1	4552	18655	603	201	YBR055C	246	8.5(10)-20	Saccharomyces cerevisiae	[ui:ybr055c] [pn:snmp:u4/u6-associated splicing factor:pre-mrna splicing factor prp6] [gn:prp6:ma6:ybr0508] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.9:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3320	11750817_f3_3	4553	18656	1242	414	YBR060C	602	9.5(10)-59	Saccharomyces cerevisiae	[ui:ybr060c] [pn:origin recognition complex, 72 kda subunit:origin recognition complex protein, subunit 2:origin recognition complex protein 71 kd subunit] [gn:orc2:rri :sir5:ybr0523] [gicfc:10.1:10.2:10.8:12.8:12.9] [keggfc:13.2] [sg]

CONTIG3647	41562877_c1_3	4554	18657	318	106	YBR081C	107	9.6(10)-5	Saccharomyces cerevisiae	[ui:ybr081c] [pn:involved in alteration of transcription start site selection:transcriptional activator spt7] [gn:sp7:ybr0739] [gtfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4860	26343875_f3_4	4555	18658	3006	1002	YBR081C	662	1.2(10)-135	Saccharomyces cerevisiae	[ui:ybr081c] [pn:involved in alteration of transcription start site selection:transcriptional activator spt7] [gn:sp7:ybr0739] [gtfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4671	4098513_f2_2	4556	18659	1347	449	YBR083W	213	1.0(10)-14	Saccharomyces cerevisiae	[ui:ybr083w] [pn:ty transcription activator:ty transcription activator tec1] [gn:tec1:roc1:ybr0750] [gtfc:10.1:10.2:12.8] [keggfc:14.2] [sgdgc:3.2.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1943	2822192_f1_1	4557	18660	261	87	YBR087W	141	3.2(10)-9	Saccharomyces cerevisiae	[ui:ybr087w] [pn:dna replication factor c, 40 kd subunit:activator 1 subunit 5:replication factor c] [gn:rfc5:ybr0810] [gtfc:10.1:10.2:10.8] [keggfc:14.2] [sgdgc:3.6.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
b3x19517.y	25652036_f2_1	4558	18661	870	290	YBR087W	692	2.7(10)-68	Saccharomyces cerevisiae	[ui:ybr087w] [pn:dna replication factor c, 40 kd subunit:activator 1 subunit 5:replication factor c] [gn:rfc5:ybr0810] [gtfc:10.1:10.2:10.8] [keggfc:14.2] [sgdgc:3.6.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2521	23939051_c2_9	4559	18662	798	266	YBR088C	740	2.2(10)-73	Saccharomyces cerevisiae	[ui:ybr088c] [pn:proliferating cell nuclear antigen:pena] [gn:pol30:ybr0811] [gicfc:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.6:0.3:7.0:9.5:0] [db:gic-saccharomyces cerevisiae]
CONTIG4482	35633436_f3_7	4560	18663	2001	667	YBR112C	1362	2.7(10)-139	Saccharomyces cerevisiae	[ui:ybr112c] [pn:general repressor of transcription:glucose repression mediator protein] [gn:ssn6:cyc8:ybr0908] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2.9:5.0] [db:gic-saccharomyces cerevisiae]
b3x1607.y	36147808_c3_4	4561	18664	303	101	YBR112C	116	7.4(10)-6	Saccharomyces cerevisiae	[ui:ybr112c] [pn:general repressor of transcription:glucose repression mediator protein] [gn:ssn6:cyc8:ybr0908] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2.9:5.0] [db:gic-saccharomyces cerevisiae]
b3x13452.y	24635752_c3_2	4562	18665	606	202	YBR112C	108	0.0018	Saccharomyces cerevisiae	[ui:ybr112c] [pn:general repressor of transcription:glucose repression mediator protein] [gn:ssn6:cyc8:ybr0908] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4298	22065680_f1_1	4563	18666	3207	1069	YBR114W	130	4.2(10)-7	Saccharomyces cerevisiae	[ui:ybr114w] [pn:nucleotide excision repair protein:dna repair protein rad16] [gn:rad16:ybr0909] [gicfc:10.1:10.10:10.2:10.8] [keggfc:14.2] [sgdfc:3.7:0.9:5.0:11.2.1] [db:gic-saccharomyces cerevisiae]

CONTIG5782	5256282_c1_18	4564	18667	2568	856	YBR114W	2633	5.7(10)-274	Saccharomyces cerevisiae	[ui:ybr114w] [pn:nucleotide excision repair protein:dna repair protein rad16] [gn:rad16] [ybr0909]
										[gicfc:10.1:10.10:10.2:10.8]
										[keggfc:14.2]
										[sgdfc:3.7:0.9:5.0:11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG863	14722182_c1_2	4565	18668	435	145	YBR123C	171	5.5(10)-12	Saccharomyces cerevisiae	[ui:ybr123c] [pn:tflii:c:transcription initiation factor subunit, 95 kd:transcription factor tau 95 kd subunit:tflii:c 95 kd subunit]
										[gn:tflii:c:ybr0919]
										[gicfc:10.1:10.2:10.3] [keggfc:14.2]
										[sgdfc:4.1:0.4:4.0:9.5.0] [db:gic-saccharomyces]
CONTIG2869	22089187_f3_1	4566	18669	1095	365	YBR150C	91	0.53	Saccharomyces cerevisiae	[ui:ybr150c] [pn:weak similarity to transcription factors:putative 126.9 kd transcriptional regulatory protein in ysw1-rib7 intergenic region]
										[gn:ybr1133] [gicfc:10.1:10.2]
										[keggfc:14.2] [sgdfc:4.12.0:9.5.0]
										[db:gic-saccharomyces cer]
CONTIG3753	26274013_f1_1	4567	18670	1422	474	YBR198C	1260	1.8(10)-128	Saccharomyces cerevisiae	[ui:ybr198c] [pn:tfid subunit:trp-associated factor, 90 kd:hypothetical trp-asp repeats containing protein in pg11 - kir4 intergenic region]
										[gn:taf90:ybr1410] [gicfc:10.1:10.2]
										[keggfc:14.2] [sgdfc:4.8.1:9.5.0]
										[db:gic-saccharomyces]

CONTIG5005	22066557_c2_4	4568	18671	1182	394	YBR198C	215	1.3(10)-14	Saccharomyces cerevisiae	[ui:ybr198c] [pn:tfid subunit:bp-associated factor, 90 kd:hypothetical trp-asp repeats containing protein in pg1 - ktr4 intergenic region] [gn:taf90:ybr1410] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:1.9:5.0] [db:gic-saccharomyces]
CONTIG5810	22438777_f3_21	4569	18672	864	288	YBR198C	199	1.0(10)-27	Saccharomyces cerevisiae	[ui:ybr198c] [pn:tfid subunit:bp-associated factor, 90 kd:hypothetical trp-asp repeats containing protein in pg1 - ktr4 intergenic region] [gn:taf90:ybr1410] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:1.9:5.0] [db:gic-saccharomyces]
CONTIG2640	13683587_c1_2	4570	18673	996	332	YBR202W	1238	3.8(10)-126	Saccharomyces cerevisiae	[ui:ybr202w] [pn:cell division control protein:cell division control protein 47] [gn:cd47:ybr1441] [gicfc:10.1:10.2:10.8:12.8] [keggfc:14.2] [sgdfc:3.6:0.3:8.0:9.5:0] [db:gic-saccharomyces cerevisiae]
CONTIG4638	16222813_c1_8	4571	18674	948	316	YBR202W	362	2.7(10)-32	Saccharomyces cerevisiae	[ui:ybr202w] [pn:cell division control protein:cell division control protein 47] [gn:cdc47:ybr1441] [gicfc:10.1:10.2:10.8:12.8] [keggfc:14.2] [sgdfc:3.6:0.3:8.0:9.5:0] [db:gic-saccharomyces cerevisiae]

CONTIG4195	6355200_c1_3	4572	18675	2007	669	YBR237W	1067	5.0(10)-108	Saccharomyces cerevisiae	[ui:ybr237w] [pn:pre-mrna processing rna-helicase:pre-mrna processing rna helicase prp5] [gn:prp5:ma5:ybr603] [gicfc: 0.1:10.2:12.16] [keggfc: 14.2] [sgdgc:4.9:0.6:4.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2066	19546878_c1_2	4573	18676	942	314	YBR239C	173	3.7(10)-14	Saccharomyces cerevisiae	[ui:ybr239c] [pn:weak similarity to transcription factor put3p:putative 60.3 kd transcriptional regulatory protein in prp5-alg7 intergenic region] [gn:ybr1622] [gicfc: 10.1:10.2] [keggfc:14.2] [sgdgc:4.12:0.9:5.0] [db:gtc-saccharomyces]
CONTIG2225	34423436_c2_2	4574	18677	294	98	YBR239C	248	1.8(10)-20	Saccharomyces cerevisiae	[ui:ybr239c] [pn:weak similarity to transcription factor put3p:putative 60.3 kd transcriptional regulatory protein in prp5-alg7 intergenic region] [gn:ybr1622] [gicfc: 10.1:10.2] [keggfc:14.2] [sgdgc:4.12:0.9:5.0] [db:gtc-saccharomyces]
CONTIG4191	20423138_c3_7	4575	18678	1941	647	YBR239C	243	5.7(10)-26	Saccharomyces cerevisiae	[ui:ybr239c] [pn:weak similarity to transcription factor put3p:putative 60.3 kd transcriptional regulatory protein in prp5-alg7 intergenic region] [gn:ybr1622] [gicfc: 10.1:10.2] [keggfc:14.2] [sgdgc:4.12:0.9:5.0] [db:gtc-saccharomyces]

CONTIG5697	20081537_f3_10	4576	18679	2427	809	YBR239C	104	0.035	Saccharomyces cerevisiae	[ui:ybr239c] [pn:weak similarity to transcription factor put3p;putative 60.3 kd transcriptional regulatory protein in prp5-alg7 intergenic region] [gn:ybr1622] [gicfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.12:0.9:5.0] [db:gicsaccharomyces]
CONTIG5532	211507_f1_1	4577	18680	351	117	YBR247C	334	2.3(10)-30	Saccharomyces cerevisiae	[ui:ybr247c] [pn:n-glycosylation protein;enp1 protein] [gn:enp1:meig1:ybr1635] [gicfc:10.1:10.2:10.7] [keggfc:14.2] [sgdgc:6.3:0.9:5.0] [db:gicsaccharomyces cerevisiae]
CONTIG4398	31292707_f3_2	4578	18681	645	215	YBR275C	90	0.54	Saccharomyces cerevisiae	[ui:ybr275c] [pn:rif1 protein;rap1-interacting factor 1] [gn:rif1:ybr1743] [gicfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.8:2.9:5.0:9.6:0] [db:gicsaccharomyces cerevisiae]
CONTIG4398	11719762_f1_1	4579	18682	1779	593	YBR275C	104	4.9(10)-7	Saccharomyces cerevisiae	[ui:ybr275c] [pn:rif1 protein;rap1-interacting factor 1] [gn:rif1:ybr1743] [gicfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.8:2.9:5.0:9.6:0] [db:gicsaccharomyces cerevisiae]
CONTIG3103	30385057_f3_2	4580	18683	1446	482	YBR279W	260	9.5(10)-30	Saccharomyces cerevisiae	[ui:ybr279w] [pn:dna-directed dna polymerase ii regulator;paf1 protein] [gn:paf1:ybr2016] [gicfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.8:2.9:5.0] [db:gicsaccharomyces cerevisiae]

CONTIG2536	437512_f1_1	4581	18684	1311	437	YBR289W	309	6.9(10)-30	Saccharomyces cerevisiae	[ui:ybr289w] [pn:component of swi/snf transcription activator complex;transcription regulatory protein snf5:swi/snf complex component snf5:transcription factor type4] [gn:snf5:ye4:swi10:ybr2036] [gtcfc:0.1:10.2:12.13:12.9] [keggfc:14]
CONTIG3809	2355208_f3_4	4582	18685	669	223	YBR289W	278	3.2(10)-23	Saccharomyces cerevisiae	[ui:ybr289w] [pn:component of swi/snf transcription activator complex;transcription regulatory protein snf5:swi/snf complex component snf5:transcription factor type4] [gn:snf5:ye4:swi10:ybr2036] [gtcfc:0.1:10.2:12.13:12.9] [keggfc:14]
CONTIG2911	24015625_f2_3	4583	18686	636	212	YCL066W	106	0.00013	Saccharomyces cerevisiae	[ui:ycl066w] [pn:mating type regulatory protein, silenced copy at hml:1 mating type regulatory protein, expressed copy at mat locus;mating-type protein alpha-1] [gn:alpha1:mata1alpha:ycl66w:mata11:mat1:mat_alpha_1:yca40w] [gtcfc:0.1:10]

CONTIG5663	6645262_c2_15	4584	18687	987	329	YCL055W	828	1.3(10)-86	Saccharomyces cerevisiae	[ui:yc[055w] [pn:regulatory protein required for pheromone induction of karyogamy genes:hypothetical 38.7 kd protein in prd1-pbni intergenic region] [gn:kar4;yc[55w];yc[432] [gicfc: 0.1:10.2:12.9] [keggfc:14.2] [sgdgc:3.3.0:4.8.2:9.5.0]
CONTIG353	36360326_f2_1	4585	18688	249	83	YCL054W	409	1.3(10)-37	Saccharomyces cerevisiae	[ui:yc[054w] [pn:transcriptional silencing protein:hypothetical 83.2 kd protein in prd1-pbni intergenic region] [gn:yc[54w];yc[431] [gicfc: 0.1:10.2] [keggfc:14.2] [sgdgc:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5623	36360326_f1_1	4586	18689	1536	512	YCL054W	1258	1.3(10)-176	Saccharomyces cerevisiae	[ui:yc[054w] [pn:transcriptional silencing protein:hypothetical 83.2 kd protein in prd1-pbni intergenic region] [gn:yc[54w];yc[431] [gicfc: 0.1:10.2] [keggfc:14.2] [sgdgc:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3731	10567301_o2_16	4587	18690	375	125	YCL029C	159	5.7(10)-11	Saccharomyces cerevisiae	[ui:yc[029c] [pn:nuclear fusion protein:nuclear fusion protein b1k1] [gn:b1k1;yc[29c] [gicfc: 0.1:10.2:12.16:12.8:12.9] [keggfc: 14.2] [sgdgc: 3.3.0:3.8.0:9.3.0:9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG5143	26741377_c1_15	4588	18691	1287	429	YCL011C	413	5.5(10)-63	Saccharomyces cerevisiae	[ui:yci011c] [pn:potential telomere-associated protein:single-strand telomeric dna-binding protein gbp2:g-strand binding protein 2:rap1 localization factor 6] [gn:gbp2:rif6:yci11c] [gicfc:10.1:10.2] [keggfc:14.2] [sgdgc:9.5:9.6:0] [
CONTIG3208	355723780_f1_1	4589	18692	1158	386	YCR042C	379	1.1(10)-33	Saccharomyces cerevisiae	[ui:ycr042c] [pn:component of taf:ii complex:tsm1 protein] [gn:tsm1:ycr42c:yer724] [gicfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.8:2:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG3956	26054813_c2_8	4590	18693	1443	481	YCR042C	879	2.7(10)-87	Saccharomyces cerevisiae	[ui:ycr042c] [pn:component of taf:ii complex:tsm1 protein] [gn:tsm1:ycr42c:yer724] [gicfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.8:2:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG3956	4800906_c3_9	4591	18694	663	221	YCR042C	212	6.9(10)-16	Saccharomyces cerevisiae	[ui:ycr042c] [pn:component of taf:ii complex:tsm1 protein] [gn:tsm1:ycr42c:yer724] [gicfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.8:2:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG3956	4007160_c3_10	4592	18695	189	63	YCR042C	144	1.2(10)-8	Saccharomyces cerevisiae	[ui:ycr042c] [pn:component of taf:ii complex:tsm1 protein] [gn:tsm1:ycr42c:yer724] [gicfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.8:2:9.5:0] [db:gtc-saccharomyces cerevisiae]

CONTIG4152	24414083_f1_2	4593	18696	720	240	YCR065W	266	2.0(10)-22	Saccharomyces cerevisiae	[ui:ycr065w] [pn:transcription factor:hcm1 protein] [gn:hcm1.ycr65w:ycr902] [gicfc: 10.1:10.2] [keggc:14.2] [sgdfc:4.8.2.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5596	23609536_f3_11	4594	18697	777	259	YCR065W	103	0.0074	Saccharomyces cerevisiae	[ui:ycr065w] [pn:transcription factor:hcm1 protein] [gn:hcm1.ycr65w:ycr902] [gicfc: 10.1:10.2] [keggc:14.2] [sgdfc:4.8.2.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5184	12140677_c2_11	4595	18698	1176	392	YCR066W	247	1.5(10)-34	Saccharomyces cerevisiae	[ui:ycr066w] [pn:dna repair protein rad18] [gn:rad18.ycr66w] [gicfc: 10.1:10.10:10.2:10.8] [keggc:14.2] [sgdfc:3.7.0.9.5:0:11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG1568	4094567_c3_4	4596	18699	942	314	YCR072C	106	0.00459	Saccharomyces cerevisiae	[ui:ycr072c] [pn:beta-transducin family:wd-40 repeat protein:hypothetical trp-asp repeats containing protein in cpr4- ssk22 intergenic region] [gn:ycr72c] [gicfc: 10.1:0.2] [keggc:14.2] [sgdfc:9.5.0:13.0.0] [db:gic-saccharomyces cere
CONTIG5040	13688762_c2_13	4597	18700	1224	408	YCR072C	122	0.00017	Saccharomyces cerevisiae	[ui:ycr072c] [pn:beta-transducin family:wd-40 repeat protein:hypothetical trp-asp repeats containing protein in cpr4- ssk22 intergenic region] [gn:ycr72c] [gicfc: 10.1:10.2] [keggc:14.2] [sgdfc:9.5.0:13.0.0] [db:gic-saccharomyces cere

CONTIG708	24797506_c2_4	4598	18701	993	331	YCR072C	1156	1.8(10)-117	Saccharomyces cerevisiae	[ui:ycr072c] [pn:beta-transducin family:wd-40 repeat protein:hypothetical trp-asp repeats containing protein in cpr4- ssk22 intergenic region] [gn:ycr72c] [gicfc: 10.1:10.2] [keggfc:14.2] [sgdfc:9.5.0:13.0.0] [db:gtc-saccharomyces cere
b9x10155,y	23693849_c1_2	4599	18702	471	157	YCR072C	594	6.7(10)-58	Saccharomyces cerevisiae	[ui:ycr072c] [pn:beta-transducin family:wd-40 repeat protein:hypothetical trp-asp repeats containing protein in cpr4- ssk22 intergenic region] [gn:ycr72c] [gicfc: 10.1:10.2] [keggfc:14.2] [sgdfc:9.5.0:13.0.0] [db:gtc-saccharomyces cere
CONTIG5601	12238550_f1_1	4600	18703	1185	395	YCR084C	1050	3.2(10)-106	Saccharomyces cerevisiae	[ui:ycr084c] [pn:general transcription repressor; glucose repression regulatory protein tup1:flocculation suppressor protein:repressor aer2] [gn:tup1:aer2:sfl2:cye9:umt7:aar1a:mml1:fkl1_orycr84c] [gicfc: 10.1:10.2] [keggfc:14.2] [sgdfc:4]
CONTIG1665	8392_c1_2	4601	18704	690	230	YCR092C	274	1.1(10)-22	Saccharomyces cerevisiae	[ui:ycr092c] [pn:dna mismatch repair protein;muts protein homolog 3:mismatch binding protein:mbp] [gn:msh3:ycr92c:ycr1152] [gicfc: 10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3957	2789050_f3_4	4602	18705	234	78	YCR092C	98	0.00067	Saccharomyces cerevisiae	[ui:ycr092c] [pn:dnamismatchrepairprotein:mutisproteinhomolog3:mismatchbindingprotein:mbp] [gn:msh3:ycr92c:ycrl152] [gtcfc:0.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.7:0.9:5.0] [db:gicsaccharomycescerevisiae]
CONTIG3957	14178130_f1_1	4603	18706	897	299	YCR092C	597	2.2(10)-57	Saccharomyces cerevisiae	[ui:ycr092c] [pn:dnamismatchrepairprotein:mutisproteinhomolog3:mismatchbindingprotein:mbp] [gn:msh3:ycr92c:ycrl152] [gtcfc:0.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.7:0.9:5.0] [db:gicsaccharomycescerevisiae]
CONTIG1046	13882630_f2_1	4604	18707	675	225	YCR093W	345	8.0(10)-30	Saccharomyces cerevisiae	[ui:ycr093w] [pn:nucleartransmembraneprotein:generalnegative regulatoroftranscriptionsubunit1] [gn:nol1:cdc39:ros1:ycr93w:ycrl151] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2.9:5.0] [db:gicsaccharomycescerevisiae]
CONTIG1046	203575_f2_2	4605	18708	282	94	YCR093W	111	6.0(10)-5	Saccharomyces cerevisiae	[ui:ycr093w] [pn:nucleartransmembraneprotein:generalnegative regulatoroftranscriptionsubunit1] [gn:nol1:cdc39:ros1:ycr93w:ycrl151] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2.9:5.0] [db:gicsaccharomycescerevisiae]

CONTIG1166	176567_c3_4	4606	18709	957.	319	YCR093W	602	3.7(10)-57	Saccharomyces cerevisiae	[ui:ycr093w] [pn:nuclear transmembrane protein:general negative regulator of transcription subunit 1] [gn:not1:cdc39:ros1:ycr93w:ycr115 1][gicfc:10.1:10.2] [keggfc:14.2][sgdgc:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG895	24398311_f2_2	4607	18710	486	162	YCR093W	224	5.9(10)-17	Saccharomyces cerevisiae	[ui:ycr093w] [pn:nuclear transmembrane protein:general negative regulator of transcription subunit 1] [gn:not1:cdc39:ros1:ycr93w:ycr115 1][gicfc:10.1:10.2] [keggfc:14.2][sgdgc:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG895	3150012_f1_1	4608	18711	678	226	YCR093W	220	1.6(10)-16	Saccharomyces cerevisiae	[ui:ycr093w] [pn:nuclear transmembrane protein:general negative regulator of transcription subunit 1] [gn:not1:cdc39:ros1:ycr93w:ycr115 1][gicfc:10.1:10.2] [keggfc:14.2][sgdgc:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3229	4332802_f3_4	4609	18712	1761	587	YCR106W	142	3.7(10)-6	Saccharomyces cerevisiae	[ui:ycr106w] [pn:weak similarity to transcription factor pip2p:putative 95.7 kd transcriptional regulatory protein in pau3 3' region] [gicfc:10.1:10.2] [keggfc:14.2][sgdgc:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG3945	2375030_c2_4	4610	18713	543	181	YDL226C	515	1.6(10)-49	Saccharomyces cerevisiae	[ui:ydl226c] [pn:cell proliferation zinc finger protein/zinc finger protein] [gn:ges1] [gicfc:10.1:10.2:12.10:12.6:2.8] [keggfc:14.2] [sgdgc:3.8:0.8:6.0:8.7:0.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5742	23609806_f3_14	4611	18714	1542	514	YDL207W	666	1.6(10)-65	Saccharomyces cerevisiae	[ui:ydl207w] [pn:rna export mediator] [gn:gie1] [gicfc:10.1:10.2:12.3] [keggfc:14.2] [sgdgc:4.11:0.8:1.0:9.2:0.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3352	2156415_c1_3	4612	18715	538	186	YDL200C	258	2.7(10)-22	Saccharomyces cerevisiae	[ui:ydl200c] [pn:06-methylguanine dna repair methyltransferase:methylated-dna--protein-cysteine methyltransferase:6-o-methylguanine-dna methyltransferase] [gn:mgt1:d1204] [gicfc:10.1:10.10:0.2:14.1] [ec:2.1.1.63] [keggfc:14.1] [sgdgc:2.1.1.63]
CONTIG5437	24350687_c3_23	4613	18716	561	187	YDL165W	324	2.7(10)-29	Saccharomyces cerevisiae	[ui:ydl165w] [pn:transcription factor:general negative regulator of transcription subunit 2] [gn:nol2:cdc36:dna19] [gicfc:10.1:10.2:12.8] [keggfc:14.2] [sgdgc:3.8:0.4:8.2:9.5:0] [db:gic-saccharomyces cerevisiae]

CONTIG5390	12896936_c1_14	4614	18717	198	66	YDL164C	112	1.5(10)-5	Saccharomyces cerevisiae	[ui:ndl164c] [pn:dnaligase:polydeoxyribonucleotidesynthase:atp] [gn:cdc9][gicfc:10.1:10.10:10.2:10.8:14.1][ec:6.5.1.1][keggfc:14.1][sgdfc:3.6.0.3.7.0.9.5.0.11.2.1][db:gic-saccharomyces cerevisiae]
CONTIG5736	203942_c3_27	4615	18718	939	313	YDL164C	1025	1.3(10)-103	Saccharomyces cerevisiae	[ui:ndl164c] [pn:dnaligase:polydeoxyribonucleotidesynthase:atp] [gn:cdc9][gicfc:10.1:10.10:10.2:10.8:14.1][ec:6.5.1.1][keggfc:14.1][sgdfc:3.6.0.3.7.0.9.5.0.11.2.1][db:gic-saccharomyces cerevisiae]
CONTIG2856	233570399_c1_4	4616	18719	1107	369	YDL164C	693	2.2(10)-68	Saccharomyces cerevisiae	[ui:ndl164c] [pn:dnaligase:polydeoxyribonucleotidesynthase:atp] [gn:cdc9][gicfc:10.1:10.10:10.2:10.8:14.1][ec:6.5.1.1][keggfc:14.1][sgdfc:3.6.0.3.7.0.9.5.0.11.2.1][db:gic-saccharomyces cerevisiae]
CONTIG2033	22334792_f1_1	4617	18720	1149	383	YDL160C	1002	3.8(10)-101	Saccharomyces cerevisiae	[ui:ndl160c] [pn:strong similarity to rna helicases of the dead box family;putative atp-dependent rna helicase] [gn:dhhl][gicfc:10.1:10.2][keggfc:14.2][sgdfc:4.12.0.9.5.0][db:gic-saccharomyces cerevisiae]
CONTIG3197	33209375_f1_2	4618	18721	621	207	YDL160C	739	2.8(10)-73	Saccharomyces cerevisiae	[ui:ndl160c] [pn:strong similarity to rna helicases of the dead box family;putative atp-dependent rna helicase] [gn:dhhl][gicfc:10.1:10.2][keggfc:14.2][sgdfc:4.12.0.9.5.0][db:gic-saccharomyces cerevisiae]

CONTIG5717	12695903_cl_8	4619	18722	1725	575	YDL154W	702	2.3(10)-69	Saccharomyces cerevisiae	[ui:ydl154w] [pn:meiosis-specific protein] [gn:msh5] [gtfcfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.5.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG1929	23597567_f1_1	4620	18723	981	327	YDL116W	179	1.2(10)-25	Saccharomyces cerevisiae	[ui:ydl116w] [pn:nucleoporin:nuclear pore protein] [gn:nup84] [gtfcfc:10.1:10.2] [keggfc:14.2] [sgdfc:8.1.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4692	14506511_f3_5	4621	18724	1479	493	YDL106C	339	6.0(10)-44	Saccharomyces cerevisiae	[ui:ydl106c] [pn:homeodomain protein:regulatory protein pho2, general regulatory factor 10] [gn:pho2:bas2:grf1:0:d2350] [gtfcfc:10.1:10.2:12.8:13.10] [keggfc:13.2] [sgdfc:1.3.5.1.4.2:4.8:2.9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG2064	10366327_f2_1	4622	18725	201	67	YDL036W	184	3.2(10)-13	Saccharomyces cerevisiae	[ui:ydl036w] [pn:transcription factor, subunit of the mbf factor:transcription factor:mbf subunit p120] [gn:mbf1] [gtfcfc:10.1:10.2:12.8] [keggfc:13.2] [sgdfc:3.8.0:4.8:2.9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3239	20751657_cl_4	4623	18726	555	185	YDL056W	282	1.1(10)-23	Saccharomyces cerevisiae	[ui:ydl056w] [pn:transcription factor, subunit of the mbf factor:transcription factor:mbf subunit p120] [gn:mbf1] [gtfcfc:10.1:10.2:12.8] [keggfc:13.2] [sgdfc:3.8.0:4.8:2.9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG3884	20488905_f2_2	4624	18727	1461	487	YDL056W	95	0.28899	Saccharomyces cerevisiae	[ui:ydI056w] [pn:transcription factor, subunit of the mbf factor:transcription factor:mbf subunit p120] [gn:mbp1] [gicfc:10.1:10.2:12.8] [keggfc:13.2] [sgdfc:3.8:0.4:8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4530	33789717_c1_8	4625	18728	2238	746	YDL056W	263	3.2(10)-25	Saccharomyces cerevisiae	[ui:ydI056w] [pn:transcription factor, subunit of the mbf factor:transcription factor:mbf subunit p120] [gn:mbp1] [gicfc:10.1:10.2:12.8] [keggfc:13.2] [sgdfc:3.8:0.4:8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG973	22269759_c2_3	4626	18729	789	263	YDL056W	194	2.7(10)-14	Saccharomyces cerevisiae	[ui:ydI056w] [pn:transcription factor, subunit of the mbf factor:transcription factor:mbf subunit p120] [gn:mbp1] [gicfc:10.1:10.2:12.8] [keggfc:13.2] [sgdfc:3.8:0.4:8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3237	4475386_c2_4	4627	18730	798	266	YDL043C	248	3.1(10)-21	Saccharomyces cerevisiae	[ui:ydI043c] [pn:pre-mrna splicing factor] [gn:ppr1] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.9:0.9:5.0] [db:gic-saccharomyces cerevisiae]

CONTIG1026	12784405_f2_1	4628	18731	918	306	YDL030W	396	6.5(10)-37	Saccharomyces cerevisiae	[ui:yd1030w] [pn:pre-mrna splicing factor:snrma-associated protein:pre-mrna splicing factor prp9] [gn:prp9:d2773] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.9:0.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG2121	29343840_f2_1	4629	18732	423	141	YDL030W	90	0.039	Saccharomyces cerevisiae	[ui:yd1030w] [pn:pre-mrna splicing factor:snrma-associated protein:pre-mrna splicing factor prp9] [gn:prp9:d2773] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.9:0.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG2648	24851018_f3_2	4630	18733	1218	406	YDL020C	217	4.2(10)-17	Saccharomyces cerevisiae	[ui:yd1020c] [pn:nuclear protein:nuclear protein son1:ub fusion degradation protein 5] [gn:son1:ufd5:d2840] [gicfc:10.1:10.11:10.2] [keggfc:14.2] [sgdfc:6.5:1:9.5:0] [db:gic-saccharomyces cerevisiae]
CONTIG5686	10759712_c2_23	4631	18734	1560	520	YDL020C	115	0.0014	Saccharomyces cerevisiae	[ui:yd1020c] [pn:nuclear protein:nuclear protein son1:ub fusion degradation protein 5] [gn:son1:ufd5:d2840] [gicfc:10.1:10.11:10.2] [keggfc:14.2] [sgdfc:6.5:1:9.5:0] [db:gic-saccharomyces cerevisiae]
CONTIG5686	21890828_c3_27	4632	18735	1506	502	YDL020C	135	7.5(10)-6	Saccharomyces cerevisiae	[ui:yd1020c] [pn:nuclear protein:nuclear protein son1:ub fusion degradation protein 5] [gn:son1:ufd5:d2840] [gicfc:10.1:10.11:10.2] [keggfc:14.2] [sgdfc:6.5:1:9.5:0] [db:gic-saccharomyces cerevisiae]

CONTIG3726	20312937_f1_1	4633	18736	480	160	YDL014W	774	5.7(10)-77	Saccharomyces cerevisiae	[ui:ydl014w] [pn:fibrillarin:nucleolar protein 1] [gn:nop1:d2870] [gicfc:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.2:0.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3726	12345187_f2_2	4634	18737	297	99	YDL014W	105	2.5(10)-5	Saccharomyces cerevisiae	[ui:ydl014w] [pn:fibrillarin:nucleolar protein 1] [gn:nop1:d2870] [gicfc:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.2:0.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5426	490917_f3_6	4635	18738	1557	519	YDR004W	252	2.7(10)-29	Saccharomyces cerevisiae	[ui:ydr004w] [pn: dna repair protein,dna repair protein rad57] [gn:rad57,yd8119] [gicfc:10.1:10.10:10.2:10.8:12.8:12.9] [keggfc:14.2] [sgdfc:3.3:0.3:0.3:7.0:9.5:0.11.2.] [db:gic-saccharomyces cerevisiae]
CONTIG4801	335803312_f3_5	4636	18739	1917	639	YDR006C	625	2.8(10)-98	Saccharomyces cerevisiae	[ui:ydr006c] [pn:high copy suppressor of a cyclic amp-dependent protein kinase mutant:sok1 protein] [gn:sok1:yd8119] [gicfc:10.1:0.2] [keggfc:14.2] [sgdfc:4.8:2.9:5.0] [db:gic-saccharomyces cerevisiae]

CONTIG1119	30250927_f1_1	4637	18740	756	252	YDR028C	107	3.0(10)-7	Saccharomyces cerevisiae	[ui:ydr028c] [pn:regulatory subunit for protein phosphatase glc7p:hex2 protein:sml1 protein:reg1 protein] [gn:hex2:sml1:reg1;spp43;yd9813] [gicfc:10.1:10.2:12.13:12.8] [keggfc:13..1] [sgdfc:1.5.2:4.9.0:9.5.0] [db:gtc-saccharomyces cere]
CONTIG2131	3929501_c1_3	4638	18741	621	207	YDR028C	105	0.00012	Saccharomyces cerevisiae	[ui:ydr028c] [pn:regulatory subunit for protein phosphatase glc7p:hex2 protein:sml1 protein:reg1 protein] [gn:hex2:sml1:reg1;spp43;yd9813] [gicfc:10.1:10.2:12.13:12.8] [keggfc:13..1] [sgdfc:1.5.2:4.9.0:9.5.0] [db:gtc-saccharomyces cere]
CONTIG2599	19632001_f1_1	4639	18742	1188	396	YDR028C	101	0.065	Saccharomyces cerevisiae	[ui:ydr028c] [pn:regulatory subunit for protein phosphatase glc7p:hex2 protein:sml1 protein:reg1 protein] [gn:hex2:sml1:reg1;spp43;yd9813] [gicfc:10.1:10.2:12.13:12.8] [keggfc:13..1] [sgdfc:1.5.2:4.9.0:9.5.0] [db:gtc-saccharomyces cere]

CONTIG2946	10833263_c3_7	4640	18743	1953	651	YDR028C	168	1.5(10)-11	Saccharomyces cerevisiae	[ui:ydrt028c] [pn:regulatory subunit for protein phosphatase glc7p:hex2 protein:sm1 protein:reg1 protein] [gn:hex2:sm1:reg1:spp43:yd9813] [gtfc:10.1:10.2:12.13:12.8] [keggfc:13.] [sgdic:1.5.24.9.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5418	19530_c3_20	4641	18744	222	74	YDR028C	117	6.0(10)-6	Saccharomyces cerevisiae	[ui:ydrt028c] [pn:regulatory subunit for protein phosphatase glc7p:hex2 protein:sm1 protein:reg1 protein] [gn:hex2:sm1:reg1:spp43:yd9813] [gtfc:10.1:10.2:12.13:12.8] [keggfc:13.] [sgdic:1.5.24.9.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG554	29550762_f1_1	4642	18745	807	269	YDR028C	381	2.1(10)-43	Saccharomyces cerevisiae	[ui:ydrt028c] [pn:regulatory subunit for protein phosphatase glc7p:hex2 protein:sm1 protein:reg1 protein] [gn:hex2:sm1:reg1:spp43:yd9813] [gtfc:10.1:10.2:12.13:12.8] [keggfc:13.] [sgdic:1.5.24.9.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG1778	11882013_c1_1	4643	18746	216	72	YDR034C	123	1.0(10)-6	Saccharomyces cerevisiae	[ui:ydrt034c] [pn:transcriptional activator of lysine pathway genes:lysine biosynthesis regulatory protein lys14] [gn:lys14:yd9673] [gtfc:10.1:10.2] [keggfc:14.2] [sgdic:1.1.24.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG271	6821877_c1_3	4644	18747	948	316	YDR034C	103	0.0016	Saccharomyces cerevisiae	[ui:ydfr034c] [pn:transcriptional activator of lysine pathway genes:lysine biosynthesis regulatory protein lys14] [gn:lys14;yd9673] [gtfc:10.1:10.2] [keggfc:14.2] [sgdgc:1.1.2.4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4112	398442_c3_6	4645	18748	696	232	YDR034C	122	1.3(10)-5	Saccharomyces cerevisiae	[ui:ydfr034c] [pn:transcriptional activator of lysine pathway genes:lysine biosynthesis regulatory protein lys14] [gn:lys14;yd9673] [gtfc:10.1:10.2] [keggfc:14.2] [sgdgc:1.1.2.4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2366	35287503_f1_1	4646	18749	873	291	YDR034C	108	0.00479	Saccharomyces cerevisiae	[ui:ydfr034c] [pn:transcriptional activator of lysine pathway genes:lysine biosynthesis regulatory protein lys14] [gn:lys14;yd9673] [gtfc:10.1:10.2] [keggfc:14.2] [sgdgc:1.1.2.4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4015	4100626_B_8	4647	18750	1917	639	YDR034C	113	0.0027	Saccharomyces cerevisiae	[ui:ydfr034c] [pn:transcriptional activator of lysine pathway genes:lysine biosynthesis regulatory protein lys14] [gn:lys14;yd9673] [gtfc:10.1:10.2] [keggfc:14.2] [sgdgc:1.1.2.4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4450	35970266_c2_9	4648	18751	1863	621	YDR034C	109	0.01099	Saccharomyces cerevisiae	[ui:yd:034c] [pn:transcriptional activator of lysine pathway genes:lysine biosynthesis regulatory protein lys14] [gn:lys14;yd9673] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdfc:1.1.24.8.2.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5002	6898551_c1_11	4649	18752	579	193	YDR034C	162	6.9(10)-11	Saccharomyces cerevisiae	[ui:yd:034c] [pn:transcriptional activator of lysine pathway genes:lysine biosynthesis regulatory protein lys14] [gn:lys14;yd9673] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdfc:1.1.24.8.2.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5632	20597288_f1_1	4650	18753	2145	715	YDR034C	289	3.2(10)-28	Saccharomyces cerevisiae	[ui:yd:034c] [pn:transcriptional activator of lysine pathway genes:lysine biosynthesis regulatory protein lys14] [gn:lys14;yd9673] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdfc:1.1.24.8.2.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5632	33441375_f2_3	4651	18754	726	242	YDR034C	145	4.5(10)-9	Saccharomyces cerevisiae	[ui:yd:034c] [pn:transcriptional activator of lysine pathway genes:lysine biosynthesis regulatory protein lys14] [gn:lys14;yd9673] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdfc:1.1.24.8.2.9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5664	15751250_f3_6	4652	18755	1197	399	YDR034C	211	5.0(10)-24	Saccharomyces cerevisiae	[ui:ydr034c] [pn:transcriptional activator of lysine pathway genes:lysine biosynthesis regulatory protein lys14] [gn:lys14.yd9673] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc: 1.1.2:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5791	4957813_f3_18	4653	18756	2070	690	YDR034C	295	1.3(10)-31	Saccharomyces cerevisiae	[ui:ydr034c] [pn:transcriptional activator of lysine pathway genes:lysine biosynthesis regulatory protein lys14] [gn:lys14.yd9673] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc: 1.1.2:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5802	4402067_f1_1	4654	18757	786	262	YDR034C	116	0.00033	Saccharomyces cerevisiae	[ui:ydr034c] [pn:transcriptional activator of lysine pathway genes:lysine biosynthesis regulatory protein lys14] [gn:lys14.yd9673] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc: 1.1.2:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
b9x11r38.x	10751640_f2_1	4655	18758	672	224	YDR034C	90	0.22	Saccharomyces cerevisiae	[ui:ydr034c] [pn:transcriptional activator of lysine pathway genes:lysine biosynthesis regulatory protein lys14] [gn:lys14.yd9673] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc: 1.1.2:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG2456	24323411_c3_4	4656	18759	1194	398	YDR052C	340	3.0(10)-34	Saccharomyces cerevisiae	[ui:yd052c] [pn:regulatory subunit for cdc7p protein kinase:dbf4 protein:dnas2 protein] [gn:dbf4;dnas2;yd9609] [gtfc:10.1:10.2:10.8:12.8] [keggfc:13.2] [sgdfc:3.6.0:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3705	182761_c3_10	4657	18760	786	262	YDR054C	622	7.2(10)-61	Saccharomyces cerevisiae	[ui:yd054c] [pn:ubiquitin-conjugating enzyme:ubiquitin-conjugating enzyme e2-34] [kd:ubiquitin-protein ligase:ubiquitin-carrier protein:cell division control protein 34] [gn:ubc3;cdc34;dnaf6;yd9609] [gtfc:10.1:10.11:10.2:10.7:10.8:12.8]
CONTIG611	4882186_c2_4	4658	18761	972	324	YDR088C	104	2.5(10)-8	Saccharomyces cerevisiae	[ui:yd088c] [pn:pre-mrna splicing factor affecting 3' splice site choice:pre-mrna splicing factor slu7] [gn:slu7;d44483] [gtfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5779	4178300_f3_12	4659	18762	1764	588	YDR097C	940	1.5(10)-94	Saccharomyces cerevisiae	[ui:yd097c] [pn:dna mismatch repair protein] [gn:msh6] [gtfc:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5779	978202_f3_13	4660	18763	1671	557	YDR097C	1524	1.8(10)-156	Saccharomyces cerevisiae	[ui:yd097c] [pn:dna mismatch repair protein] [gn:msh6] [gtfc:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5779	9946877_f1_3	4661	18764	261	87	YDR097C	142	1.7(10)-8	Saccharomyces cerevisiae	[ui:ydr097c] [pn: dna mismatch repair protein] [gn:msh6] [gtfc:10.1:10.2:10.8] [keggc:14.2] [sgdfc:3.7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4241	4772125_f1_2	4662	18765	1719	573	YDR159W	1095	5.5(10)-111	Saccharomyces cerevisiae	[ui:ydr159w] [pn:leucine permease transcriptional regulator] [gn:sac3:lep1:yd8358] [gtfc:10.1:10.2] [keggc:14.2] [sgdfc:1.1.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG864	20901562_f2_2	4663	18766	711	237	YDR159W	210	1.0(10)-15	Saccharomyces cerevisiae	[ui:ydr159w] [pn:leucine permease transcriptional regulator] [gn:sac3:lep1:yd8358] [gtfc:10.1:10.2] [keggc:14.2] [sgdfc:1.1.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4895	7206462_c3_6	4664	18767	954	318	YDR173C	463	5.2(10)-44	Saccharomyces cerevisiae	[ui:ydr173c] [pn:arginine metabolism transcription factor:arginine metabolism regulation protein iii] [gn:argR3:arg82:yd9395] [gtfc:10.1:10.2:12.15] [keggc:14.2] [sgdfc:1.1.2:3.4.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG969	24335417_c3_4	4665	18768	891	297	YDR176W	470	1.8(10)-44	Saccharomyces cerevisiae	[ui:ydr176w] [pn:general transcriptional adaptor or co-activator:ada3 protein:mgg1 protein] [gn:ada3:ngg1:yd9395] [gtfc:10.1:10.2:12.13] [keggc:14.2] [sgdfc:1.5.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1884	975012_f1_1	4666	18769	876	292	YDR217C	132	3.5(10)-6	Saccharomyces cerevisiae	[ui:ydrl217c] [pn: dna repair checkpoint protein:dna repair protein] [gn:rad9] [gicfc:10.1:10.2:12.8] [keggc:14.2] [sgdfc:3.8:0.4.8:2.9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3962	16835925_c2_7	4667	18770	399	133	YDR224C	466	2.5(10)-44	Saccharomyces cerevisiae	[ui:ydrl224c] [pn: histone h2b:histone h2b] [gn:htbl:h2b]:[sp1:12:yd9334] [gicfc:10.1:10.2] [keggc:14.2] [sgdfc:4.8:2.9.5:0.9.6.0] [db:gic-saccharomyces cerevisiae]
CONTIG4359	4741062_f1_1	4668	18771	549	183	YDR225W	518	7.7(10)-50	Saccharomyces cerevisiae	[ui:ydrl225w] [pn: histone h2a:histone h2a] [gn:htal:h2a]:[sp1:1:yd9934] [gicfc:10.1:10.2] [keggc:14.2] [sgdfc:4.8:2.9.5:0.9.6.0] [db:gic-saccharomyces cerevisiae]
CONTIG3853	11117280_f3_4	4669	18772	1134	378	YDR228C	154	2.8(10)-22	Saccharomyces cerevisiae	[ui:ydrl228c] [pn: component of pre-mma 3"-end processing factor cf1] [gn:pcfl] [gicfc:10.1:10.2:10.9] [keggc:14.2] [sgdfc:4.10.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5337	4812525_f3_2	4670	18773	954	318	YDR228C	242	1.2(10)-19	Saccharomyces cerevisiae	[ui:ydrl228c] [pn: component of pre-mma 3"-end processing factor cf1] [gn:pcfl] [gicfc:10.1:10.2:10.9] [keggc:14.2] [sgdfc:4.10.0:9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG5312	9922131_f3_7	4671	18774	912	304	YDR216W	204	4.5(10)-15	Saccharomyces cerevisiae	[ui:ydr216w] [pn:zinc-finger transcription factor:regulatory protein adr1] [gn:adr1:yd8142] [gicfc:10.1:10.2:12.13] [keggfc:14.2] [sgdfc:1.5.2:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG927	11828957_f1_1	4672	18775	873	291	YDR216W	225	2.6(10)-17	Saccharomyces cerevisiae	[ui:ydr216w] [pn:zinc-finger transcription factor:regulatory protein adr1] [gn:adr1:yd8142] [gicfc:10.1:10.2:12.13] [keggfc:14.2] [sgdfc:1.5.2:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3333	13867037_c1_4	4673	18776	957	319	YDR243C	426	4.2(10)-40	Saccharomyces cerevisiae	[ui:ydr243c] [pn:pre-mrna splicing factor rna helicase of dead box family:pre-mrna splicing factor rna helicase prp28:helicase ca8] [gn:prp28:yd8419] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.9:0.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4458	11737891_c2_6	4674	18777	381	127	YDR243C	188	7.0(10)-14	Saccharomyces cerevisiae	[ui:ydr243c] [pn:pre-mrna splicing factor rna helicase of dead box family:pre-mrna splicing factor rna helicase prp28:helicase ca8] [gn:prp28:yd8419] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.9:0.9:5.0] [db:gic-saccharomyces cerevisiae]

CONTIG2065	167625_f3_2	4675	18778	591	197	YDR254W	140	7.0(10)-9	Saccharomyces cerevisiae	[uri:ydr254w] [pn:chromosome segregation protein:putative cell segregation machinery component chl4] [gn:chl4:ctfl7.yd9320a] [gicfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8:0.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4619	12506512_f2_4	4676	18779	564	188	YDR254W	208	2.8(10)-16	Saccharomyces cerevisiae	[uri:ydr254w] [pn:chromosome segregation protein:putative cell segregation machinery component chl4] [gn:chl4:ctfl7.yd9320a] [gicfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8:0.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG1848	10814002_c1_2	4677	18780	210	70	YDR257C	97	0.00034	Saccharomyces cerevisiae	[uri:ydr257c] [pn:regulatory protein] [gn:rms1] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3873	120157_c2_3	4678	18781	1167	389	YDR257C	253	1.8(10)-40	Saccharomyces cerevisiae	[uri:ydr257c] [pn:regulatory protein] [gn:rms1] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG1274	9797251_f1_1	4679	18782	762	254	YDR285W	94	0.14999	Saccharomyces cerevisiae	[uri:ydr285w] [pn:synaptonemal complex protein:synaptonemal complex protein zip1] [gn:zip1.d9819] [gicfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.5:0.3:8.0:9.5:0:9.6:0] [db:gic-saccharomyces cerevisiae]

CONTIG4344	12118760_c2_8	4680	18783	543	181	YDR285W	113	0.00036	Saccharomyces cerevisiae	[ui:yd285w] [pn:synaptonemal complex protein:synaptonemal complex protein zip1] [gn:zip1:d9819] [gfcfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.5.0:3.8.0:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4822	30117187_c2_12	4681	18784	1350	450	YDR285W	106	0.023	Saccharomyces cerevisiae	[ui:yd285w] [pn:synaptonemal complex protein:synaptonemal complex protein zip1] [gn:zip1:d9819] [gfcfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.5.0:3.8.0:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5780	16147626_f1_1	4682	18785	405	135	YDR285W	93	0.01499	Saccharomyces cerevisiae	[ui:yd285w] [pn:synaptonemal complex protein:synaptonemal complex protein zip1] [gn:zip1:d9819] [gfcfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.5.0:3.8.0:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG270	10005011_c3_2	4683	18786	387	129	YDR301W	234	3.0(10)-18	Saccharomyces cerevisiae	[ui:yd301w] [pn:pre-mrna 3'-end processing factor cf ii] [gn:cft1] [gfcfc:10.1:10.2:10.9] [keggfc:14.2] [sgdfc:4.10.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3074	4892288_c3_6	4684	18787	1587	529	YDR301W	694	4.5(10)-74	Saccharomyces cerevisiae	[ui:yd301w] [pn:pre-mrna 3'-end processing factor cf ii] [gn:cft1] [gfcfc:10.1:10.2:10.9] [keggfc:14.2] [sgdfc:4.10.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3248	29882938_f1_2	4685	18788	1107	369	YDR301W	185	8.5(10)-18	Saccharomyces cerevisiae	[ui:yd301w] [pn:pre-mrna 3"-end processing factor cf ii] [gnc:ctf1] [gtcfc:10.1:10.2:10.9] [keggfc:14.2] [sgdfc:4.10.9:5.0] [db:gtc-saccharomyces cerevisiae]
b2x18140.y	26375442_f1_1	4686	18789	465	155	YDR301W	141	2.3(10)-8	Saccharomyces cerevisiae	[ui:yd301w] [pn:pre-mrna 3"-end processing factor cf ii] [gnc:ctf1] [gtcfc:10.1:10.2:10.9] [keggfc:14.2] [sgdfc:4.10.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4614	33773307_c2_6	4687	18790	672	224	YDR308C	165	2.0(10)-12	Saccharomyces cerevisiae	[ui:yd308c] [pn:dna-directed dna polymerase ii holoenzyme and komberg's mediator:srb subcomplex subunit:suppressor of ma polymerase b srb7] [gn:srb7:d9740] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:1:9.5.0] [db:gtc-saccharomyces_c
CONTIG5785	7228218_c3_34	4688	18791	1716	572	YDR311W	433	6.4(10)-58	Saccharomyces cerevisiae	[ui:yd311w] [pn:tfiih subunit:transcription initiation factor, 7S rna polymerase ii transcription factor b 73 kd subunit] [gn:tfb1:d9740] [gtcfc:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:4.8.1:9.5:0:11.2.1] [db:gtc-saccharomyces_cerev

CONTIG5785	21875078_c1_24	4689	18792	423	141	YDR311W	125	4.7(10)-7	Saccharomyces cerevisiae	[ui:yd311w] [pn:tfiih subunit:transcription initiation factor, 75 kda polymerase ii transcription factor b 73 kd subunit] [gn:ifb1:d9740] [gtcfc:10.1:10.10:10.2] [keggfc:4.8.1:9.5.0:11.2..1] [db:gtc-saccharomyces cerev]
CONTIG4764	9782136_f1_1	4690	18793	549	183	YDR328C	469	1.5(10)-54	Saccharomyces cerevisiae	[ui:yd328c] [pn:kinetochore protein complex cbf3, subunit d:centromere dna-binding protein complex cbf3 subunit d:suppressor of kinetochore protein 1] [gn:cbf3d:skp1:d9798] [gtcfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.5.0:9.6.
CONTIG1200	1267200_f2_1	4691	18794	714	238	YDR356W	132	3.3(10)-6	Saccharomyces cerevisiae	[ui:yd356w] [pn:spindle pole body component:nuf1 protein:spindle poly body spacer protein spc110] [gn:nuf1:spc110:d9476] [gtcfc:10.1:10.2:12.16:12.8] [keggfc:4.2] [sgdfc:3.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3798	2909500_f3_5	4692	18795	690	230	YDR356W	106	0.00719	Saccharomyces cerevisiae	[ui:ydr356w] [pn:spindle pole body component:nuf1 protein:spindle poly body spacer protein spc110] [gn:nuf1:spc110:d9476] [gicfc: 10.1:10.2:12.16:12.8] [keggfc: 14.2] [sgdfc: 3.8:0.9:3.0:9.5:0] [db:gic-saccharomyces cerevisiae]
CONTIG4570	4800451_f2_3	4693	18796	1449	483	YDR356W	102	0.05299	Saccharomyces cerevisiac	[ui:ydr356w] [pn:spindle pole body component:nuf1 protein:spindle poly body spacer protein spc110] [gn:nuf1:spc110:d9476] [gicfc: 10.1:10.2:12.16:12.8] [keggfc: 14.2] [sgdfc: 3.8:0.9:3.0:9.5:0] [db:gic-saccharomyces cerevisiae]
CONTIG4836	15042311_c3_6	4694	18797	900	300	YDR356W	98	0.095	Saccharomyces cerevisiae	[ui:ydr356w] [pn:spindle pole body component:nuf1 protein:spindle poly body spacer protein spc110] [gn:nuf1:spc110:d9476] [gicfc: 10.1:10.2:12.16:12.8] [keggfc: 14.2] [sgdfc: 3.8:0.9:3.0:9.5:0] [db:gic-saccharomyces cerevisiae]

CONTIG4987	30352067_f3_3	4695	18798	2775	925	YDR356W	315	1.7(10)-24	Saccharomyces cerevisiae	[ui:ydr356w] [pn:spindle pole body component:nuf1 protein:spindle poly body spacer protein spc110] [gn:nuf1:spc110:d9476] [gicfc:10.:10.2:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3315	991577_f3_5	4696	18799	1011	337	YDR356W	95	0.22	Saccharomyces cerevisiae	[ui:ydr356w] [pn:spindle pole body component:nuf1 protein:spindle poly body spacer protein spc110] [gn:nuf1:spc110:d9476] [gicfc:10.1:10.2:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5767	6034681_c1_33	4697	18800	2166	722	YDR356W	128	0.00017	Saccharomyces cerevisiae	[ui:ydr356w] [pn:spindle pole body component:nuf1 protein:spindle poly body spacer protein spc110] [gn:nuf1:spc110:d9476] [gicfc:10.1:10.2:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3581	954436_f1_1	4698	18801	813	271	YDR364C	451	2.7(10)-49	Saccharomyces cerevisiae	[ui:ydr364c] [pn:cell division control protein:cde40-xrs2] [gn:cde40-xrs2] [gicfc:10.1:10.2:10.8:12.8] [keggfc:14.2] [sgdfc:3.6.0:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2012	2922000_f3_2	4699	18802	984	328	YDR390C	685	7.7(10)-76	Saccharomyces cerevisiae	[ui:ydR390c] [pn:similarity to ubalp and human ubiquitin-activating enzyme e1:ubiquitin-activating enzyme e1-like:polymerase-interacting protein 2] [gn:uba2:ual1:pip2:d9509] [gtfc: 10.1:10.11:10.2:10.9] [keggfc: 14.2] [sgdfc:4.10.0:6.5]
CONTIG4290	875288_c2_9	4700	18803	777	259	YDR390C	175	2.0(10)-12	Saccharomyces cerevisiae	[ui:ydR390c] [pn:similarity to ubalp and human ubiquitin-activating enzyme e1:ubiquitin-activating enzyme e1-like:polymerase-interacting protein 2] [gn:uba2:ual1:pip2:d9509] [gtfc: 10.1:10.11:10.2:10.9] [keggfc: 14.2] [sgdfc:4.10.0:6.5]
CONTIG2068	4102290_f2_1	4701	18804	828	276	YDR392W	784	5.0(10)-78	Saccharomyces cerevisiae	[ui:ydR392w] [pn:regulatory protein:spt3 protein:positive regulator of ty transcription] [gn:spf3:d9509] [gtfc: 10.1:10.2:12.9] [keggfc: 14.2] [sgdfc:3.3.0:4.8.2:9.5.0] [db:gc-saccharomyces cerevisiae]
CONTIG5754	29554682_c3_37	4702	18805	1026	342	YDR432W	237	1.3(10)-19	Saccharomyces cerevisiae	[ui:ydR432w] [pn:nucleolar protein:nucleolar protein 3:mitochondrial targeting suppressor 1 protein] [gn:nop3,npf3:msl1:d9461] [gtfc: 10.1:10.2:10.3:10.7:11.1:12.3] [keggfc: 14.2] [sgdfc:4.2.0:4.11.0:6.2:0.8.1.0:9.5.0] [db:gtc-saccharom]

CONTIG3941	605208_f2_1	4703	18806	2769	923	YDR443C	119	1.8(10)-12	Saccharomyces cerevisiae	[ui:yd443c] [pn:dnad-directed rna polymerase ii holoenzyme and kornberg's mediator:srb subcomplex subunit:suppressor of rna polymerase b srb9:scal1 protein] [gn:srb9:scal1:ssn2] [gtfc:10.1:10.2:12.13] [keggc:14.2] [sgdgc:1.5.2.4.8.1.9]
CONTIG5734	9792001_f1_2	4704	18807	1734	578	YDR443C	262	4.9(10)-19	Saccharomyces cerevisiae	[ui:yd443c] [pn:dnad-directed rna polymerase ii holoenzyme and kornberg's mediator:srb subcomplex subunit:suppressor of rna polymerase b srb9:scal1 protein] [gn:srb9:scal1:ssn2] [gtfc:10.1:10.2:12.13] [keggc:14.2] [sgdgc:1.5.2.4.8.1.9]
CONTIG2067	33364063_c3_8	4705	18808	630	210	YDR448W	369	4.7(10)-34	Saccharomyces cerevisiae	[ui:yd448w] [pn:transcriptional adaptor:potential transcriptional adaptor] [gn:ada2:d9461] [gtfc:10.1:10.2] [keggc:14.2] [sgdgc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2067	20507813_c1_6	4706	18809	768	256	YDR448W	803	4.7(10)-80	Saccharomyces cerevisiae	[ui:yd448w] [pn:transcriptional adaptor:potential transcriptional adaptor] [gn:ada2:d9461] [gtfc:10.1:10.2] [keggc:14.2] [sgdgc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3191	4945755_f2_1	4707	18810	1497	499	YEL061C	463	1.8(10)-47	Saccharomyces cerevisiae	[ui:yel061c] [pn:kinesin-related protein:kinesin-like protein cin8] [gn:cin8:ks12] [gtfc:10.1:10.2:12.16:12.8] [keggc:14.2] [sgdgc:3.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5049	14537503_f2_4	4708	18811	1083	361	YEL037C	297	3.2(10)-35	Saccharomyces cerevisiae	[ui:yel037cl] [pn:nucleotide excision repair protein:uv excision repair protein rad23] [gn:rad23;sg:gp-orf29] [gtfc:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:9.5:0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1546	250700_c1_3	4709	18812	798	266	YEL032W	315	4.0(10)-27	Saccharomyces cerevisiae	[ui:yel032w] [pn:replication initiation protein:minichromosome maintenance protein 3] [gn:mcm3;sg:gp-orf23] [gtfc:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.6:0:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG2343	10022567_c3_5	4710	18813	186	62	YEL032W	98	0.00062	Saccharomyces cerevisiae	[ui:yel032w] [pn:replication initiation protein:minichromosome maintenance protein 3] [gn:mcm3;sg:gp-orf23] [gtfc:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.6:0:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG2767	26600302_c1_2	4711	18814	1305	435	YEL032W	1162	1.8(10)-125	Saccharomyces cerevisiae	[ui:yel032w] [pn:replication initiation protein:minichromosome maintenance protein 3] [gn:mcm3;sg:gp-orf23] [gtfc:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.6:0:9.5:0] [db:gtc-saccharomyces cerevisiae]

CONTIG4538	79808_c3_4	4712	18815	945	315	YEL009C	239	2.7(10)-20	Saccharomyces cerevisiae	[ui:yel009c] [pn:transcriptional activator of amino acid biosynthetic genes:general control protein gcn4:amino acid biosynthesis regulatory protein] [gn:gcn4,arg9:aas3] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdgc:1.1.2.4.8.2.9.5.0] [db:gtc]
CONTIG1851	5175257_c1_2	4713	18816	1176	392	YER013W	346	2.6(10)-30	Saccharomyces cerevisiae	[ui:yer013w] [pn:pre-mrna splicing factor:pre-mrna splicing factor rna helicase] [gn:prp22] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.9.0.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5798	7120932_c3_41	4714	18817	1857	619	YER013W	2018	8.5(10)-209	Saccharomyces cerevisiae	[ui:yer013w] [pn:pre-mrna splicing factor:pre-mrna splicing factor rna helicase] [gn:prp22] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.9.0.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5798	22454051_c2_35	4715	18818	1287	429	YER013W	314	8.3(10)-52	Saccharomyces cerevisiae	[ui:yer013w] [pn:pre-mrna splicing factor:pre-mrna splicing factor rna helicase] [gn:prp22] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.9.0.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4666	2401009_c1_10	4716	18819	558	186	YER013W	248	7.5(10)-20	Saccharomyces cerevisiae	[ui:yer013w] [pn:pre-mrna splicing factor:pre-mrna splicing factor rna helicase] [gn:prp22] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.9.0.9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5728	23649056_f2_8	4717	18820	1467	489	YER022W	457	4.5(10)-43	Saccharomyces cerevisiae	[ui:yer022w] [pn:dna-directed dna polymerase ii holoenzyme and kornberg's mediator:srb subcomplex subunit:suppressor of rna polymerase b] [gn:srb4] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.1:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5601	26605093_c2_27	4718	18821	858	286	YER045C	114	1.2(10)-9	Saccharomyces cerevisiae	[ui:yer045c] [pn:weak similarity to transcription factor sko1p:hypothetical 54.6 kd protein in mei4-caj1 intergenic region] [gtcfc:10.2] [keggfc:14.2] [sgdfc:9.5.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5813	34422150_f3_28	4719	18822	1734	578	YER068W	737	4.7(10)-73	Saccharomyces cerevisiae	[ui:yer068w] [pn:transcriptional repressor:general negative regulator of transcription subunit 4] [gr:not4:mot2:ssfl1:sg1:ccl1] [gtcfc:10.1:10.2:12.9] [keggfc:14.2] [sgdfc:3.3.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3009	12580327_c2_6	4720	18823	774	258	YER088C	248	3.1(10)-20	Saccharomyces cerevisiae	[ui:yer088c] [pn:weak similarity human transforming proteins:b-myb:hypothetical 73.0 kd protein in seb1-trp2 intergenic region] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3394	1044271_f2_2	4721	18824	651	217	YER095W	866	1.0(10)-86	Saccharomyces cerevisiae	[ui:yer095w] [pn:dna repair protein] [gn:rad51] [gtcfc:10.1:10.10:10.2:10.8:12.9] [keggfc:14.2] [sgdfc:3.3.0:3.7.0:9.5.0:11.2.] [db:gtc-saccharomyces cerevisiae]
CONTIG6555	468950_c3_21	4722	18825	1152	384	YER107C	159	2.8(10)-9	Saccharomyces cerevisiae	[ui:yer107c] [pn:required for nuclear pore complex structure and function:hypothetical 40.5 kd protein in nup157-pdh5 intergenic region][gn:gle2] [gtcfc:10.1:10.2:12.3] [keggfc:14.2] [sgdfc:4.11.0:8.1.0:9.2.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3390	14113300_c1_2	4723	18826	1773	591	YER111C	114	0.00449	Saccharomyces cerevisiae	[ui:yer111c] [pn:transcription factor:regulatory protein swi4:cell-cycle box factor, chain swi4:art1 protein][gn:swi4:art1] [gtcfc:10.1:10.2:12.8] [keggfc:13.1] [sgdfc:3.8.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3587	433332_f2_1	4724	18827	711	237	YER111C	194	4.0(10)-14	Saccharomyces cerevisiae	[ui:yer111c] [pn:transcription factor:regulatory protein swi4:cell-cycle box factor, chain swi4:art1 protein][gn:swi4:art1] [gtcfc:0.1:10.2:12.8] [keggfc:13.1] [sgdfc:3.8.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2567	20319501_f2_3	4725	18828	390	130	YER112W	96	1.0(10)-15	Saccharomyces cerevisiae	[ui:yer112w] [pn:u6 snma-associated protein:u6 snma-associated protein][gnussl:sd23]
CONTIG2741	598342_c3_12	4726	18829	1455	485	YER122C	488	5.5(10)-71	Saccharomyces cerevisiae	[ui:yer122c] [pn:zinc finger protein][gn:gio3] [gicfc:10.1:10.2] [keggfc:14.2][sgdfc:4.9.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5574	7226587_f1_1	4727	18830	951	317	YER142C	398	4.0(10)-37	Saccharomyces cerevisiae	[ui:yer142c] [pn:dna-3-methyladenine glycosidase:3-methyladenine dna glycosylase][gn:mag1_mag][gicfc:10.1:10.10:10.2:14.1][ec:3.2.2.21] [keggfc:14.1][sgdfc:9.5.0:11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG4776	15718812_f3_4	4728	18831	759	253	YER148W	813	4.2(10)-81	Saccharomyces cerevisiae	[ui:yer148w] [pn:tfiId and tfiIib subunit; transcription initiation factor (tfiD-tata-box factor:tata sequence-binding protein:tpf) transcription factor d][gn:spf15_btf1][gicfc:10.1:10.2:10.3] [keggfc:14.2][sgdfc:4.1.0:4.4.0:4.8.1:9]

CONTIG2031	16485801_f3_4	4729	18832	1038	346	YER161C	163	1.1(10)-11	Saccharomyces cerevisiae	[ui:yer 61 c] [pn:multifunctional hmg-like chromatin protein spf2 protein:negative regulator of ty transcription] [gn:spf2:spm2:sin1] [gicfc:10.1:10.2] [keggc:14.2] [sgdfc:4.8:2.9:5.0:9.6.0] [db:gic-saccharomyces cerevisiae]
CONTIG2681	20410150_f1_1	4730	18833	1179	393	YER162C	476	7.0(10)-45	Saccharomyces cerevisiae	[ui:yer 62 c] [pn:excision repair protein:dna repair protein] [gn:rad4] [gicfc:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:9.5:0:11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG4672	35798416_c3_9	4731	18834	774	258	YER162C	279	1.8(10)-23	Saccharomyces cerevisiae	[ui:yer 62 c] [pn:excision repair protein:dna repair protein] [gn:rad4] [gicfc:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:9.5:0:11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG4715	9930401_f3_6	4732	18835	894	298	YER165W	574	8.9(10)-56	Saccharomyces cerevisiae	[ui:yer 65 w] [pn:mmra polyadenylate-binding protein, cytoplasmic and nuclear:pabp:ars consensus binding protein acbp-67:polyadenylate tail-binding protein] [gn:pab1] [gicfc:10.1:10.2:10.7:10.9] [keggfc:14]

CONTIG479	10975405_f2_1	4733	18836	531	177	YER165W	509	6.9(10)-49	Saccharomyces cerevisiae	[ui:yer165w] [pn:mmna polyadenylate-binding protein:polyadenylate-binding protein, cytoplasmic and nuclear:pabp] [ars consensus binding protein acbp-67:polyadenylylate tail-binding protein] [gn:pab1] [gtfc:10.1:10.2:10.7:10.9] [keggfc:14]
CONTIG4129	30085927_c1_12	4734	18837	2121	707	YER171W	2837	1.3(10)-295	Saccharomyces cerevisiae	[ui:yer171w] [pn:dna helicase/atpase:dna repair helicase rad3] [gn:rad3:rem1] [gtfc:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:4.8.1.9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1980	36226442_f2_2	4735	18838	564	188	YER179W	767	3.1(10)-76	Saccharomyces cerevisiae	[ui:yer179w] [pn:meiosis-specific protein:meiotic recombination protein dmc1] [gn:dmc1:isc2] [gtfc:10.1:10.2:10.8:12.8] [keggfc:14.2] [sgdfc:3.5.0:3.7.0:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG820	6423252_f1_1	4736	18839	711	237	YER184C	98	0.021	Saccharomyces cerevisiae	[ui:yer184c] [pn:similarity to multidrug resistance proteins pdr3p and pdr1p;putative 91.1 kd transcriptional regulatory protein in isc10.3'region] [gtfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2763	2736251_f1_1	4737	18840	744	248	YFL031W	230	2.5(10)-19	Saccharomyces cerevisiae	[ui:yfl031w] [pn:transcription factor:hac1 protein] [gn:hac1:ire2] [gicfc:10.1:10.2] [keggc:14.2] [sgdfc:4.8:2.9:5.0] [db:gc-saccharomyces cerevisiae]
CONTIG5803	14488952_c1_20	4738	18841	1416	472	YFL008W	831	1.5(10)-82	Saccharomyces cerevisiae	[ui:yfl008w] [pn:chromosome segregation protein:chromosome segregation protein smc1:da-box protein smc1] [gn:smc1:chl10] [gicfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8:0.9:5.0] [db:gc-saccharomyces cerevisiae]
CONTIG5803	10656932_03_33	4739	18842	2379	793	YFL008W	1224	1.2(10)-124	Saccharomyces cerevisiae	[ui:yfl008w] [pn:chromosome segregation protein:chromosome segregation protein smc1:da-box protein smc1] [gn:smc1:chl10] [gicfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8:0.9:5.0] [db:gc-saccharomyces cerevisiae]
CONTIG5276	14631563_f1_2	4740	18843	2481	827	YFL003C	1155	2.3(10)-117	Saccharomyces cerevisiae	[ui:yfl003c] [pn:meiosis-specific protein:muis protein homolog 4] [gn:msh4] [gicfc:10.1:10.2:10.8:12.8] [keggfc:14.2] [sgdfc:3.5:0.3:7.0:9.5.0] [db:gc-saccharomyces cerevisiae]
CONTIG413	33406877_03_5	4741	18844	489	163	YFL002C	344	8.8(10)-31	Saccharomyces cerevisiae	[ui:yfl002c] [pn:atp-dependent rna helicase of deah box family:atp-dependent rna helicase] [gn:spb4] [gicfc:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.2:0.9:5.0] [db:gc-saccharomyces cerevisiae]

CONTIG413	24410682_c3_4	4742	18845	315	105	YFL002C	216	7.2(10)-17	Saccharomyces cerevisiae	[ui:yfl002c] [pn:atp-dependent rna helicase of deah box family:atp-dependent rna helicase] [gn:spb4] [gtfc:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.2.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG500	30367268_f1_1	4743	18846	384	128	YFL002C	109	2.2(10)-5	Saccharomyces cerevisiae	[ui:yfl002c] [pn:atp-dependent rna helicase of deah box family:atp-dependent rna helicase] [gn:spb4] [gtfc:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.2.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5037	19953762_f2_2	4744	18847	1233	411	YFR002W	367	7.7(10)-33	Saccharomyces cerevisiae	[ui:yfr002w] [pn:nuclear pore protein:96 kd nucleoporin-interacting component] [gn:nic96] [gtfc:10.1:10.2] [keggfc:14.2] [sgdfc:8.1.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5037	24062751_f3_3	4745	18848	1839	613	YFR002W	608	2.2(10)-59	Saccharomyces cerevisiae	[ui:yfr002w] [pn:nuclear pore protein:96 kd nucleoporin-interacting component] [gn:nic96] [gtfc:10.1:10.2] [keggfc:14.2] [sgdfc:8.1.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4980	1195277_c1_5	4746	18849	2469	823	YFR031C	1751	1.7(10)-180	Saccharomyces cerevisiae	[ui:yfr031c] [pn:chromosome segregation protein:da-box protein] [gn:smc2] [gtfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG5730	22141556_c2_13	4747	188530	903	301	YFR031C	1054	1.2(10)-106	Saccharomyces cerevisiae	[ui:yfr031c] [pn:chromosome segregation protein:da-box protein] [gn:smc2] [gicfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8:0.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3742	13846061_c1_7	4748	18851	711	237	YFR034C	109	0.00023	Saccharomyces cerevisiae	[ui:yfr034c] [pn:transcription factor:phosphate system positive regulatory protein] [gn:pho4] [gicfc:10.1:10.2:12.8:13.10] [keggfc:13.2] [sgdfc:1.4.2:4.8:2.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG1011	26172255_c2_3	4749	18852	840	280	YGL251C	443	9.0(10)-41	Saccharomyces cerevisiae	[ui:ygl251c] [pn:dna/ma helicase:hfm1 protein] [gn:hfm1:nre1046] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.12.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5468	26223519_c1_13	4750	18853	906	302	YGL251C	170	8.3(10)-10	Saccharomyces cerevisiae	[ui:ygl251c] [pn:dna/ma helicase:hfm1 protein] [gn:hfm1:nre1046] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.12.0:9.5.0] [db:gic-saccharomyces cerevisiae]
b3x11387_y	26188424_c1_4	4751	18854	594	198	YGL251C	441	1.5(10)-40	Saccharomyces cerevisiae	[ui:ygl251c] [pn:dna/ma helicase:hfm1 protein] [gn:hfm1:nre1046] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.12.0:9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG2495	4119381_f3_1	4752	18855	1392	464	YGL238W	515	1.2(10)-48	Saccharomyces cerevisiae	[ui:yg]238w [pn:probable kinetochore protein:chromosome segregation protein] [gn:cse1] [gtfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8:0.9:5.0:9.6.0] [db:gic-saccharomyces cerevisiae]
CONTIG4965	25428812_c2_7	4753	18856	192	64	YGL238W	161	1.2(10)-10	Saccharomyces cerevisiae	[ui:yg]238w [pn:probable kinetochore protein:chromosome segregation protein] [gn:cse1] [gtfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8:0.9:5.0:9.6.0] [db:gic-saccharomyces cerevisiae]
b9x13e15.y	14896887_f1_1	4754	18857	906	302	YGL238W	641	1.8(10)-62	Saccharomyces cerevisiae	[ui:yg]238w [pn:probable kinetochore protein:chromosome segregation protein] [gn:cse1] [gtfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8:0.9:5.0:9.6.0] [db:gic-saccharomyces cerevisiae]
CONTIG2187	39511_f3_3	4755	18858	642	214	YGL237C	195	1.3(10)-15	Saccharomyces cerevisiae	[ui:yg]237c [pn:ccaa-t-binding factor subunit:transcriptional activator] [gn:hap2] [gtfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG2563	14882907_f3_2	4756	18859	840	280	YGL237C	279	1.6(10)-24	Saccharomyces cerevisiae	[ui:yg]237c [pn:ccaa-t-binding factor subunit:transcriptional activator] [gn:hap2] [gtfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2:9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG2845	23595207_c3_4	4757	18860	1605	535	YGL208W	185	1.1(10)-11	Saccharomyces cerevisiae	[uri:yg][208w] [pn:dominant suppressor of some ts mutations in rpo21 and rpr4:sip2:spm2 protein] [gn:sip2:spm2]
CONTIG4654	24410451_f3_8	4758	18861	1182	394	YGL207W	611	6.5(10)-59	Saccharomyces cerevisiae	[uri:yg][207w] [pn:general chromatin factor:cell division control protein 68] [gn:cdc68:spt16:ssf1]
CONTIG4654	9978176_f1_3	4759	18862	1350	450	YGL207W	1013	2.7(10)-102	Saccharomyces cerevisiae	[uri:yg][207w] [pn:general chromatin factor:cell division control protein 68] [gn:cdc68:spt16:ssf1]
CONTIG4654	1993950_f2_6	4760	18863	291	97	YGL207W	327	2.3(10)-28	Saccharomyces cerevisiae	[uri:yg][207w] [pn:general chromatin factor:cell division control protein 68] [gn:cdc68:spt16:ssf1]

CONTIG563	12207031_c3_5	4761	18864	234	78	YGL207W	209	9.5(10)-16	Saccharomyces cerevisiae	[ui:yg1207w] [pn:general chromatin factor;cell division control protein 68] [gn:cde68;spt16:ssf1] [gicfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8 0.4 8.3:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5011	5120427_c3_11	4762	18865	1638	546	YGL192W	1023	2.2(10)-103	Saccharomyces cerevisiae	[ui:yg1192w] [pn:positive transcription factor for ime2:transcriptional regulator spo8] [gn:spo8;ime4,g1337] [gicfc:10.1:10.2:12.15] [keggfc:14.2] [sgdfc:3.4 0.4 8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4386	12000402_f1_1	4763	18866	1023	341	YGL172W	221	1.0(10)-26	Saccharomyces cerevisiae	[ui:yg1172w] [pn:nuclear pore protein;nucleoporin nup49/nsp49;nuclear pore protein nup49/nsp49] [gicfc:10.1:10.2:12.3] [keggfc:14.2] [sgdfc:4.11 0.8 1.0 9.5.0] [db:gic-saccharomyces cerevisiae]
b9x10w60.x	29847157_f1_1	4764	18867	528	176	YGL172W	101	0.00012	Saccharomyces cerevisiae	[ui:yg1172w] [pn:nuclear pore protein;nucleoporin nup49/nsp49;nuclear pore protein nup49/nsp49] [gicfc:10.1:10.2:12.3] [keggfc:14.2] [sgdfc:4.11 0.8 1.0 9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG3057	12782292_B3_2	4765	18868	1212	404	YGL166W	118	5.9(10)-5	Saccharomyces cerevisiae	[ui:yg1166w] [pn:copper-dependent transcription factor:transcriptional activator protein acel :copper-fist transcription factor] [gn:acc1:cup2:g1810] [gtcfc:10.1:10.2:12.6] [keggfc:14.2] [sgdfc:1.8.1:4.8.2:9.5.0] [db:grc-saccharomyces]
CONTIG1666	480126_f1_1	4766	18869	816	272	YGL163C	1014	2.1(10)-102	Saccharomyces cerevisiae	[ui:yg1163c] [pn: dna-dependent nuclease of the snf2p family:dna repair and recombination protein rad54] [gn:rad54:g1821] [gtcfc:10.1:10.10:10.2:10.8:12.8] [keggfc:14.2] [sgdfc:3.5.0:3.7.0:9.5.0:11.2.1] [db:grc-saccharomyces cerevisiae]
CONTIG2995	11723211_c2_8	4767	18870	1257	419	YGL163C	486	3.8(10)-82	Saccharomyces cerevisiae	[ui:yg1163c] [pn: dna-dependent nuclease of the snf2p family:dna repair and recombination protein rad54] [gn:rad54:g1821] [gtcfc:10.1:10.10:10.2:10.8:12.8] [keggfc:14.2] [sgdfc:3.5.0:3.7.0:9.5.0:11.2.1] [db:grc-saccharomyces cerevisiae]
b3x16060.y	35838517_B3_1	4768	18871	378	126	YGL163C	129	2.7(10)-7	Saccharomyces cerevisiae	[ui:yg1163c] [pn: dna-dependent nuclease of the snf2p family:dna repair and recombination protein rad54] [gn:rad54:g1821] [gtcfc:10.1:10.10:10.2:10.8:12.8] [keggfc:14.2] [sgdfc:3.5.0:3.7.0:9.5.0:11.2.1] [db:grc-saccharomyces cerevisiae]

CONTIG2515	25509687_c3_3	4769	18872	762	254	YGL115W	763	8.3(10)-76	Saccharomyces cerevisiae	[ui:ygl115w] [pn:nuclear regulatory protein:nuclear protein snf4,regulatory protein cat3] [gn:snf4;cat3] [gtfc:10.1:10.2:12.13:13.2] [keggc:14.2] [sgdfc:1.5.24.8.2:9.5.0:11.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2496	33754007_c1_5	4770	18873	906	302	YGL112C	653	3.7(10)-64	Saccharomyces cerevisiae	[ui:ygl112c] [pn:tfid subunit:tfp-associated protein complex, 60kd:transcription initiation factor tfid 60 kd subunit:tafi-60] [gn:taf60;g2985] [gtfc:10.1:10.2] [keggc:14.2] [sgdfc:4.8.1:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4476	31921888_f1_1	4771	18874	528	176	YGL112C	95	0.01099	Saccharomyces cerevisiae	[ui:ygl112c] [pn:tfid subunit:tfp-associated protein complex, 60kd:transcription initiation factor tfid 60 kd subunit:tafi-60] [gn:taf60;g2985] [gtfc:10.1:10.2] [keggc:14.2] [sgdfc:4.8.1:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5761	33207500_c1_18	4772	18875	1140	380	YGL100W	735	9.0(10)-94	Saccharomyces cerevisiae	[ui:ygl100w] [pn:nuclear pore protein] [gn:seh1] [gtfc:10.1:10.2] [keggc:14.2] [sgdfc:8.1:0.9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1734	15664163_12_1	4773	18876	462	154	YGL097W	479	1.0(10)-45	Saccharomyces cerevisiae	[ui:yg 097w] [pn:gdp/gtp exchange factor for gsp1p/gsp2p:regulator of chromosome condensation:prp20 protein:pheromone response pathway component sml1] [gn:prp20:sml1:mtr1] [gtcfc:10.1:10.2:10.3:10.6:10.9:12.3 :12.8:12.9] [keggfc:13.3]
CONTIG4261	16853436_c3_6	4774	18877	1014	318	YGL097W	839	7.4(10)-84	Saccharomyces cerevisiae	[ui:yg 097w] [pn:gdp/gtp exchange factor for gsp1p/gsp2p:regulator of chromosome condensation:prp20 protein:pheromone response pathway component sml1] [gn:prp20:sml1:mtr1] [gtcfc:10.1:10.2:10.3:10.6:10.9:12.3 :12.8:12.9] [keggfc:13.3]
CONTIG4989	5254555_c3_7	4775	18878	1215	405	YGL097W	109	5.2(10)-5	Saccharomyces cerevisiae	[ui:yg 097w] [pn:gdp/gtp exchange factor for gsp1p/gsp2p:regulator of chromosome condensation:prp20 protein:pheromone response pathway component sml1] [gn:prp20:sml1:mtr1] [gtcfc:10.1:10.2:10.3:10.6:10.9:12.3 :12.8:12.9] [keggfc:13.3]

CONTIG5116	14885931_c1_6	4776	18879	1464	488	YGL097W	134	1.0(10)-5	Saccharomyces cerevisiae	[ui:yg[097w] [pn:gdp/gtp exchange factor for gsp1p/gsp2p/regulator of chromosome condensation:pp20 protein:pheromone response pathway component smr1] [gn:pp20:smr1:mtr1] [gtcfc:10.1:10.2:10.3:10.6:10.9:12.3:12.8:12.9] [keggfc:13.3]
CONTIG1557	24788942_f1_1	4777	18880	942	314	YGL092W	111	4.5(10)-7	Saccharomyces cerevisiae	[ui:yg[092w] [pn:nucleoporin:nuclear pore protein] [gn:nup145] [gtcfc:10.1:10.2:10.6:12.3] [keggfc:14.2] [sgdic:4.5.0:4.11.0:8.1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2555	23524192_c3_3	4778	18881	1656	552	YGL092W	231	1.3(10)-15	Saccharomyces cerevisiae	[ui:yg[092w] [pn:nucleoporin:nuclear pore protein] [gn:nup145] [gtcfc:10.1:10.2:10.6:12.3] [keggfc:14.2] [sgdic:4.5.0:4.11.0:8.1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2189	19734676_f1_2	4779	18882	1194	398	YGL086W	121	0.00029	Saccharomyces cerevisiae	[ui:yg[086w] [pn:spindle assembly checkpoint protein:spindle assembly checkpoint component:mitotic protein] [gn:mad1] [gtcfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2444	4806436_c2_3	4780	18883	1923	641	YGL086W	346	1.2(10)-28	Saccharomyces cerevisiae	[ui:yg[086w] [pn:spindle assembly checkpoint protein:spindle assembly checkpoint component:mitotic protein] [gn:mad1] [gtcfc:10.1:0.2:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5431	26692299_c1_9	4781	18884	960	320	YGL078C	1095	5.5(10)-111	Saccharomyces cerevisiae	[ui:yg[078c] [pn:putative rna helicase required for pre-rna processing;probable atp-dependent rna helicase ca3] [gn:dbp3] [gtcfc:10.1:0.2:10.3] [keggfc:14.2] [sgdfc:4.2.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3275	33407202_c1_17	4782	18885	915	305	YGL071W	95	6.5(10)-6	Saccharomyces cerevisiae	[ui:yg[071w] [pn:iron-regulated transcriptional repressor:iron-regulated transcriptional repressor aft1] [gn:aft1:res1] [gtcfc:10.1:0.2:12.6] [keggfc:14.2] [sgdfc:1.8.14.8.2.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4253	12611055_c3_8	4783	18886	411	137	YGL058W	483	3.8(10)-46	Saccharomyces cerevisiae	[ui:yg[058w] [pn:ubiquitin conjugating enzyme:ubiquitin-conjugating enzyme e2-20 kd:ubiquitin- protein ligase:ubiquitin carrier protein] [gn:ubc2:rafd6] [gtcfc:10.1:10.10:10.2:10.7:10.8:12.15:14.1] [ec:6.3.2.19] [keggfc:14.1] [sgdfc:3]

CONTIG4173	9801537_c2_9	4784	18887	1122	374	YGL044C	112	0.00052	Saccharomyces cerevisiae	[ui:yg 044c] [pn:component of pre-mrna 3"-end processing factor of i:mRNA 3"-end processing protein] [gn:ma15] [gicfc:10.1:10.2:10.9] [keggfc:14.2] [sgdfc:4.10.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5749	20742187_c2_22	4785	18888	837	279	YGL044C	218	4.7(10)-18	Saccharomyces cerevisiae	[ui:yg 044c] [pn:component of pre-mrna 3"-end processing factor of i:mRNA 3"-end processing protein] [gn:ma15] [gicfc:10.1:10.2:10.9] [keggfc:14.2] [sgdfc:4.10.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5749	19615635_f3_10	4786	18889	939	313	YGL043W	455	5.5(10)-63	Saccharomyces cerevisiae	[ui:yg 043w] [pn:tfis:transcription elongation factor:transcription elongation factor s-ii:dna strand transfer protein alpha:stp-alpha:dna strand transferase I:pyrimidine pathway regulatory protein 2] [gn:dst1:ppr2] [gicfc:10.1:10.2:1]
CONTIG1873	785627_f1_3	4787	18890	753	251	YGL035C	241	9.1(10)-20	Saccharomyces cerevisiae	[ui:yg 035c] [pn:transcriptional repressor:regulatory protein cat4] [gn:mig1:cat4:ssn1] [gicfc:10.1:10.2:12.13] [keggfc:14.2] [sgdfc:1.5.2.4.8.2.9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG2619	783132_c3_9	4788	18891	1527	509	YGL035C	241	1.3(10)-18	Saccharomyces cerevisiae	[ui:yg1035c] [pn:transcriptional repressor:regulatory protein mig1:regulatory protein cat4] [gn:mig1:ca4:ssn1] [gtfc:10.1:10.2:12.13] [keggc:14.2] [sgdfc:1.5.2.4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5297	24407812_f2_7	4789	18892	528	176	YGL035C	273	2.7(10)-23	Saccharomyces cerevisiae	[ui:yg1035c] [pn:transcriptional repressor:regulatory protein mig1:regulatory protein cat4] [gn:mig1:ca4:ssn1] [gtfc:10.1:10.2:12.13] [keggc:14.2] [sgdfc:1.5.2.4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5245	15630261_c3_23	4790	18893	909	303	YGL019W	667	1.2(10)-65	Saccharomyces cerevisiae	[ui:yg1019w] [pn:casein kinase ii beta subunit:casein kinase ii beta chain:ck iii] [gn:ctkb1] [gtfc:10.1:10.2:12.13:14.1] [ec:2.7.1.37] [keggc:14.1] [sgdfc:4.4.0:9.5.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3649	260_c2_7	4791	18894	696	232	YGL013C	113	0.00027	Saccharomyces cerevisiae	[ui:yg1013c] [pn:transcription factor:pleiotropic drug resistance regulatory protein 1] [gn:pdf1:ant1:bor2:cyh3:nra2:smr2] [gtfc:10.1:10.2:12.12] [keggc:14.2] [sgdfc:4.8.2:9.5.0:11.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4336	476550_c1_7	4792	18895	564	188	YGL013C	117	6.5(10)-6	Saccharomyces cerevisiae	[ui:yg[013c] [pn:transcription factor:pleiotropic drug resistance regulatory protein 1] [gn:prd1:ant1:bor2:cyh3:nra2:smf2] [gicfc:10.1:0.2:12.12] [keggfc:14.2] [sgdfc:4.8:2.9:5.0:11.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG472	4797027_f1_1	4793	18896	909	303	YGR005C	325	2.2(10)-29	Saccharomyces cerevisiae	[ui:yg[005c] [pn:tfifif subunit:transcription initiation factor, 54 kd:transcription initiation factor iif, beta subunit:tfifif- beta:tfifif medium subunit:transcription factor g 54 kd subunit] [gn:tfg2] [gicfc:10.1:0.2] [keggfc:14.2] [
CONTIG981	5875001_f2_2	4794	18897	684	228	YGR006W	123	4.5(10)-6	Saccharomyces cerevisiae	[ui:yg[006w] [pn:u5 snRNA-associated protein:pre-mRNA splicing factor] [gn:prp18] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.9:0.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3978	35332807_f1_1	4795	18898	1218	406	YGR044C	154	1.3(10)-8	Saccharomyces cerevisiae	[ui:yg[044c] [pn:zinc-finger transcription factor:zinc finger protein] [gn:rme1] [gicfc:10.1:0.2:12.8] [keggfc:13.1] [sgdfc:3.5:0.3:8.0:4.8:2.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5713	13706525_c3_21	4796	18899	351	117	YGR063C	259	2.1(10)-22	Saccharomyces cerevisiae	[ui:yg[063c] [pn:transcription initiation protein] [gn:spf4] [gicfc:10.1:0.2:10.8] [keggfc:14.2] [sgdfc:3.7:0.4:8.1:4.8:3.9:5.0] [db:gic-saccharomyces cerevisiae]

CONTIG5447	22054035_c1_13	4797	18900	366	122	YGR074W	100	1.5(10)-5	Saccharomyces cerevisiae	[ui:ygr074w] [pn:snrna-associated protein;small nuclear ribonucleoprotein d1 homolog] [gn:smd1] [gtcfc:10.1:10.2:12.16] [keggc:14.2] [sgdfc:4.9:0.6:4.0:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG1368	25502175_f2_1	4798	18901	942	314	YGR091W	345	1.5(10)-35	Saccharomyces cerevisiae	[ui:ygr091w] [pn:pre-mrna splicing protein;pre-mrna splicing factor] [gn:prp31] [gtcfc:10.1:10.2] [keggc:14.2] [sgdfc:4.9:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3144	448957_f1_1	4799	18902	2007	669	YGR098C	237	5.2(10)-16	Saccharomyces cerevisiae	[ui:ygr098c] [pn:required for normal spindle structure;protein] [gn:esp1] [gtcfc:10.1:10.2:12.8] [keggc:14.2] [sgdfc:3.8:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG582	4695411_c1_3	4800	18903	735	245	YGR098C	255	2.2(10)-20	Saccharomyces cerevisiae	[ui:ygr098c] [pn:required for normal spindle structure;protein] [gn:esp1] [gtcfc:10.1:10.2:12.8] [keggc:14.2] [sgdfc:3.8:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4432	6407830_f3_8	4801	18904	753	251	YGR099W	144	1.1(10)-7	Saccharomyces cerevisiae	[ui:ygr099w] [pn:involved in controlling telomere length and position effect telomere length regulation protein] [gn:tel2] [gtcfc:10.1:10.2] [keggc:14.2] [sgdfc:9.5:0.9:6.0] [db:gtc-saccharomyces cerevisiae]

CONTIG432	21666581_f1_1	4802	18905	585	195	YGR099W	103	0.00489	Saccharomyces cerevisiae	[ui:ygr099w] [pn:involved in controlling telomere length and position effect:telomer length regulation protein] [gn:tel2] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:9.5.0:9.6.0] [db:gic-saccharomyces cerevisiae]
CONTIG5789	6855033_c3_30	4803	18906	897	299	YGR104C	143	8.9(10)-13	Saccharomyces cerevisiae	[ui:ygr104c] [pn:dna-directed rna polymerase ii holoenzyme and kornberg's mediator:srb subcomplex subunit:suppressor of rna polymerase b] [gn:srb5] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.1:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG801	26750450_c3_3	4804	18907	1119	373	YGR116W	501	1.1(10)-46	Saccharomyces cerevisiae	[ui:ygr116w] [pn:transcription initiation protein:transcription initiation protein spf6] [gn:spf6:ssm20:cre2:g6169] [gicfc: 10.1:10.2:10.8] [keggfc: 14.2] [sgdfc:3.7.0:4.8.1:4.8.3:9.5.0] [db:gic-saccharomyces cerevisiae]
b2x10868_y	10828302_f1_1	4805	18908	522	174	YGR116W	203	6.5(10)-15	Saccharomyces cerevisiae	[ui:ygr116w] [pn:transcription initiation protein:transcription initiation protein spf6] [gn:spf6:ssm20:cre2:g6169] [gicfc: 10.1:10.2:10.8] [keggfc: 14.2] [sgdfc:3.7.0:4.8.1:4.8.3:9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG892	10347312_f1_1	4806	18909	606	202	YGR119C	192	2.2(10)-14	Saccharomyces cerevisiae	[ui:ygr119c] [pn:nuclear pore protein:nucleoporin nup57;nuclear pore protein nup57] [gn:nup57:g6320] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdgc:8.1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5795	16829705_c3_42	4807	18910	1209	403	YGR159C	698	6.4(10)-69	Saccharomyces cerevisiae	[ui:ygr159c] [pn:nuclear localization sequence binding protein:p67] [gn:nsl1:g7001] [gtcfc:10.1:10.2:10.3:13.2] [keggfc:14.2] [sgdgc:4.2:0:9.5:0:11.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4405	15019625_f1_1	4808	18911	1635	545	YGR186W	387	2.5(10)-56	Saccharomyces cerevisiae	[ui:ygr186w] [pr:tfif subunit;transcription initiation factor, 105 kd:transcription initiation factor iif, alpha subunit:tfif-alpha:tfif large subunit:transcription factor g 105 kd subunit:p105] [gn:tsf1:ssu71:g7526] [gtcfc:10.1:10]
CONTIG1831	819637_c3_4	4809	18912	633	211	YGR229C	131	5.4(10)-7	Saccharomyces cerevisiae	[ui:ygr229c] [pn:beta-1,3-glucan synthesis protein:sm1 protein:killer toxin resistant protein 4] [gn:sm1:knr4:kir4:g8553] [gtcfc:10.1:10.2:12.13] [keggfc:14.2] [sgdgc:1.5:2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3039	33250311_c1_3	4810	18913	1296	432	YGR229C	306	6.0(10)-27	Saccharomyces cerevisiae	[ui:ygr229c] [pn:beta-1,3-glucan synthesis protein:sm1 protein:killer toxin resistant protein 4] [gn:sm1.knr4:kir4.g8553] [gtfc:10.1:10.2:12.13] [keggc:14.2] [sgdgc:1.5.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3039	2907182_c3_4	4811	18914	426	142	YGR229C	106	3.7(10)-5	Saccharomyces cerevisiae	[ui:ygr229c] [pn:beta-1,3-glucan synthesis protein:sm1 protein:killer toxin resistant protein 4] [gn:sm1.knr4:kir4.g8553] [gtfc:10.1:10.2:12.13] [keggc:14.2] [sgdgc:1.5.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3774	24432937_f1_2	4812	18915	693	231	YGR229C	244	4.2(10)-20	Saccharomyces cerevisiae	[ui:ygr229c] [pn:beta-1,3-glucan synthesis protein:sm1 protein:killer toxin resistant protein 4] [gn:sm1.knr4:kir4.g8553] [gtfc:10.1:10.2:12.13] [keggc:14.2] [sgdgc:1.5.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4159	23829656_f3_2	4813	18916	1083	361	YGR252W	1398	4.2(10)-143	Saccharomyces cerevisiae	[ui:ygr252w] [pn:histone acetyltransferase:transcriptional activator gcn5] [gn:gcn5.ada4] [gtfc:10.1:10.2:10.7] [keggc:14.2] [sgdgc:4.8.2:4.8.3:6.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG360	10757661_f1_1	4814	18917	948	316	YGR258C	104	0.024	Saccharomyces cerevisiae	[ui:gr258c] [pn:structure-specific nuclease of the nucleotide excision repairosome:dna repair protein] [gn:rad2] [gicfc:10.1:10:10:2:12.8] [Keggfc:14.2] [sgdfc:3.5:0:9.5:0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5692	6812900_f1_3	4815	18918	447	149	YGR258C	448	2.5(10)-41	Saccharomyces cerevisiae	[ui:gr258c] [pn:structure-specific nuclease of the nucleotide excision repairosome:dna repair protein] [gn:rad2] [gicfc:10.1:10:10:2:12.8] [Keggfc:14.2] [sgdfc:3.5:0:9.5:0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5692	21660937_f2_5	4816	18919	2385	795	YCR258C	647	4.2(10)-103	Saccharomyces cerevisiae	[ui:gr258c] [pn:structure-specific nuclease of the nucleotide excision repairosome:dna repair protein] [gn:rad2] [gicfc:10.1:10:10:2:12.8] [Keggfc:14.2] [sgdfc:3.5:0:9.5:0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1591	24429567_f2_1	4817	18920	1089	363	YGR274C	241	2.0(10)-29	Saccharomyces cerevisiae	[ui:gr274c] [pn:tfIID subunit:bp-associated factor, 145 kd:transcription initiation factor tfIID 145 kd subunit:bp- associated factor 145 kd:tafI-145:tafI-130] [gn:tafI_45] [gicfc:10.1:10:2] [Keggfc:14.2] [sgdfc:4.8:1:4.8:3:9.5:0:

CONTIG3332	35433287_f2_1	4818	18921	564	188	YGR274C	167	3.0(10)-11	Saccharomyces cerevisiae	[ui:yg274c] [pn:tfid subunit:bp-associated factor, 145 kd:transcription initiation factor tfid 145 kd subunit:bp-associated factor 145 kdafti-145:taftii-130] [gn:taf145] [gtfc:10.1:0.2] [keggfc:14.2] [sgdgc:4.8:14.8:3.9:5.0]
b3x13754.x	196075_c3_5	4819	18922	528	176	YGR285C	320	7.2(10)-29	Saccharomyces cerevisiae	[ui:yg285c] [pn:zuo1in, a putative z-dna binding protein:zuo1n] [gn:zuo1] [gtfc:10.1:10.2] [keggfc:14.2] [sgdgc:9.5:0.9:6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5554	1406325_c3_21	4820	18923	615	205	YGR288W	134	3.2(10)-8	Saccharomyces cerevisiae	[ui:yg288w] [pn:maltose pathway regulatory protein:maltose fermentation regulatory protein mal1rl] [gn:mal1rl:mal3:gs591] [gtfc:10.1:10.2:12.13] [keggfc:14.2] [sgdgc:1.5:2.4.8:2.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4046	10972175_c3_8	4821	18924	855	285	YHL034C	116	6.0(10)-5	Saccharomyces cerevisiae	[ui:yhl034c] [pn:single-strand nucleic acid binding protein:single-stranded nucleic acid-binding protein] [gn:ssbr1:ssbp1] [gtfc:10.1:10.2:10.3] [keggfc:4.2:0.9:5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3312	24298461_f2_4	4822	18925	342	114	YHL027W	92	0.0016	Saccharomyces cerevisiae	[ui.yhl027w] [pn:meiotic regulatory protein] [gn:rim101] [gicfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.5.0:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3535	19728432_f1_1	4823	18926	1062	354	YHL027W	358	2.8(10)-32	Saccharomyces cerevisiae	[ui.yhl027w] [pn:meiotic regulatory protein] [gn:rim101] [gicfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.5.0:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3064	33985001_f2_3	4824	18927	993	331	YHL022C	139	8.5(10)-7	Saccharomyces cerevisiae	[ui.yhl022c] [pn:meiosis specific protein.meiosis-specific sporulation protein] [gn:spo11] [gicfc:10.1:10.2:10.8:12.8] [keggfc:14.2] [sgdfc:3.5.0:3.7:0.9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5717	10939550_f3_3	4825	18928	624	208	YHR041C	146	7.2(10)-10	Saccharomyces cerevisiae	[ui.yhr041c] [pn:dna-directed rna polymerase ii holoenzyme and kornberg's mediator:srb subcomplex subunit:suppressor of rna polymerase b] [gn:srb2] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.1:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3621	975077_f1_2	4826	18929	453	151	YHR089C	286	2.8(10)-25	Saccharomyces cerevisiae	[ui.yhr089c] [pn:nucleolar rna processing protein:protein] [gn:gar1] [gicfc:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.2:0:9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG1193	10315750_c2_9	4827	18930	567	189	YHR118C	104	0.0002	Saccharomyces cerevisiae	[uiyhr118c] [pn:origin recognition complex, 50 kd subunit:origin recognition complex protein, subunit 6:origin recognition complex protein 50 kd subunit:acs associated protein 1] [gn:orc6AAP] [gtcfc:0.1:10.2:10.8:12.8:12.9] [keggf]
CONTIG259	14472916_f2_1	4828	18931	2652	884	YHR119W	715	8.5(10)-105	Saccharomyces cerevisiae	[uiyhr119w] [pn:regulatory protein:hypothetical 123.9 kd protein in orf6-msh1 intergenic region] [gn:yix1] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.8.3.9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5721	5864036_02_23	4829	18932	258	86	YHR129C	178	3.5(10)-13	Saccharomyces cerevisiae	[uiyhr129c] [pn:contractin:actin-like protein] [gn:act5:act3] [gtcfc:10.1:10.2:12.16:12.8] [keggfc:14.2] [sgdgc:3.8.0:9.3.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3192	4687927_03_6	4830	18933	660	220	YHR164C	368	1.8(10)-32	Saccharomyces cerevisiae	[uiyhr164c] [pn:dna helicase:dna replication helicase] [gn:dnah2] [gtcfc:0.1:10.2:10.8] [keggfc:14.2] [sgdgc:3.6.0:9.5.0] [db:gic-saccharomyces cerevisiae]
b2x10687.x	10829568_f1_1	4831	18934	765	255	YHR164C	231	7.2(10)-18	Saccharomyces cerevisiae	[uiyhr164c] [pn:dna helicase:dna replication helicase] [gn:dnah2] [gtcfc:10.1:10.2:10.8] [keggfc:14.2] [sgdgc:3.6.0:9.5.0] [db:gic-saccharomyces cerevisiae]

b2x12186.x	444801_f3_1	4832	18935	519	173	YHR164C	240	7.9(10)-19	Saccharomyces cerevisiae	[ui:yhr164c] [pn: dna helicase:dna replication helicase] [gn: dna2] [gicfc:10.1:10.2:10.8] [keggfc:14.2] [sgdgc:3.6.0:9.5.0] [db:gic-saccharomyces cerevisiae]
b3x15670.y	12756438_f2_1	4833	18936	486	162	YHR164C	255	2.8(10)-25	Saccharomyces cerevisiae	[ui:yhr164c] [pn: dna helicase:dna replication helicase] [gn: dna2] [gicfc:10.1:10.2:10.8] [keggfc:14.2] [sgdgc:3.6.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG1677	433332_f2_1	4834	18937	1128	376	YHR165C	723	6.2(10)-70	Saccharomyces cerevisiae	[ui:yhr165c] [pn: u5 snmp protein, pre-mrna splicing factor:pre-mrna splicing factor prp8] [gn: prp8:ma8:dbf3:dna39] [gicfc:10.1:10.2:12.8] [keggfc:14.2] [sgdgc:3.8.0:4.9:0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG1685	21521891_c1_5	4835	18938	846	282	YHR165C	895	3.1(10)-88	Saccharomyces cerevisiae	[ui:yhr165c] [pn: u5 snmp protein, pre-mrna splicing factor:pre-mrna splicing factor prp8] [gn: prp8:ma8:dbf3:dna39] [gicfc:10.1:10.2:12.8] [keggfc:14.2] [sgdgc:3.8.0:4.9:0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG606	5900312_f3_2	4836	18939	1254	418	YHR165C	1602	7.5(10)-164	Saccharomyces cerevisiae	[ui:yhr165c] [pn: u5 snmp protein, pre-mrna splicing factor:pre-mrna splicing factor prp8] [gn: prp8:ma8:dbf3:dna39] [gicfc:10.1:10.2:12.8] [keggfc:14.2] [sgdgc:3.8.0:4.9:0:9.5.0] [db:gic-saccharomyces cerevisiae]

b9x13cl5.x	4428442_c3_3	4837	18940	201	67	YHR166C	131	1.1(10)-7	Saccharomyces cerevisiae	[ui:yhr166c] [pn:subunit of anaphase-promoting complex:cyclosome;cell division control protein 23] [gn:cdc23] [gicfc:10.1:10.11:10.2:12.16:12.8] [keggfc:13..3] [sgdfc:3..8.0:6.5.1:9.3.0:9.5.0] [db:gic-saccharomyces cerevisiae]
b9x13cl5.x	2917251_c2_2	4838	18941	477	159	YHR166C	523	2.2(10)-50	Saccharomyces cerevisiae	[ui:yhr166c] [pn:subunit of anaphase-promoting complex:cyclosome;cell division control protein 23] [gn:cdc23] [gicfc:10.1:10.11:10.2:12.16:12.8] [keggfc:13..3] [sgdfc:3..8.0:6.5.1:9.3.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG549	19782885_B3_1	4839	18942	516	172	YHR193C	338	9.0(10)-31	Saccharomyces cerevisiae	[ui:yhr193c] [pn:similarity to human alpha-nac:protein] [gn:egd2] [gicfc:10.1:10.2:12.13] [keggfc:14..2] [sgdfc:1.5.2:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4001	12683582_c2_12	4840	18943	240	80	YHR206W	221	2.2(10)-17	Saccharomyces cerevisiae	[ui:yhr206w] [pn:transcription factor with similarity to hsf1p:putative transcription factor skn7:pos9 protein] [gn:skn7:pos9] [gicfc:10.1:10.2:12.8:13.2] [keggfc:14..2] [sgdfc:3..1.0:3..8.0:4..8.2:9.5.0:11.1.0] [db:gic-saccharomyces cere

CONTIG4001	34563212_c3_15	4841	18944	948	316	YHR206W	184	1.8(10)-19	Saccharomyces cerevisiae	[ui:yer206w] [pn:transcription factor with similarity to hsf1p;putative transcription factor skn7:pos9 protein] [gn:skn7:pos9] [gtcfc:10.1:10.2:12.8:13.2] [keggfc:14.2] [sgdgc:3.1.0:3.8:0.4.8:2.9.5:0:11.1.0] [db:gtc-saccharomyces cere]
CONTIG5462	860077_f3_7	4842	18945	477	159	YHR206W	383	4.7(10)-35	Saccharomyces cerevisiae	[ui:yer206w] [pn:transcription factor with similarity to hsf1p;putative transcription factor skn7:pos9 protein] [gn:skn7:pos9] [gtcfc:10.1:10.2:12.8:13.2] [keggfc:14.2] [sgdgc:3.1.0:3.8:0.4.8:2.9.5:0:11.1.0] [db:gtc-saccharomyces cere]
CONTIG1455	4490885_c3_6	4843	18946	942	314	YIL143C	1435	5.0(10)-147	Saccharomyces cerevisiae	[ui:yil143c] [pn:dna helicase:dna repair helicase rad25] [gn:rad25:ssl2:uvv112] [gtcfc:10.1:10.10:10.2] [keggfc:14.2] [sgdgc:4.8.1:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2685	15792336_c1_5	4844	18947	708	236	YIL143C	823	3.7(10)-82	Saccharomyces cerevisiae	[ui:yil143c] [pn:dna helicase:dna repair helicase rad25] [gn:rad25:ssl2:uvv112] [gtcfc:10.1:10.10:10.2] [keggfc: 14.2] [sgdgc:4.8.1:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]

CONTIG5706	10970255_c1_19	4845	18948	831	277	YIL143C	714	1.3(10)-70	Saccharomyces cerevisiae	[ui:yil143c] [pn: dna helicase: dna repair helicase rad25] [gn:rad25;ssl2;uvst112] [gtfc:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:4.8.1.9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1299	20597211_f3_3	4846	18949	1272	424	YIL126W	588	4.9(10)-56	Saccharomyces cerevisiae	[ui:yil126w] [pn: subunit of the rsc complex:nuclear protein sth1(npst1)] [gn:sth1;npst1] [gtfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0:4.8.2:4.8.3:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3504	39756_f1_1	4847	18950	1722	574	YIL126W	1555	1.7(10)-169	Saccharomyces cerevisiae	[ui:yil126w] [pn: subunit of the rsc complex:nuclear protein sth1(npst1)] [gn:sth1;npst1] [gtfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0:4.8.2:4.8.3:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4330	16453251_c2_6	4848	18951	1254	418	YIL115C	218	2.0(10)-14	Saccharomyces cerevisiae	[ui:yil115c] [pn: nuclear pore protein:nucleoporin nup159] [gn:nup159;rat7] [gtfc:10.1:10.2] [keggfc:14.2] [sgdfc:8.1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3472	22050877_c3_6	4849	18952	786	262	YIL061C	193	2.3(10)-15	Saccharomyces cerevisiae	[ui:yil061c] [pn:u1 small nuclear ribonucleoprotein;u1 small nuclear ribonucleoprotein 70 kd homolog] [gn:snp1] [gtfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.9:0.9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG1816	25433132_c1_3	4850	18953	1119	373	YIL046W	718	1.2(10)-83	Saccharomyces cerevisiae	[ui:yil046w] [pn:involved in regulation of sulfur assimilation genes;protein] [gn:met30] [gtfc:10.1:10.2] [keggfc:1.1:2.4:8.2:9.5.0] [sgdgc: [db:gic-saccharomyces cerevisiae]
CONTIG4732	23944625_c1_12	4851	18954	1149	383	YIL038C	214	2.0(10)-16	Saccharomyces cerevisiae	[ui:yil038c] [pn:general negative regulator of transcription, subunit 3; general negative regulator of transcription subunit 3] [gn:not3_cdc39] [gtfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.8:2.9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5775	26370317_c2_27	4852	18955	2334	778	YIL038C	94	1.1(10)-15	Saccharomyces cerevisiae	[ui:yil038c] [pn:general negative regulator of transcription, subunit 3; general negative regulator of transcription subunit 3] [gn:not3_cdc39] [gtfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.8:2.9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4311	4431966_f3_4	4853	18956	633	211	YIL035C	777	2.7(10)-77	Saccharomyces cerevisiae	[ui:yil035c] [pn:casein kinase ii, catalytic alpha chain:casein kinase ii, alpha chain:ck ii] [gn:cka1] [gtfc:10.1:10.2:12.13:12.8] [ec:2.7.1.37] [keggfc:14.1] [sgdgc:3.8:0.4:7.0:9.5:0.15.0.0] [db:gic-saccharomyces cerevisiae]

CONTIG3781	2735001_f3_1	4854	18957	1491	497	YJL194W	240	6.2(10)-31	Saccharomyces cerevisiae	[ui:yjl194w] [pn:cell division control protein:cell division control protein 6] [gn:cdc6;jo347] [gicfc:10.1:10.2:10.8:12.8] [keggfc:13.2] [sgdfc:3.6:0.3.8:0.9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG20	25587825_c3_1	4855	18958	561	187	YJL176C	218	7.5(10)-17	Saccharomyces cerevisiae	[ui:yjl176c] [pn:transcription regulatory protein:transcription regulatory protein swi3;swi/snf complex component swi3:transcription factor tye2] [gn:swi3;tye2;j0495] [gicfc:10.1:10.2:12.13:12.9] [keggfc:14.2] [sgdfc:1.5.2:3.3.0:4.8.2]
CONTIG3498	36382067_c1_6	4856	18959	1686	562	YJL176C	103	0.05	Saccharomyces cerevisiae	[ui:yjl176c] [pn:transcription regulatory protein:transcription regulatory protein swi3;swi/snf complex component swi3:transcription factor tye2] [gn:swi3;tye2;j0495] [gicfc:10.1:10.2:12.13:12.9] [keggfc:14.2] [sgdfc:1.5.2:3.3.0:4.8.2]
CONTIG4493	24508433_f2_3	4857	18960	2754	918	YJL176C	414	2.1(10)-65	Saccharomyces cerevisiae	[ui:yjl176c] [pn:transcription regulatory protein:transcription regulatory protein swi3;swi/snf complex component swi3:transcription factor tye2] [gn:swi3;tye2;j0495] [gicfc:10.1:10.2:12.13:12.9] [keggfc:14.2] [sgdfc:1.5.2:3.3.0:4.8.2]

CONTIG4854	36025277_f2_1	4858	18961	1413	471	YJL127C	475	6.2(10)-66	Saccharomyces cerevisiae	[ui:yj1127c] [pn:transcription regulatory protein:sp10 protein] [gn:sp10:std1 :cre1:j0702] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2:9.5.0] [db:gic-saccharomyces cerevisiae]
b3x13313.y	53836_c3_3	4859	18962	576	192	YJL127C	108	0.00092	Saccharomyces cerevisiae	[ui:yj1127c] [pn:transcription regulatory protein:sp10 protein] [gn:sp10:std1 :cre1:j0702] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5539	3913925_f1_1	4860	18963	2226	742	YJL090C	255	1.2(10)-22	Saccharomyces cerevisiae	[ui:yj090c] [pn:involved in dna replication and s-phase checkpoint/hypothetical 87.2 kd protein in srs2-sip4 intergenic region] [gn:dpb11:j0918] [gicfc:10.1:10.2:10.8:12.8] [keggfc:13.2] [sgdfc:3.6:0.3.8:0.9:5.0] [db:gic-saccharomyce]
CONTIG2690	4882175_f1_1	4861	18964	1317	439	YJL089W	209	6.0(10)-14	Saccharomyces cerevisiae	[ui:yj089w] [pn:interacts with snf1 protein kinase:sip4 protein] [gn:spip4:j0922] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG2958	14650187_c1_2	4862	18965	1491	497	YJL081C	505	1.3(10)-71	Saccharomyces cerevisiae	[ui:yj081c] [pn:actin-related protein:actin-like protein act3] [gn:arp4:act3:j1012] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:9.5:0.9:6.0] [db:gic-saccharomyces cerevisiae]

CONTIG5135	36354678_c1_17	4863	18966	510	170	YJL080C	257	9.0(10)-21	Saccharomyces cerevisiae	[ui:yi 080c] [pn:histone-like protein:scp160 protein:protein hx] [gn:scp160:hxj1017] [gicfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5135	12922152_c3_20	4864	18967	2499	833	YJL080C	914	8.3(10)-92	Saccharomyces cerevisiae	[ui:yi 080c] [pn:histone-like protein:sep160 protein:protein hx] [gn:scp160:hxj1017] [gicfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5522	507186_c1_20	4865	18968	1635	545	YJL061W	132	3.6(10)-5	Saccharomyces cerevisiae	[ui:yi 061w] [pn:nuclear pore protein:nucleoporin nup82:nuclear pore protein nup82] [gn:nup82:j1135:hrb187] [gicfc:10.1:10.2:12.3] [keggfc:14.2] [sgdfc:4.11.0:8.1.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG140	515762_c2_2	4866	18969	243	81	YJL050W	187	2.2(10)-13	Saccharomyces cerevisiae	[ui:yi 050w] [pn:involved in nucleocytoplasmic transport of mrna:hypothetical helicase in tdh1-Eyp6 intergenic region] [gn:mtr4:j1158] [gicfc:10.1:10.2:12.3] [keggfc:14.2] [sgdfc:4.11.0:8.1.0:9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG4785	33492200_f2_2	4867	18970	516	172	YJL050W	494	3.2(10)-46	Saccharomyces cerevisiae	[ui:yl050w] [pn:involved in nucleocytoplasmic transport of mrna:hypothetical helicase in tdh1-gyp6 intergenic region] [gn:mir4; j1158] [gicfc:10.1:10.2:12.3] [keggfc:14.2] [sgdfc:4.11.0.8.1.0.9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5293	26351677_f2_2	4868	18971	2757	919	YJL050W	2832	4.7(10)-295	Saccharomyces cerevisiae	[ui:yl050w] [pn:involved in nucleocytoplasmic transport of mrna:hypothetical helicase in tdh1-gyp6 intergenic region] [gn:mir4; j1158] [gicfc:10.1:10.2:12.3] [keggfc:14.2] [sgdfc:4.11.0.8.1.0.9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3153	32553328_f3_1	4869	18972	366	122	YJL041W	109	3.3(10)-5	Saccharomyces cerevisiae	[ui:yl041w] [pn:nuclear pore protein:nucleoporin nsp1:nuclear pore protein nsp1:nucleoskeletal-like protein p110] [gn:nsp1;j1207] [gicfc:10.1] [keggfc:14.2] [sgdfc:4.7.0.8.1.0.9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5819	22522577_f2_7	4870	18973	1314	438	YJL025W	322	1.0(10)-28	Saccharomyces cerevisiae	[ui:yl025w] [pn:polymerase i specific transcription initiation factor:rn polymerase i specific transcription initiation factor rm7] [gn:rm7;j1273] [gicfc:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.1.0.9.5.0] [db:gic-saccharomyces cere

CONTIG4926	23554843_f2_3	4871	18974	1041	347	YJR035W	1128	1.8(10)-114	Saccharomyces cerevisiae	[ui:yjr035w] [pn:dna repair and recombination protein:dna repair and recombination protein rad26] [gn:rad26;gra1085;j1606] [gtfc:10.1:0.2:10.8] [keggfc:14.2] [sgdc:3.7:0.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4926	1212937_f3_5	4872	18975	1575	525	YJR035W	921	1.5(10)-92	Saccharomyces cerevisiae	[ui:yjr035w] [pn:dna repair and recombination protein:dna repair and recombination protein rad26] [gn:rad26;gra1085;j1606] [gtfc:10.1:0.2:10.8] [keggfc:14.2] [sgdc:3.7:0.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3117	14542311_c3_9	4873	18976	1101	367	YJR042W	154	6.4(10)-8	Saccharomyces cerevisiae	[ui:yjr042w] [pn:nuclear pore protein:nucleoporin nup85:nuclear pore protein nup85] [gn:nup85;rat9;j1624] [gtfc:10.1:10.2:10.6] [keggfc:14.2] [sgdc:4.5:0.8:1.0:9.5:0] [db:gic-saccharomyces cerevisiae]
CONTIG4183	14640660_f1_1	4874	18977	1191	397	YJR042W	283	8.5(10)-23	Saccharomyces cerevisiae	[ui:yjr042w] [pn:nuclear pore protein:nucleoporin nup85:nuclear pore protein nup85] [gn:nup85;rat9;j1624] [gtfc:10.1:10.2:10.6] [keggfc:14.2] [sgdc:4.5:0.8:1.0:9.5:0] [db:gic-saccharomyces cerevisiae]

CONTIG5049	23834438_c1_13	4875	18978	366	122	YJR052W	192	2.5(10)-14	Saccharomyces cerevisiae	[ui:yjr052w] [pn:nucleotide excision repair protein rad7] [gn:rad7;j1665] [gicfc:10.:10.10.:10.2] [keggfc:14.2] [sgdgc:9.5.0;11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG5049	33337805_c1_12	4876	18979	1596	532	YJR052W	524	2.7(10)-55	Saccharomyces cerevisiae	[ui:yjr052w] [pn:nucleotide excision repair protein rad7] [gn:rad7;j1665] [gicfc:10.:10.10.:10.2] [keggfc:14.2] [sgdgc:9.5.0;11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG5280	32220142_f2_5	4877	18980	747	249	YJR060W	324	2.7(10)-29	Saccharomyces cerevisiae	[ui:yjr060w] [pn:kinetochore protein:centromere-binding protein 1:cbp-1:centromere-binding factor 1:centromere promoter factor 1] [gn:cbf1:cpfl:cp1:cep1;j1730] [gicfc:10.1;10.2;12.8] [keggfc:14.2] [sgdgc:1.1.2;3.8;0.4;8.2;9.5.0;9.6.0]
CONTIG1577	2066431_c2_5	4878	18981	186	62	YJR068W	126	1.3(10)-7	Saccharomyces cerevisiae	[ui:yjr068w] [pn:dna replication factor c, 41 kd subunit:activator 1 41 kd subunit:replication factor c 41 kd subunit][gn:rfc2;j1808] [gicfc:10.1;10.2;10.8] [keggfc:14.2] [sgdgc:3.6.0;9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG3110	12597803_c3_8	4879	18982	741	247	YJR068W	622	7.2(10)-61	Saccharomyces cerevisiae	[ui:yyj068w] [pn:dna replication factor c, 41 kd subunit:activator 1 41 kd subunit:replication factor c 41 kd subunit][gn:rrc2;j108] [gicfc:10.1:10.2:10.8] [keggfc:14.2] [sgdgc:3.6.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3182	448958_c2_8	4880	18983	693	231	YTR093C	202	3.7(10)-16	Saccharomyces cerevisiae	[ui:yyj093c] [pn:component of pre-mma polyadenylation factor pf ifip1 protein][gn:fip1;j191] [gicfc:10.1:10.2:10.9] [keggfc:14.2] [sgdgc:4.10.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5318	36503155_f1_1	4881	18984	654	218	YJR112W	177	1.0(10)-13	Saccharomyces cerevisiae	[ui:yyj112w] [pn:nuclear envelope protein:hypothetical 23.6 kd protein in cpa2-aitp2 intergenic region][gn:nnfl1;j2011] [gicfc:10.1:10.2:12.8] [keggfc:14.2] [sgdgc:3.8.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG53351	19562875_c3_13	4882	18985	1023	341	YTR122W	280	4.5(10)-24	Saccharomyces cerevisiae	[ui:yyj122w] [pn:ccr4 associated factor:hypothetical 57.1 kd protein in aitp2-rrps5 intergenic region][gn:ccf17;j2033] [gicfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG1075	24666043_f2_1	4883	18986	870	290	YKL210W	924	7.2(10)-93	Saccharomyces cerevisiae	[ui:yyk1210w] [pn:ubiquitin-activating enzyme e1] [gn:yuba] [gicfc:10.1:10.11:10.2:10.7:13.2] [keggfc:14.2] [sgdgc:6.3.0:6.5.1:9.2.0:9.5.0:11.1.0] [db:gic-saccharomyces cerevisiae]

b1x13259_x	11024166_f2_2	4884	18987	216	72	YKL210W	122	1.8(10)-6	Saccharomyces cerevisiae	[ui:ykl1210w] [pn:ubiquitin--protein ligase:ubiquitin-activating enzyme e1] [gn:ubal] [gtfc:10.1:10.11:10.2:10.7:13.2] [keggfc:14.2] [sgdfc:6.3.0:6.5.1:9.2:0.9.5.0:11.1.0] [db:gtc:saccharomyces cerevisiae]
b1x13259_x	3923451_f3_3	4885	18988	747	249	YKL210W	808	1.3(10)-80	Saccharomyces cerevisiae	[ui:ykl1210w] [pn:ubiquitin--protein ligase:ubiquitin-activating enzyme e1] [gn:ubal] [gtfc:10.1:10.11:10.2:10.7:13.2] [keggfc:14.2] [sgdfc:6.3.0:6.5.1:9.2:0.9.5.0:11.1.0] [db:gtc:saccharomyces cerevisiae]
CONTIG5818	34491277_c1_32	4886	18989	1080	360	YKL205W	214	1.2(10)-14	Saccharomyces cerevisiae	[ui:ykl205w] [pn:pre-trna splicing protein:protein] [gn:los1] [gtfc:10.1:10.2:10.6:12.3] [keggfc:14.2] [sgdfc:4.5.0:4.11.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5818	272813_c2_41	4887	18990	1773	591	YKL205W	488	1.5(10)-45	Saccharomyces cerevisiae	[ui:ykl205w] [pn:pre-trna splicing protein:protein] [gn:los1] [gtfc:10.1:10.2:10.6:12.3] [keggfc:4.5.0:4.11.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2637	33725012_f3_1	4888	18991	1083	361	YKL193C	91	0.16	Saccharomyces cerevisiae	[ui:ykl193c] [pn:regulatory subunit for the mitotic function of type i protein phosphatase;protein phosphatases pp1 regulatory subunit sds22] [gn:sds22;egp1]
										[gtcfc:10.1:10.2:10.7:12.8] [keggfc:13.3] [sgdfc:3.8.0:6.3.0:9.5.0] [db:gtc-]
CONTIG4464	470306_f2_2	4889	18992	1512	504	YKL193C	149	1.2(10)-7	Saccharomyces cerevisiae	[ui:ykl193c] [pn:regulatory subunit for the mitotic function of type i protein phosphatase;protein phosphatases pp1 regulatory subunit sds22] [gn:sds22;egp1]
										[gtcfc:10.1:10.2:10.7:12.8] [keggfc:13.3] [sgdfc:3.8.0:6.3.0:9.5.0] [db:gtc-]
CONTIG4718	32206956_f2_1	4890	18993	2154	718	YKL193C	139	2.2(10)-6	Saccharomyces cerevisiae	[ui:ykl193c] [pn:regulatory subunit for the mitotic function of type i protein phosphatase;protein phosphatases pp1 regulatory subunit sds22] [gn:sds22;egp1]
										[gtcfc:10.1:10.2:10.7:12.8] [keggfc:13.3] [sgdfc:3.8.0:6.3.0:9.5.0] [db:gtc-]

CONTIG5101	26375392_f1_1	4891	18994	1431	477	YKL193C	100	0.014	Saccharomyces cerevisiae	[ui:ykl193c] [pn:regulatory subunit for the mitotic function of type i protein phosphatase;protein phosphatases pp1 regulatory subunit sds22] [gn:sds22;egp1] [gicfc:10.1:10.2:10.7:12.8] [keggfc:13.3] [sgdgc:3.8.0:6.3.0:9.5.0] [db:gic-
CONTIG5479	20157632_f2_6	4892	18995	657	219	YKL193C	94	0.032	Saccharomyces cerevisiae	[ui:ykl193c] [pn:regulatory subunit for the mitotic function of type i protein phosphatase;protein phosphatases pp1 regulatory subunit sds22] [gn:sds22;egp1] [gicfc:10.1:10.2:10.7:12.8] [keggfc:13.3] [sgdgc:3.8.0:6.3.0:9.5.0] [db:gic-
CONTIG5506	25523502_c3_15	4893	18996	918	306	YKL193C	342	5.5(10)-55	Saccharomyces cerevisiae	[ui:ykl193c] [pn:regulatory subunit for the mitotic function of type i protein phosphatase;protein phosphatases pp1 regulatory subunit sds22] [gn:sds22;egp1] [gicfc:10.1:10.2:10.7:12.8] [keggfc:13.3] [sgdgc:3.8.0:6.3.0:9.5.0] [db:gic-

CONTIG5644	4394002_f1_2	4894	18997	2145	715	YKL193C	90	0.46	Saccharomyces cerevisiae	[ui:ykl1193c] [pn:regulatory subunit for the mitotic function of type i protein phosphatase:protein phosphatases pp1 regulatory subunit sds22] [gn:sds22;egp1] [gicfc:10.1:10.2:10.7:12.8] [keggfc:13.3] [sgdfc:3.8.0/6.3.0/9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5815	16438261_c3_48	4895	18998	540	180	YKL186C	222	1.8(10)-18	Saccharomyces cerevisiae	[ui:ykl1186c] [pn:mRNA transport protein:mRNA transport regulator] [gn:mtr2] [gicfc::12.3:10.1:10.2] [keggfc:14.2] [sgdfc:4.11.0/8.1.0/9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5667	5945317_f1_2	4896	18999	1083	361	YKL114C	1098	2.6(10)-111	Saccharomyces cerevisiae	[ui:ykl114c] [pn:dNA:apurinic or apyrimidinic site lyase:ap endonuclease:apurinic-apyrimidinic endonuclease] [gn:apn1;ykl1513] [gicfc:10.1:10.10:10.2:14.1] [ec:4.2.99.18] [keggfc:14.1] [sgdfc:9.5.0/11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2060	16204092_f1_1	4897	19000	1104	368	YKL109W	95	0.12	Saccharomyces cerevisiae	[ui:ykl109w] [pn:ccaa-t-binding factor subunit:hap4 transcriptional activator] [gn:hap4;ykl465] [gicfc:10.1:10.2] [keggfc:4.2] [sgdfc:4.8.2/9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3756	11756587_c2_7	4898	19001	1575	525	YKL109W	95	0.19	Saccharomyces cerevisiae	[ui:yk109w] [pn:ccat-binding factor subunit:hap4 transcriptional activator] [gn:hap4.yk1465] [gtfc:10.1:10.2] [keggc:14.2] [sgdc:4.8:2.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5791	165882_f1_1	4899	19002	1566	522	YKL089W	207	4.9(10)-21	Saccharomyces cerevisiae	[ui:yk089w] [pn:required for normal chromosome segregation and spindle integrity/protein] [gn:mit2] [gtfc:10.1:10.2:12.8:4.1] [ec:3.4.24.64] [keggc:14.1] [sgdc:3.8:0.9:5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5100	14073342_c3_8	4900	19003	309	103	YKL074C	125	3.6(10)-7	Saccharomyces cerevisiae	[ui:yk1074c] [pn:pre-mrna splicing factor:splicing factor mud2] [gn:mud2.ykl358] [gtfc:10.1:10.2] [keggc:14.2] [sgdc:4.9:0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5189	13103542_f1_1	4901	19004	387	129	YKL062W	153	4.5(10)-10	Saccharomyces cerevisiae	[ui:yk062w] [pn:transcriptional activator:zinc finger protein:multicopy suppressor of snf1 protein-4] [gn:msn4] [gtfc:10.1:10.2:12.13:13.2] [keggc:14.2] [sgdc: 1.5:2:4.8:2.9:5.0:11.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5755	10970308_f3_10	4902	19005	2283	761	YKL062W	181	9.0(10)-11	Saccharomyces cerevisiae	[ui:ykl062w] [pn:transcriptional activator:zinc finger protein:multiplex suppressor of snf1 protein 4] [gn:msn4] [lgtfc:10.1:10.2:12.13:13.2] [keggc:14.2] [sgdfc:1.5.2.4.8.2.9.5.0:11.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4060	11878775_f3_3	4903	19006	492	164	YKL058W	318	1.2(10)-28	Saccharomyces cerevisiae	[ui:ykl058w] [pn:tfia subunit:transcription initiation factor, 13.5 kd transcription initiation factor lla small chain:tfia 13.5 kd subunit] [gn:toa2] [lgtfc:10.1:10.2] [keggc:14.2] [sgdfc:4.8.1:9.5.0] [db:gtc-saccharomyces cerevis]
CONTIG3752	21507692_c2_4	4904	19007	2121	707	YKL038W	167	6.5(10)-9	Saccharomyces cerevisiae	[ui:ykl038w] [pn:regulator of glucose-induced genes:putative 1.28.2 kd transcriptional regulatory protein in pml1-ixr1 intergenic region] [gn:rgtl:ykl125.1] [lgtfc:10.1:10.2:12.13] [keggc:14.2] [sgdfc:1.5.2.4.8.2.9.5.0] [db:gtc-saccharo
CONTIG4152	26443927_c1_6	4905	19008	1230	410	YKL028W	639	1.2(10)-62	Saccharomyces cerevisiae	[ui:ykl028w] [pn:tfie subunit:transcription initiation factor iie, alpha subunit:tfie-alpha:transcription factor a large subunit:factor a 66 kd subunit] [gn:fal] [lgtfc:10.1:10.2] [keggc:14.

CONTIG3951	14553275_c1_5	4906	19009	1401	467	YKL022C	748	3.2(10)-74	Saccharomyces cerevisiae	[ui:yk 022c] [pn:subunit of anaphase-promoting complex:cyclosome:cell division control protein 16] [gn:cdc16] [gtfc:10.1:10.11:10.2:12.16:12.8] [keggc:13.3] [sgdfc:3.8:0:6.5:1.9:3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2112	26290902_f3_3	4907	19010	1443	481	YKL020C	244	2.6(10)-37	Saccharomyces cerevisiae	[ui:yk 020c] [pn:dosage-dependent suppressor of ty-induced promotor mutations:protein] [gn:spf23] [gtfc:10.2] [keggfc:14.2] [sgdfc:9.5.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1305	1961462_c3_4	4908	19011	1089	363	YKL015W	802	6.2(10)-80	Saccharomyces cerevisiae	[ui:yk 015w] [pn:positive activator of the proline utilisation pathway:proline utilization trans-activator] [gn:put3] [gtfc:10.1:10.2] [keggfc:14.2] [sgdfc: 1.1.2:4.8:2.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3445	54187_c3_6	4909	19012	1524	508	YKL015W	95	0.33	Saccharomyces cerevisiae	[ui:yk 015w] [pn:positive activator of the proline utilisation pathway:proline utilization trans-activator] [gn:put3] [gtfc:10.1:10.2] [keggfc:14.2] [sgdfc: 1.1.2:4.8:2.9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3566	29376655_c2_9	4910	19013	627	209	YKL015W	220	5.9(10)-17	Saccharomyces cerevisiae	[ui:yk[015w] [pn:positive activator of the proline utilisation pathway;proline utilization trans-activator] [gn:put3] [gfcfc:10.1:10.2] [keggfc:14.2] [sgdfc:1.1.24.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3982	18760890_c3_8	4911	19014	1914	638	YKL015W	131	7.5(10)-5	Saccharomyces cerevisiae	[ui:yk[015w] [pn:positive activator of the proline utilisation pathway;proline utilization trans-activator] [gn:put3] [gfcfc:10.1:10.2] [keggfc:14.2] [sgdfc:1.1.24.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4660	21884677_c1_8	4912	19015	696	232	YKL015W	125	1.7(10)-10	Saccharomyces cerevisiae	[ui:yk[015w] [pn:positive activator of the proline utilisation pathway;proline utilization trans-activator] [gn:put3] [gfcfc:10.1:10.2] [keggfc:14.2] [sgdfc:1.1.24.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5235	35432156_c2_17	4913	19016	1128	376	YKL015W	94	0.29999	Saccharomyces cerevisiae	[ui:yk[015w] [pn:positive activator of the proline utilisation pathway;proline utilization trans-activator] [gn:put3] [gfcfc:10.1:10.2] [keggfc:14.2] [sgdfc:1.1.24.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5732	4085937_c2_30	4914	19017	2490	830	YKL015W	126	0.0004	Saccharomyces cerevisiae	[ui:yk[015w] [pn:positive activator of the proline utilisation pathway;proline utilization trans-activator] [gn:put3] [gfcfc:10.1:10.2] [keggfc:14.2] [sgdfc:1.1.24.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG2948	2613901_c1_4	4915	19018	1203	401	YKL005C	107	0.0051	Saccharomyces cerevisiae	[ui:ykl005c] [pn:weak similarity to ykr029c and d.melanogaster transcription elongation factor dms-ii:hypothetical 67.9 kd protein rp114a-aur1 intergenic region] [gn:ykl150] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.12.0.9.5.0] [db:gic]
CONTIG4205	976013_c3_7	4916	19019	888	296	YKL005C	94	0.13	Saccharomyces cerevisiae	[ui:ykl005c] [pn:weak similarity to ykr029c and d.melanogaster transcription elongation factor dms-ii:hypothetical 67.9 kd protein rp114a-aur1 intergenic region] [gn:ykl150] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.12.0.9.5.0] [db:gic]
CONTIG5102	26441557_c2_5	4917	19020	387	129	YKL005C	172	3.7(10)-12	Saccharomyces cerevisiae	[ui:ykl005c] [pn:weak similarity to ykr029c and d.melanogaster transcription elongation factor dms-ii:hypothetical 67.9 kd protein rp114a-aur1 intergenic region] [gn:ykl150] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.12.0.9.5.0] [db:gic]
CONTIG1056	21490677_c2_2	4918	19021	738	246	YKR002W	892	1.8(10)-89	Saccharomyces cerevisiae	[ui:ykr002w] [pn:poly:a polymerase] [gn:pap1] [gicfc:10.1:10.2:10.9:14.1] [ec:2.7.7.19] [keggfc:14.1] [sgdfc:4.10.0:9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG2615	393775_f2_1	4919	19022	1353	451	YKR002W	1446	3.5(10)-148	Saccharomyces cerevisiae	[ui:ykr002w] [pn:poly-a polymerase] [gn:pap] [gtcfc: 10.1:10.2:10.9:14.1] [ec:2.7.7.19] [keggfc:14.1] [sgdfc:4.10.0.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG911	24609517_f3_1	4920	19023	453	151	YKR002W	128	1.8(10)-7	Saccharomyces cerevisiae	[ui:ykr002w] [pn:poly-a polymerase] [gn:pap] [gtcfc:10.1:10.2:10.9:14.1] [ec:2.7.7.19] [keggfc:14.1] [sgdfc:4.10.0.9.5.0] [db:gtc-saccharomyces cerevisiae]
b2x15963.y	4792178_f3_1	4921	19024	492	164	YKR008W	149	1.2(10)-9	Saccharomyces cerevisiae	[ui:ykr008w] [pn:similarity to s.pombe and chicken bromodomain proteins:hypothetical 72.3 kd protein in mlp113-fox2:intergenic region] [gn:yk107] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1427	7111541_f1_1	4922	19025	252	84	YKR054C	98	0.00289	Saccharomyces cerevisiae	[ui:ykr054c] [pn:dynein heavy chain, cytosolic:dhc] [gn:dynl-dhc] [gtcfc:10.1:10.2:12.10:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0.8.3.0.8.8.0.9.3.0.9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1427	29330380_f1_2	4923	19026	1104	363	YKR054C	648	1.2(10)-61	Saccharomyces cerevisiae	[ui:yk054c] [pn:dynein heavy chain, cytosolic:dyhc] [gn: dyn1.dhc1] [gtfc:10.1:10.2:12.10:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0.8.3.0.8.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1148	6303188_c2_2	4924	19027	612	204	YKR054C	401	2.0(10)-35	Saccharomyces cerevisiae	[ui:yk054c] [pn:dynein heavy chain, cytosolic:dyhc] [gn: dyn1.dhc1] [gtfc:10.1:10.2:12.10:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0.8.3.0.8.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4169	19822202_c2_3	4925	19028	2328	776	YKR054C	1077	3.5(10)-107	Saccharomyces cerevisiae	[ui:yk054c] [pn:dynein heavy chain, cytosolic:dyhc] [gn: dyn1.dhc1] [gtfc:10.1:10.2:12.10:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0.8.3.0.8.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2880	972203_f3_1	4926	19029	1224	408	YKR054C	271	1.2(10)-27	Saccharomyces cerevisiae	[ui:yk054c] [pn:dynein heavy chain, cytosolic:dyhc] [gn: dyn1.dhc1] [gtfc:10.1:10.2:12.10:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0.8.3.0.8.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4797	4801525_c3_4	4927	19030	1467	489	YKR054C	248	4.5(10)-17	Saccharomyces cerevisiae	[ui:yk:054c] [pn:dynein heavy chain, cytosolic:dyhc] [gn: dyn1.dhc1] [gtfc:10.1:0.2:12.10:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0.8.3.0.8.8.0:9.3:0.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5802	22476703_c3_36	4928	19031	423	141	YKR054C	169	8.5(10)-11	Saccharomyces cerevisiae	[ui:yk:054c] [pn:dynein heavy chain, cytosolic:dyhc] [gn: dyn1.dhc1] [gtfc:10.1:0.2:12.10:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0.8.3.0.8.8.0:9.3:0.9.5.0] [db:gtc-saccharomyces cerevisiae]
b9x13s62.x	23555426_f3_1	4929	19032	396	132	YKR054C	293	5.9(10)-24	Saccharomyces cerevisiae	[ui:yk:054c] [pn:dynein heavy chain, cytosolic:dyhc] [gn: dyn1.dhc1] [gtfc:10.1:0.2:12.10:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0.8.3.0.8.8.0:9.3:0.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5328	7070312_c3_18	4930	19033	1665	555	YKR056W	1260	1.8(10)-128	Saccharomyces cerevisiae	[ui:yk:056w] [pn:endo-exonuclease:endo-exonuclease nucr] [gn:mcl.mud1] [gtfc:10.1:10.10:10.2:10.8:14.1] [ec:3.-.-.] [keggfc:14.1] [sgdfc:3.7.0.9.5.0:11.2.] [db:gtc-saccharomyces cerevisiae]

CONTIG3280	6064135_f3_4	4931	19034	423	141	YKR062W	352	3.0(10)-32	Saccharomyces cerevisiae	[ui:ykr062w] [pn:tfie subunit:transcription initiation factor, 43 kd transcription initiation factor iic, beta subunit:tfie-beta transcription factor a small subunit:factor a 43 kd subunit [gn:1fa2] [gtcfc:10.1:10.2] [keggfc:14.2]
CONTIG5588	14157757_c2_13	4932	19035	771	257	YKR063C	381	2.5(10)-35	Saccharomyces cerevisiae	[ui:ykr063c] [pn:involved in cell morphogenesis, cytoskeletal regulation and bud formation:protein] [gn:las] [gtcfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.2.0:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3308	3020818_c3_4	4933	19036	1377	459	YKR072C	292	7.0(10)-24	Saccharomyces cerevisiae	[ui:ykr072c] [pn:involved in cell cycle-specific gene expression:sis2 protein:halotolerance protein hal3] [gn:sis2:hal3] [gtcfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1054	957875_f3_4	4934	19037	621	207	YKR082W	99	0.041	Saccharomyces cerevisiae	[ui:ykr082w] [pn:nuclear pore protein:nucleoporin nup133:pore protein nup133] [gn:nup133:ykr02] [gtcfc:10.1:10.2:12.3] [keggfc:14.2] [sgdfc:4.11.0:8.1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2223	23673186_c1_4	4935	19038	819	273	YKR082W	102	0.03699	Saccharomyces cerevisiae	[ui:ycr082w] [pn:nuclear pore protein:nucleoporin nup133;nuclear pore protein nup133] [gn:nup133;ycr402] [gtfc:10.1:10.2:12.3] [keggfc:14.2] [sgdfc:4.11:0.8:1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5159	12286705_f2_3	4936	19039	726	242	YKR086W	372	3.7(10)-33	Saccharomyces cerevisiae	[ui:ycr086w] [pn:rnase-dependent apnase;pre-mrna splicing factor rna helicase prp16] [gn:prp16;ycr406] [gtfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.9:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3107	35291466_f2_1	4937	19040	2172	724	YKR086W	1200	1.8(10)-127	Saccharomyces cerevisiae	[ui:ycr086w] [pn:rnase-dependent apnase;pre-mrna splicing factor rna helicase prp16] [gn:prp16;ycr406] [gtfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.9:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4377	34172162_f2_1	4938	19041	2262	754	YKR092C	98	0.00048	Saccharomyces cerevisiae	[ui:ycr092c] [pn:suppressor of mutant ac40 of rna polymerase i and iii:suppressor protein srp40] [gn:srp40;ycr412a] [gtfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.12:0.9:5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4393	24018807_c1_7	4939	19042	1248	416	YKR092C	98	0.047.	Saccharomyces cerevisiae	[ui:ykr092c] [pn:suppressor of mutant ac40 of ma polymerase i and iii:suppressor protein srp40] [gn:sp40:ykr412a] [gtfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.12.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5299	4867180_f1_2	4940	19043	3681	1227	YKR092C	108	0.01499	Saccharomyces cerevisiae	[ui:ykr092c] [pn:suppressor of mutant ac40 of ma polymerase i and iii:suppressor protein srp40] [gn:sp40:ykr412a] [gtfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.12.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5594	43550787_f3_8	4941	19044	2511	837	YKR092C	107	0.012	Saccharomyces cerevisiae	[ui:ykr092c] [pn:suppressor of mutant ac40 of ma polymerase i and iii:suppressor protein srp40] [gn:sp40:ykr412a] [gtfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.12.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5660	24020325_c2_22	4942	19045	2130	710	YKR092C	99	0.04299	Saccharomyces cerevisiae	[ui:ykr092c] [pn:suppressor of mutant ac40 of ma polymerase i and iii:suppressor protein srp40] [gn:sp40:ykr412a] [gtfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.12.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5706	26772711_c3_25	4943	19046	1245	415	YKR092C	358	6.9(10)-33	Saccharomyces cerevisiae	[ui:ykr092c] [pn:suppressor of mutant ac40 of ma polymerase i and iii:suppressor protein srp40] [gn:sp40:ykr412a] [gtfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.12.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG759	10945193_f1_1	4944	19047	1185	395	YKR092C	98	0.047	Saccharomyces cerevisiae	[ui: ykr092c] [pn: suppressor of mutant ac40 of rna polymerase i and iii: suppressor protein srp40] [gn: srp40; ykr412a] [gicfc: 10.1:10.2] [keggfc: 14.2] [sgdfc: 4.12:0.9:5.0] [db: gic-saccharomyces cerevisiae]
CONTIG1263	979711_f1_4	4945	19048	378	126	YKR095W	99	0.001	Saccharomyces cerevisiae	[ui: ykr095w] [pn: myosin-like protein related to uso1p; myosin-like protein mlp1] [gn: mlp1; ykr415] [gicfc: 10.1:10:10:0.2] [keggfc: 14.2] [sgdfc: 9.5:0:11.2.1] [db: gic-saccharomyces cerevisiae]
CONTIG1719	23438942_f2_1	4946	19049	855	285	YKR095W	91	0.65	Saccharomyces cerevisiae	[ui: ykr095w] [pn: myosin-like protein related to uso1p; myosin-like protein mlp1] [gn: mlp1; ykr415] [gicfc: 10.1:10:10:10:0.2] [keggfc: 14.2] [sgdfc: 9.5:0:11.2.1] [db: gic-saccharomyces cerevisiae]
CONTIG2276	24431336_f3_2	4947	19050	1062	354	YKR095W	106	0.028	Saccharomyces cerevisiae	[ui: ykr095w] [pn: myosin-like protein related to uso1p; myosin-like protein mlp1] [gn: mlp1; ykr415] [gicfc: 10.1:10:10:10:0.2] [keggfc: 14.2] [sgdfc: 9.5:0:11.2.1] [db: gic-saccharomyces cerevisiae]
CONTIG2699	24492005_f1_1	4948	19051	738	246	YKR095W	123	0.00012	Saccharomyces cerevisiae	[ui: ykr095w] [pn: myosin-like protein related to uso1p; myosin-like protein mlp1] [gn: mlp1; ykr415] [gicfc: 10.1:10:10:10:0.2] [keggfc: 14.2] [sgdfc: 9.5:0:11.2.1] [db: gic-saccharomyces cerevisiae]

CONTIG3289	19573957_f1_1	4949	19052	1110	370	YKR095W	133	4.5(10)-5	Saccharomyces cerevisiae	[ui:yr095w] [pn:myosin-like protein related to uso1p myosin-like protein mlp1] [gn:mlp1:yr415] [gtfc:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:9.5:0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG33870	9861078_f3_1	4950	19053	2229	743	YKR095W	176	1.5(10)-12	Saccharomyces cerevisiae	[ui:yr095w] [pn:myosin-like protein related to uso1p myosin-like protein mlp1] [gn:mlp1:yr415] [gtfc:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:9.5:0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4435	1379415_f2_5	4951	19054	792	264	YKR095W	123	0.00019	Saccharomyces cerevisiae	[ui:yr095w] [pn:myosin-like protein related to uso1p myosin-like protein mlp1] [gn:mlp1:yr415] [gtfc:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:9.5:0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5711	34187660_f3_7	4952	19055	2574	858	YKR095W	93	0.68	Saccharomyces cerevisiae	[ui:yr095w] [pn:myosin-like protein related to uso1p myosin-like protein mlp1] [gn:mlp1:yr415] [gtfc:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:9.5:0:11.2.1] [db:gtc-saccharomyces cerevisiae]
b9x10449_y	26773516_c3_2	4953	19056	516	172	YKR095W	163	1.6(10)-10	Saccharomyces cerevisiae	[ui:yr095w] [pn:myosin-like protein related to uso1p myosin-like protein mlp1] [gn:mlp1:yr415] [gtfc:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:9.5:0:11.2.1] [db:gtc-saccharomyces cerevisiae]

b9x11865.x	1050933_c1_2	4954	19057	819	273	YKR095W	182	1.5(10)-12	Saccharomyces cerevisiae	[ui:ykr095w] [pn:myosin-like protein related to uso1p:myosin-like protein mlp1] [gn:mlp1:ykr415] [gtfc:10.1:10.10:10.2] [keggc:14.2] [sgdgc:9.5:0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5679	25594034_c2_19	4955	19058	690	230	YKR095W	93	0.29999	Saccharomyces cerevisiae	[ui:ykr095w] [pn:myosin-like protein related to uso1p:myosin-like protein mlp1] [gn:mlp1:ykr415] [gtfc:10.1:10.10:10.2] [keggc:14.2] [sgdgc:9.5:0:11.2.1] [db:gtc-saccharomyces cerevisiae]
b2x10471.y	9807969_c2_2	4956	19059	789	263	YKR095W	103	0.033	Saccharomyces cerevisiae	[ui:ykr095w] [pn:myosin-like protein related to uso1p:myosin-like protein mlp1] [gn:mlp1:ykr415] [gtfc:10.1:10.10:10.2] [keggc:14.2] [sgdgc:9.5:0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5544	4098427_c1_16	4957	19060	951	317	YKR099W	51	4.7(10)-53	Saccharomyces cerevisiae	[ui:ykr099w] [pn:transcription factor:myb-like dna-binding protein] [gn:bas1] [gtfc:10.1:10.2] [keggc:14.2] [sgdgc:1.1:2:1.3:5:4:8:2:9:5:0] [db:gtc-saccharomyces cerevisiae]
CONTRIG4661	10626412_f2_2	4958	19061	273	91	YLL039C	164	1.2(10)-11	Saccharomyces cerevisiae	[ui:yll039c] [pn:ubiquitin precursor] [gn:abi4] [gtfc:10.1:1:10.2:10.7:12.15:1 2.16:13:2] [keggc:14.2] [sgdgc:3.4:0:5:5:0:6:4:0:6:5:1:9:2:0:9 5:0:11:1:0] [db:gtc-saccharomyces cerevisiae]

CONTIG5683	13834636_c2_22	4959	19062	714	238	YLL039C	1141	7.2(10)-116	Saccharomyces cerevisiae	[ui:y]l039c] [pn:ubiquitin precursor] [gn:ubi4] [gicfc:10.1:0.1.1:10.2:10.7:12.15:1 2.16:13.2] [keggfc:14.2] [sgdfc:3.4.0.5.5.0.6.4.0.6.5.1.9.2:0.9 .5.0:11.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4777	3907830_c3_10	4960	19063	891	297	YLL036C	252	5.7(10)-21	Saccharomyces cerevisiae	[ui:y]l036c] [pn:non-stump sliceosome component required for dna repair:pre-mirna splicing factor prp19] [gn:prp19;ps04] [gicfc:10.1:0.2] [keggfc:14.2] [sgdfc:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1469	26692142_f3_2	4961	19064	444	148	YLL011W	95	0.01	Saccharomyces cerevisiae	[ui:y]l011w] [pn:involved in 18s pre-rna production:soft protein] [gn:soft1;113:39] [gicfc:10.1:0.2:10.3] [keggfc:14.2] [sgdfc:4.2.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG53367	23865811_c1_11	4962	19065	741	247	YLL011W	637	1.8(10)-62	Saccharomyces cerevisiae	[ui:y]l011w] [pn:involved in 18s pre-rna production:soft protein] [gn:soft1;113:39] [gicfc:10.1:0.2:10.3] [keggfc:14.2] [sgdfc:4.2.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5792	5079717_f2_6	4963	19066	1719	573	YLL008W	1466	5.7(10)-156	Saccharomyces cerevisiae	[ui:y]l008w] [pn:ma helicase of the dead box family:putative aip-dependent ma helicase drs1] [gn:drs1;113:45] [gicfc:10.1:0.2:10.3:12.16] [keggfc:14.2] [sgdfc:4.2.0:6.4.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5612	10553426_f2_4	4964	19067	1758	586	YLL004W	120	0.00056	Saccharomyces cerevisiae	[ui:yl004w] [pn:origin recognition complex, 62 kda subunit:origin recognition complex protein, subunit 3:origin recognition complex protein 62 kd subunit]
										[gn:orc3:orf1:11365] [gicfc:10.1:10.2:10.8:12.8:12.9] [keggfc:13.2] [sgdf]
CONTIG5612	672342_f3_6	4965	19068	330	110	YLL004W	149	1.2(10)-9	Saccharomyces cerevisiae	[ui:yl004w] [pn:origin recognition complex, 62 kda subunit:origin recognition complex protein, subunit 3:origin recognition complex protein 62 kd subunit]
										[gn:orc3:orf1:11365] [gicfc:10.1:10.2:10.8:12.8:12.9] [keggfc:13.2] [sgdf]
CONTIG4626	19938160_c1_4	4966	19069	2445	815	YLR014C	449	6.9(10)-87	Saccharomyces cerevisiae	[ui:yl014c] [pn:transcription factor regulating pyrimidine pathway/pyrimidine pathway regulatory protein 1] [gn:pprl]
										[gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:1.3.5:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3082	6027043_f1_1	4967	19070	483	161	YLR025W	135	5.0(10)-9	Saccharomyces cerevisiae	[ui:yl025w] [pn:nuclear protein]
										[gn:snf7] [gicfc:10.1:10.2:12.13:12.15] [keggfc:14.2] [sgdfc:1.5.2:3.4.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4349	4491052_c3_5	4968	19071	690	230	YLR025W	204	1.3(10)-16	Saccharomyces cerevisiae	[ui:yl025w] [pn:nuclear protein]
										[gn:snf7] [gicfc:10.1:10.2:12.13:12.15] [keggfc:14.2] [sgdfc: 1.5.2:3.4.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5645	24488443_c3_22	4969	19072	3270	1090	YLR032W	1383	8.6(10)-162	Saccharomyces cerevisiae	[ui:yh032w] [pn: dna helicase:dna repair protein rad5] [gn:rad5.rev2.snm2] [gicfc:10.1:10.10:10.2:10.8] [keggfc:14.2] [sgdfc:3.7:0.9.5.0:11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG5212	33406553_c3_19	4970	19073	1671	557	YLR055C	279	7.0(10)-22	Saccharomyces cerevisiae	[ui:yh055c] [pn:transcription factor spf8] [gn:spf8.12.144] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5484	12304525_c3_20	4971	19074	4026	1342	YLR086W	1879	4.5(10)-194	Saccharomyces cerevisiae	[ui:yh086w] [pn:similarity to chromosome condensation proteins] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:9.5.0:9.6.0] [db:gic-saccharomyces cerevisiae]
CONTIG4418	16412511_f2_6	4972	19075	885	295	YLR098C	115	0.00069	Saccharomyces cerevisiae	[ui:yh098c] [pn:transcription factor:cha4 activatory protein] [gn:cha4.18.004] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:1.1.2:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG431	12696886_c3_3	4973	19076	672	224	YLR105C	182	1.2(10)-13	Saccharomyces cerevisiae	[ui:yh105c] [pn:rna splicing endonuclease beta subunit:rna-splicing endonuclease beta subunit] [gn:sen2.18.004] [gicfc:10.1:10.2:10.6] [keggfc:14.2] [sgdfc:4.5.0:9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG1820	22850662_c3_3	4974	19077	534	178	YLR131C	227	7.2(10)-18	Saccharomyces cerevisiae	[uii:ylr131c] [pn:metallothionein expression activator] [gn:ace2;13123;19606] [gicfc:10.1:10.2:12.13:12.8] [keggc:14.2] [sgdic:1.5.2.3.9.0:4.8:2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4941	10979555_c2_6	4975	19078	327	109	YLR147C	280	1.3(10)-24	Saccharomyces cerevisiae	[uii:ylr147c] [pn:strong similarity to small nuclear ribonucleoprotein d3;small nuclear ribonucleoprotein d3 homolog] [gn:smd3;19634] [gicfc:10.1:10.2] [keggc:14.2] [sgdic:4.9.0:4.12.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1039	6646892_c3_5	4976	19079	576	192	YLR175W	638	1.5(10)-62	Saccharomyces cerevisiae	[uii:ylr175w] [pn:centromere/microtubule binding protein cbf5;p64"] [gn:cbf5;19470] [gicfc:10.1:10.2:12.16:12.8] [keggc:14.2] [sgdic:3.1.0:3.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2834	10634652_c3_6	4977	19080	303	101	YLR175W	398	4.0(10)-37	Saccharomyces cerevisiae	[uii:ylr175w] [pn:centromere/microtubule binding protein cbf5;p64"] [gn:cbf5;19470] [gicfc:10.1:10.2:12.16:12.8] [keggc:14.2] [sgdic:3.1.0:3.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1246	13791410_f3_1	4978	19081	1074	358	YLR176C	135	7.4(10)-6	Saccharomyces cerevisiae	[ui.ylr176c] [pn:dnabindingprotein] [gn:rfx1] [gtfc:10.1:10.2:12.8] [keggfc:13.1] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4976	6270908_f2_3	4979	19082	2577	859	YLR176C	300	6.5(10)-37	Saccharomyces cerevisiae	[ui.ylr176c] [pn:dnabindingprotein] [gn:rfx1] [gtfc:10.1:10.2:12.8] [keggfc:13.1] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1268	15049000_f3_2	4980	19083	993	331	YLR212C	524	2.3(10)-60	Saccharomyces cerevisiae	[ui.ylr212c] [pn:gamma tubulin:tubulin gamma chain] [gn:tub4.18167] [gtfc:10.1:10.2:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4646	25423593_f3_2	4981	19084	408	136	YLR212C	105	4.4(10)-5	Saccharomyces cerevisiae	[ui.ylr212c] [pn:gamma tubulin:tubulin gamma chain] [gn:tub4.18167] [gtfc:10.1:10.2:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3156	33395062_f3_2	4982	19085	1497	499	YLR234W	819	1.5(10)-112	Saccharomyces cerevisiae	[ui.ylr234w] [pn:dna topoisomeraseii] [gn:top3:edr1:18083] [gtfc:10.1:10.2:12.8:14.1] [ec:5.99.1.2] [keggfc:14.1] [sgdfc:3.5.0:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4303	2948838_c2_5	4983	19086	1527	509	YLR256W	134	1.8(10)-5	Saccharomyces cerevisiae	[ui:ylr256w] [pn:transcription factor:cyp1 activatory protein] [gn:cyp1:hap1] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2.9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4762	2757655_f2_6	4984	19087	897	299	YLR256W	105	0.025	Saccharomyces cerevisiae	[ui:ylr256w] [pn:transcription factor:cyp1 activatory protein] [gn:cyp1:hap1] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2.9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5745	2504676_f2_5	4985	19088	2961	987	YLR256W	120	0.0032	Saccharomyces cerevisiae	[ui:ylr256w] [pn:transcription factor:cyp1 activatory protein] [gn:cyp1:hap1] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2.9.5.0] [db:gic-saccharomyces cerevisiae]
b2x10621.y	5163942_f3_2	4986	19089	762	254	YLR256W	165	7.5(10)-11	Saccharomyces cerevisiae	[ui:ylr256w] [pn:transcription factor:cyp1 activatory protein] [gn:cyp1:hap1] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2.9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG2166	4948336_f3_4	4987	19090	747	249	YLR274W	802	6.2(10)-80	Saccharomyces cerevisiae	[ui:ylr274w] [pn:cell division control protein 46:minichromosome maintenance protein 5] [gn:cdc46:mcm5:19328] [gicfc:10.1:10.2:10.8:12.8] [keggfc:13.2] [sgdfc:3.6:0.3:8.0:9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG3544	4351426_f3_5	4988	19091	1290	430	YLR274W	481	1.6(10)-80	Saccharomyces cerevisiae	[ui:ylr274w] [pn:cell division control protein:cell division control protein 46:minichromosome maintenance protein 5] [gn:cd46:rncm5:19228] [gicfc:10.1:10.2:10.8:12.8] [keggfc:13.2] [sgdfc:3.6:0.3:8:0.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG2166	22303177_c1_5	4989	19092	444	148	YLR275W	275	4.2(10)-24	Saccharomyces cerevisiae	[ui:ylr275w] [pn:strong similarity to human snrnp chain d2 involved in systemic lupus erythematosus] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.9:0.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG1262	565757_f2_3	4990	19093	939	313	YLR277C	711	2.7(10)-70	Saccharomyces cerevisiae	[ui:ylr277c] [pn:component of pre-mrna polyadenylation factor pf i] [gn:brr5] [gicfc:10.1:10.2:10.9] [keggfc:14.2] [sgdfc:4.10:0.9:5.0] [db:gic-saccharomyces cerevisiae]
b9x12m23.x	35328538_f3_1	4991	19094	258	86	YLR277C	198	9.5(10)-15	Saccharomyces cerevisiae	[ui:ylr277c] [pn:component of pre-mrna polyadenylation factor pf i] [gn:brr5] [gicfc:10.1:10.2:10.9] [keggfc:14.2] [sgdfc:4.10:0.9:5.0] [db:gic-saccharomyces cerevisiae]
b9x12m23.x	17007937_f3_2	4992	19095	297	99	YLR277C	95	0.001	Saccharomyces cerevisiae	[ui:ylr277c] [pn:component of pre-mrna polyadenylation factor pf i] [gn:brr5] [gicfc:10.1:10.2:10.9] [keggfc:14.2] [sgdfc:4.10:0.9:5.0] [db:gic-saccharomyces cerevisiae]

CONTIG731	390750_f2_1	4993	19096	708	236	YLR293C	1052	2.0(10)-106	Saccharomyces cerevisiae	[uiylyt293cl] [pn:gtp-binding protein of the ras superfamily:gtp-binding nuclear protein gsp1/cnrl] [gn:gsp1:cnrl:cst17:18003] [gicfc:10.1:10.2:12.3] [keggfc:14.2] [sgdfc:4.11:0.8:1.0:9.5:0] [db:gic-saccharomyces cerevisiae]
CONTIG3079	26189181_f1_1	4994	19097	468	156	YLR298C	174	2.2(10)-13	Saccharomyces cerevisiae	[uiylyt298cl] [pn:part of the u1 complex] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.9:0.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3116	6767786_f2_2	4995	19098	1314	438	YLR335W	142	1.8(10)-16	Saccharomyces cerevisiae	[uiylyt335w] [pn:nucleoporin:nuclear pore protein:p95] [gn:nup2] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:8.1:0:9.5:0] [db:gic-saccharomyces cerevisiae]
CONTIG4375	24398461_o3_9	4996	19099	1998	666	YLR335W	155	1.3(10)-7	Saccharomyces cerevisiae	[uiylyt335w] [pn:nucleoporin:nuclear pore protein:p95] [gn:nup2] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:8.1:0:9.5:0] [db:gic-saccharomyces cerevisiae]
CONTIG3399	26429087_f2_2	4997	19100	762	254	YLR335W	221	2.8(10)-17	Saccharomyces cerevisiae	[uiylyt335w] [pn:nucleoporin:nuclear pore protein:p95] [gn:nup2] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:8.1:0:9.5:0] [db:gic-saccharomyces cerevisiae]

CONTIG4994	471041_f3_5	4998	19101	1044	348	YLR398C	832	1.8(10)-82	Saccharomyces cerevisiae	[ui:ylr398c] [pn:antiviral protein and putative helicase:antiviral protein] [gn:sk12] [gtfc:10.1:10.2:12.12] [keggfc:14.2] [sgdfc:9.5.0:11.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG5760	4728438_c1_29	4999	19102	2208	736	YLR398C	1757	8.6(10)-199	Saccharomyces cerevisiae	[ui:ylr398c] [pn:antiviral protein and putative helicase:antiviral protein] [gn:sk12] [gtfc:10.1:10.2:12.12] [keggfc:14.2] [sgdfc:9.5.0:11.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG5733	1210287_f1_1	5000	19103	498	166	YLR403W	128	2.5(10)-7	Saccharomyces cerevisiae	[ui:ylr403w] [pn:zinc finger protein:zinc finger protein sfp1] [gn:sfp1:18084] [gtfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.1.0:3.8.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5733	19738337_f2_5	5001	19104	864	288	YLR403W	479	1.8(10)-58	Saccharomyces cerevisiae	[ui:ylr403w] [pn:zinc finger protein:zinc finger protein sfp1] [gn:sfp1:18084] [gtfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.1.0:3.8.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3247	866708_f3_3	5002	19105	819	273	YLR430W	193	1.3(10)-12	Saccharomyces cerevisiae	[ui:ylr430w] [pn:positive effector of tRNA-splicing endonuclease:tRNA-splicing endonuclease positive effector] [gn:sen1] [gtfc:10.1:10.2:10.6] [keggfc:14.2] [sgdfc:4.5.0:9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG3653	12985630_c3_8	5003	19106	2400	800	YLR430W	493	5.0(10)-61	Saccharomyces cerevisiae	[ui.ylr430w] [pn:positive effector of tRNA-splicing endonuclease:tRNA-splicing endonuclease positive effector] [gn:sen1] [gicfc:10.1:10.2:10.6] [keggfc:14.2] [sgdic:4.5.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4822	975727_f2_6	5004	19107	1218	406	YLR430W	594	2.8(10)-56	Saccharomyces cerevisiae	[ui.ylr430w] [pn:positive effector of tRNA-splicing endonuclease:tRNA-splicing endonuclease positive effector] [gn:sen1] [gicfc:10.1:10.2:10.6] [keggfc:14.2] [sgdic:4.5.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
b1x10463_y	32244792_f2_1	5005	19108	729	243	YLR430W	392	8.8(10)-35	Saccharomyces cerevisiae	[ui.ylr430w] [pn:positive effector of tRNA-splicing endonuclease:tRNA-splicing endonuclease positive effector] [gn:sen1] [gicfc:10.1:10.2:10.6] [keggfc:14.2] [sgdic:4.5.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5665	2915831_f2_3	5006	19109	2970	990	YLR451W	919	4.0(10)-121	Saccharomyces cerevisiae	[ui.ylr451w] [pn:transcription factor:regulatory protein leu3] [gn:leu3:19324] [gicfc:0.1:10.2] [keggfc:14.2] [sgdic:1.1.2:4.8:2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5199	4475886_c1_9	5007	19110	3396	1132	YML103C	522	1.6(10)-61	Saccharomyces cerevisiae	[ui.yml103c] [pn:nucleoporin:nuclear pore protein] [gn:nup188] [gicfc:10.1:10.2] [keggfc:14.2] [sgdic:8.1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

b9x11910.y	31304582_f3_1	5008	19111	816	272	YML103C	354	6.5(10)-31	Saccharomyces cerevisiae	[ui:ym1103c] [pn:nucleoporin:nuclear pore protein] [gr:nup 88] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:8.1.0-9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3719	24804033_f3_4	5009	19112	249	83	YML103C	93	0.0038	Saccharomyces cerevisiae	[ui:ym1103c] [pn:nucleoporin:nuclear pore protein] [gr:nup 88] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:8.1.0-9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5722	6287811_f2_6	5010	19113	537	179	YML098W	166	1.5(10)-12	Saccharomyces cerevisiae	[ui:ym098w] [pn:ffid subunit:bp-associated factor, 19 kd:protein] [gn:taf19.fun81] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.1:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4302	20422716_c1_4	5011	19114	2253	751	YML076C	277	1.3(10)-40	Saccharomyces cerevisiae	[ui:ym076c] [pn:weak similarity to transcription factor] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3857	803758_f3_4	5012	19115	315	105	YML074C	30	7.0(10)-8	Saccharomyces cerevisiae	[ui:ym074c] [pn:proline cis-trans isomerase:R506-binding nuclear protein:peptidyl-prolyl cis- trans isomerase:ppase:proline rotamase:nucleolar proline isomerase:kbp-70] [gr:ipr3.npi46] [gicfc:10.1:10.2:10.5:10.7:12.7:14.1] [ec:5.2]

CONTIG4014	9776061_f3_5	5013	19116	699	233	YML069W	591	1.3(10)-57	Saccharomyces cerevisiae	[ui:yml069w] [pn:similarity to hmg proteins] [gn:pbp3] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4014	25948302_f3_6	5014	19117	207	69	YML069W	146	2.1(10)-9	Saccharomyces cerevisiae	[ui:yml069w] [pn:similarity to hmg proteins] [gn:pbp3] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG481	23836502_c3_8	5015	19118	753	251	YML065W	201	5.7(10)-15	Saccharomyces cerevisiae	[ui:yml065w] [pn:origin recognition complex, 104 kd subunit:origin recognition complex protein, subunit 1:origin recognition complex protein 120 kd subunit] [gn:orc] [gicfc:10.1:10.2:10.8:12.8:12.9] [keggfc:13.2] [sgdfc:3.3.0:3.6:0.4]
CONTIG4399	14746043_f2_2	5016	19119	990	330	YML065W	279	2.6(10)-23	Saccharomyces cerevisiae	[ui:yml065w] [pn:origin recognition complex, 104 kd subunit:origin recognition complex protein, subunit 1:origin recognition complex protein 120 kd subunit] [gn:orc] [gicfc:10.1:10.2:10.8:12.8:12.9] [keggfc:13.2] [sgdfc:3.3.0:3.6:0.4]
CONTIG465	20008541_c3_8	5017	19120	669	223	YML060W	466	2.5(10)-44	Saccharomyces cerevisiae	[ui:yml060w] [pn:8-oxoguanine dna glycosylase] [gn:ogg1ym9958] [gicfc:10.1:10.1:10.2:14.1] [ec:3.2.2.-] [keggfc:14.1] [sgdfc:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]

CONTIG275	3913128_c1_1	5018	19121	786	262	YML046W	102	0.00869	Saccharomyces cerevisiae	[ui:ym 046w] [pn:pre-mrna splicing factor:pre-mrna processing protein prp39] [gn:prp39;ym9827] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.9.0:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5049	25601563_f3_5	5019	19122	912	304	YML046W	105	0.0061	Saccharomyces cerevisiae	[ui:ym 046w] [pn:pre-mrna splicing factor:pre-mrna processing protein prp39] [gn:prp39;ym9827] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.9.0:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3214	1213380_f3_1	5020	19123	1710	570	YML043C	260	8.9(10)-20	Saccharomyces cerevisiae	[ui:ym 043c] [pn:ma polymerase i specific transcription initiation factor] [gn:rml1] [gicfc:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.1.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5467	23844680_f1_4	5021	19124	507	169	YML032C	164	2.1(10)-11	Saccharomyces cerevisiae	[ui:ym 032c] [pn:recombination and dna repair protein:dna repair and recombination protein] [gn:rad52] [gicfc:10.1:10.10:10.2:10.8:12.9] [keggfc:14.2] [sgdfc:3.3.0:3.7:0.9:5.0:11.2.1] [db:gic-saccharomyces cerevisiae]

CONTIG5726	82_c1_17	5022	19125	1839	613	YML032C	485	4.9(10)-54	Saccharomyces cerevisiae	[ui:yml032c] [pn:recombination and dna repair protein:dna repair and recombination protein] [gn:rad52] [gtfc:10.1:10.10:10.2:10.8:12.9] [keggfc:14.2] [sgdfc:3.3.0:3.7:0:9.5:0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5467	33384427_c3_19	5023	19126	1029	343	YML031W	123	0.00012	Saccharomyces cerevisiae	[ui:yml031w] [pn:nuclear envelope protein] [gn:ndc1] [gtfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG3652	10243751_c3_3	5024	19127	651	217	YML027W	142	3.1(10)-9	Saccharomyces cerevisiae	[ui:yml027w] [pn:homeobox protein] [gn:yox1] [gtfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.12.0:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG5589	33150_f3_12	5025	19128	2799	933	YML010W	1134	4.0(10)-115	Saccharomyces cerevisiae	[ui:yml010w] [pn:transcription initiation protein:spt5] [gn:spt5;ym9571] [gtfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.1:4.8.3:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG3572	26290937_f3_2	5026	19129	1056	352	YML007W	139	6.7(10)-14	Saccharomyces cerevisiae	[ui:yml007w] [pn:transcriptional activator involved in oxidative stress response:transcriptional activator pdr4:yap-1 protein] [gn:pdr4;yap1;snp3;par1;ym9571] [gtfc:10.1:10.2:13.2] [keggfc:14.2] [sgdfc:4.8.2:9.5:0:11.1:0] [db:gtc-sac]

CONTIG3590	21910777_B_1	5027	19130	258	86	YML007W	212	2.2(10)-16	Saccharomyces cerevisiae	[ui:ym007w] [pn:transcriptional activator involved in oxidative stress response;transcriptional activator pd4:yap-1 protein] [gn:pd4:yap1:snq3:part1:ym9571] [gicfc:10.1:0.2:13.2] [keggfc:14.2] [sgdic:4.8.2.9.5.0:11.1.0] [db:gic-sac]
CONTIG5215	33750027_c3_14	5028	19131	543	181	YML007W	109	0.00083	Saccharomyces cerevisiae	[ui:ym007w] [pn:transcriptional activator involved in oxidative stress response;transcriptional activator pd4:yap-1 protein] [gn:pd4:yap1:snq3:part1:ym9571] [gicfc:10.1:0.2:13.2] [keggfc:14.2] [sgdic:4.8.2.9.5.0:11.1.0] [db:gic-sac]
CONTIG1922	33254630_f2_2	5029	19132	1002	334	YMR016C	516	3.2(10)-49	Saccharomyces cerevisiae	[ui:ymr016c] [pn:regulatory protein in the pka signal transduction pathway;sok2 protein] [gn:sok2:ym9711] [gicfc:12.13] [keggfc:14.2] [sgdic:3.2.0.4.8.2.9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5673	6331442_f1_1	5030	19133	480	160	YMR039C	171	8.0(10)-13	Saccharomyces cerevisiae	[ui:ymr039c] [pn:transcriptional coactivator;sub1 protein] [gn:sub1:ym9532] [gicfc:10.1:10.2] [keggfc:14.2] [sgdic:4.8.2.9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG4526	23906250_cl_7	5031	19134	1914	638	YMR047C	299	1.3(10)-35	Saccharomyces cerevisiae	[ui:ymr047c] [pn:nuclear pore protein:nucleoporin nup116/nsp116] [gn:nup116:nsp116:ym9532] [gicfc:10.1:10.2:10.6] [keggfc:14.2] [sgdfc:4.5.08.1.0.9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5667	34410090_f1_3	5032	19135	1344	448	YMR047C	199	2.1(10)-17	Saccharomyces cerevisiae	[ui:ymr047c] [pn:nuclear pore protein:nucleoporin nup116/nsp116:ym9532] [gicfc:10.1:10.2:10.6] [keggfc:14.2] [sgdfc:4.5.08.1.0.9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4321	21657628_c2_9	5033	19136	2076	692	YMR061W	572	1.8(10)-70	Saccharomyces cerevisiae	[ui:ymr061w] [pn:component of pre-mrna 3"-end processing factor cf1:mmra 3"-end processing protein mra14] [gn:mra14:ym9796] [gicfc:10.1:10.2:10.9] [keggfc:14.2] [sgdfc:4.10.0.9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5784	26285905_f2_5	5034	19137	2346	782	YMR078C	258	2.2(10)-38	Saccharomyces cerevisiae	[ui:ymr078c] [pn:required for accurate chromosome transmission in mitosis and maintenance of normal telomere length chl12 protein] [gn:chl12:cflf18:ym9582] [gicfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0.9.5.0] [db:gic-saccharomyces]

CONTIG5784	24010800_f3_9	5035	19138	312	104	YMR078C	165	3.0(10)-11	Saccharomyces cerevisiae	[ui:ymr078c] [pn:required for accurate chromosome transmission in mitosis and maintenance of normal telomere length:chi12 protein] [gn:chi12;ctf18;ym9582] [gcfc:10.1:10.2:12.8] [keggfc:14.2] [sgdc:3.8.0;9.5.0] [db:gtc-saccharomyces]
CONTIG5813	30209777_f3_31	5036	19139	1596	532	YMR106C	181	1.2(10)-10	Saccharomyces cerevisiae	[ui:ymr106c] [pn:component of dna end-joining repair pathway] [gn:hd12] [gcfc:10.1:10.2:10.8] [keggfc:14.2] [sgdc:3.7:0;9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1251	35589436_f2_1	5037	19140	1236	412	YMR129W	269	7.5(10)-21	Saccharomyces cerevisiae	[ui:ymr129w] [pn:nuclear pore membrane glycoprotein;nuclear envelope pore membrane protein pom152;p150] [gn:pom152;ym9553] [gcfc:10.1:10.2] [keggfc:14.2] [sgdc:8.1:0;9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1780	10426006_f2_2	5038	19141	792	264	YMR129W	280	3.6(10)-23	Saccharomyces cerevisiae	[ui:ymr129w] [pn:nuclear pore membrane glycoprotein;nuclear envelope pore membrane protein pom152;p150] [gn:pom152;ym9553] [gcfc:10.1:10.2] [keggfc:14.2] [sgdc:8.1:0;9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3661	161018_c3_5	5039	19142	273	91	YMR129W	225	2.6(10)-17	Saccharomyces cerevisiae	[ui:ymr129w] [pn:nuclear pore membrane glycoprotein;nuclear envelope pore membrane protein pom152;p150] [gn:pom152;ym9553] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:8.1:0.9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG2419	26455011_f1_2	5040	19143	1257	419	YMR137C	121	9.0(10)-17	Saccharomyces cerevisiae	[ui:ymr137c] [pn: dna repair protein] [gn:pso21] [gicfc:10.1:10.10.10.2] [keggfc:14.2] [sgdfc:9.5.0:11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG5566	24414092_f2_11	5041	19144	1677	559	YMR137C	129	6.9(10)-5	Saccharomyces cerevisiae	[ui:ymr137c] [pn: dna repair protein] [gn:pso2] [gicfc:10.1:10.10.10.2] [keggfc:14.2] [sgdfc:9.5.0:11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG1457	6834800_c3_1	5042	19145	549	183	YMR167W	340	5.0(10)-30	Saccharomyces cerevisiae	[ui:ymr167w] [pn: dna mismatch repair protein;mutl protein homolog 1:dna mismatch repair protein mlh1] [gn:mlh1;ym8520] [gicfc:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.7.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG2822	24428937_c3_1	5043	19146	1221	407	YMR167W	375	6.0(10)-50	Saccharomyces cerevisiae	[ui:ymr167w] [pn: dna mismatch repair protein;mutl protein homolog 1:dna mismatch repair protein mlh1] [gn:mlh1;ym8520] [gicfc:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.7.0:9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG3961	21917137_f2_2	5044	19147	735	245	YMR167W	670	6.0(10)-66	Saccharomyces cerevisiae	[ui:ymr167w] [pn: dna mismatch repair protein:mutl protein homolog 1: dna mismatch repair protein mlh1] [gn:mlh1:ym8520] [gicfc:10.1:10.2:10.2] [sgdfc:3.7:0.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4228	12540775_c3_11	5045	19148	654	218	YMR167W	297	2.2(10)-25	Saccharomyces cerevisiae	[ui:ymr167w] [pn: dna mismatch repair protein:mutl protein homolog 1: dna mismatch repair protein mlh1] [gn:mlh1:ym8520] [gicfc:10.1:10.2:10.2] [sgdfc:3.7:0.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5344	6027165_f1_4	5046	19149	684	228	YMR197C	333	3.1(10)-30	Saccharomyces cerevisiae	[ui:ymr197c] [pn:similarity to nuf1 p] [gicfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.9:0.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5111	16838411_c1_13	5047	19150	1197	399	YMR201C	564	3.3(10)-59	Saccharomyces cerevisiae	[ui:ymr201c] [pn:nucleotide excision repair protein: dna repair protein rad14] [gn:rad14:ym8325] [gicfc:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:9.5:0:11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG4328	24883563_c1_3	5048	19151	810	270	YMR224C	782	8.0(10)-78	Saccharomyces cerevisiae	[ui:ymr224c] [pn: dna repair and meiotic recombination protein:mre11 protein] [gn:mre11:ym9959] [gicfc:10.1:10.2:10.8:12.8] [keggfc:14.2] [sgdfc:3.5:0.3:7.0:9.5:0] [db:gic-saccharomyces cerevisiae]

CONTIG648	4885950_c2_5	5049	19152	717	239	YMR224C	108	3.5(10)-5	Saccharomyces cerevisiae	[ui:ymr224c] [pn: dna repair and meiotic recombination protein.mre11 protein] [gn:mre11;ym9959] [gtfc:10.1:10.2:10.8:12.8] [keggc:4.2] [sgdgc:3.5.0:3.7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG648	15801542_c1_4	5050	19153	246	82	YMR224C	156	2.5(10)-10	Saccharomyces cerevisiae	[ui:ymr224c] [pn: dna repair and meiotic recombination protein.mre11 protein] [gn:mre11;ym9959] [gtfc:10.1:10.2:10.8:12.8] [keggc:4.2] [sgdgc:3.5.0:3.7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5817	24807938_c3_63	5051	19154	5262	1754	YMR229C	2455	0	Saccharomyces cerevisiae	[ui:ymr229c] [pn: processing of pre-ribosomal rna][gn:rrp5] [gtfc:10.1:10.2:10.3] [keggc:14.2] [sgdgc:4.2:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5046	32087818_F2_2	5052	19155	255	85	YMR240C	156	1.2(10)-10	Saccharomyces cerevisiae	[ui:ymr240c] [pn: u2 snmp protein] [gn:cus1] [gtfc:10.1:10.2] [keggc:14.2] [sgdgc:4.9:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5046	26620138_f3_3	5053	19156	804	268	YMR240C	178	4.7(10)-13	Saccharomyces cerevisiae	[ui:ymr240c] [pn: u2 snmp protein] [gn:cus1] [gtfc:10.1:10.2] [keggc:14.2] [sgdgc:4.9:0.9:5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3657	24413880_c1_3	5054	19157	1824	608	YMR239C	449	1.6(10)-42	Saccharomyces cerevisiae	[ui:ymr239c] [pn:double-stranded ribonuclease] [gn:mt1] [gtcfc:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.2.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5748	21692010_f3_10	5055	19158	2049	683	YMR239C	160	1.8(10)-8	Saccharomyces cerevisiae	[ui:ymr239c] [pn:double-stranded ribonuclease] [gn:mt1] [gtcfc:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.2.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5739	21914553_f1_6	5056	19159	2889	963	YMR268C	281	1.0(10)-21	Saccharomyces cerevisiae	[ui:ymr268c] [pn:pre-mrna splicing factor:u4/u6 snrna-associated splicing factor prp24:u4/u6snrp protein] [gn:prp24;ym8156] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5322	10975930_f1_2	5057	19160	1026	342	YMR276W	570	2.3(10)-55	Saccharomyces cerevisiae	[ui:ymr276w] [pn:ubiquitin-like protein:ubiquitin-like protein dsk2] [gn:dsk2;she4;ym8021] [gtcfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5482	1365936_f3_13	5058	19161	2466	822	YMR284W	144	1.2(10)-25	Saccharomyces cerevisiae	[ui:ymr284w] [pn:high-affinity dna-binding protein:high affinity dna-binding factor subunit 1:kif70 homolog] [gn:hdf1;nes24;yku70;ym8021] [gtcfc:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.6.0:3.7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5428	2432827_c1_12	5039	19162	564	188	YNL330C	117	2.0(10)-6	Saccharomyces cerevisiae	[ui:ynl330c] [pn:transcription modifier protein:histone deacetylase;transcriptional regulatory protein rpd3] [gn:rpd3:sd12:n0305] [gicfc:10.1:10.2:12.15:12.9:13.10] [keggfc:14.2] [sgdfc:.4.1:3.3.0:3.4.0:4.8:2.9:5.0] [db:gic-saccharom]
CONTIG5428	390932_c3_17	5060	19163	1347	449	YNL330C	1756	5.0(10)-181	Saccharomyces cerevisiae	[ui:ynl330c] [pn:transcription modifier protein:histone deacetylase;transcriptional regulatory protein rpd3] [gn:rpd3:sd12:n0305] [gicfc:10.1:10.2:12.15:12.9:13.10] [keggfc:14.2] [sgdfc:.4.1:3.3.0:3.4.0:4.8:2.9:5.0] [db:gic-saccharom]
CONTIG5485	24492127_f3_6	5061	19164	1524	508	YNL330C	1678	9.0(10)-173	Saccharomyces cerevisiae	[ui:ynl330c] [pn:transcription modifier protein:histone deacetylase;transcriptional regulatory protein rpd3] [gn:rpd3:sd12:n0305] [gicfc:10.1:10.2:12.15:12.9:13.10] [keggfc:14.2] [sgdfc:.4.1:3.3.0:3.4.0:4.8:2.9:5.0] [db:gic-saccharom]
CONTIG4245	21745192_f2_3	5062	19165	543	181	YNL312W	254	7.2(10)-22	Saccharomyces cerevisiae	[ui:ynl312w] [pn:dna replication factor a, 36 kda subunit replication factor-a protein 2:rf-a:dna binding protein bbf1] [gn:rfa2:bbf1:n0368] [gicfc:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.6.0:9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG4341	9851567_f2_2	5063	19166	1098	366	YNL290W	1044	1.3(10)-105	Saccharomyces cerevisiae	[ui:ynl290w] [pn: dna replication factor c, 40 kda subunit:activator 1 40 kd subunit] [gn:rfc3.n0533] [gctfc:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.6.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5417	24407812_f1_2	5064	19167	765	255	YNL282W	159	8.4(10)-12	Saccharomyces cerevisiae	[ui:ynl282w] [pn: involved in processing of tRNAs and rRNAs:hypothetical 22.6 kd protein in mrp110-erg24 intergenic region] [gn:pop3.n0586] [gctfc:10.1:10.2:10.3:10.6] [keggfc:14.2] [sgdfc:4.2:0.4:5.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG2384	36117188_f2_2	5065	19168	573	191	YNL261W	113	1.6(10)-9	Saccharomyces cerevisiae	[ui:ynl261w] [pn: origin recognition complex, 50 kda subunit:origin recognition complex protein, subunit 5:origin recognition complex protein 53 kd subunit] [gn:orc5.n0834] [gctfc:10.1:10.2:10.8:12.8:12.9] [keggfc:13.2] [sgdfc:3.3.0:3.]
CONTIG5793	4898311_c3_24	5066	19169	2073	691	YNL251C	628	3.7(10)-80	Saccharomyces cerevisiae	[ui:ynl251c] [pn: involved in regulation of nuclear pre-mRNA abundance:nd1 protein] [gn:mrd1.n0868] [gctfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG1211	16282280_f3_1	5067	19170	609	203	YNL250W	159	2.7(10)-10	Saccharomyces cerevisiae	[ui:ynl250w] [pn: dna repair protein: dna repair protein rad50:153 kd protein] [gn:rad50:n0872] [gicfc:10.:10.2:10.8:12.8] [keggfc:14.:2] [sgdgc:3.5.0;3.7:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2192	797518_c2_2	5068	19171	723	241	YNL250W	604	8.6(10)-58	Saccharomyces cerevisiae	[ui:ynl250w] [pn: dna repair protein: dna repair protein rad50:153 kd protein] [gn:rad50:n0872] [gicfc:10.:10.2:10.8:12.8] [keggfc:14.:2] [sgdgc:3.5.0;3.7:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4056	9788502_f1_1	5069	19172	1038	346	YNL250W	103	0.03599	Saccharomyces cerevisiae	[ui:ynl250w] [pn: dna repair protein: dna repair protein rad50:153 kd protein] [gn:rad50:n0872] [gicfc:10.:10.2:10.8:12.8] [keggfc:14.:2] [sgdgc:3.5.0;3.7:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5341	24854706_c1_14	5070	19173	1335	445	YNL250W	891	7.0(10)-89	Saccharomyces cerevisiae	[ui:ynl250w] [pn: dna repair protein: dna repair protein rad50:153 kd protein] [gn:rad50:n0872] [gicfc:10.:10.2:10.8:12.8] [keggfc:14.:2] [sgdgc:3.5.0;3.7:0.9:5.0] [db:gtc-saccharomyces cerevisiae]

blx11175.y	11194187_f3_1	5071	19174	279	93	YNL250W	118	6.4(10)-6	Saccharomyces cerevisiae	[ui:ynl250w] [pn:dna repair protein:dna repair protein rad50:153 kd protein] [gn:rad50:n0872] [gicfc:10.1:10.2:10.8:12.8] [keggfc:14.2] [sgdfc:3.5:0.3:7.0:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG4568	24804628_c1_6	5072	19175	1008	336	YNL236W	119	0.00038	Saccharomyces cerevisiae	[ui:ynl236w] [pn:global regulator protein:global transcriptional regulator sin4] [gn:sin4;tsf3;bel2;gal22:ssf5;n1135] [gicfc:10.1:10.2:12.13:12.15:12.9] [keggfc:14.2] [sgdfc:1.1.2:1.5.2:3.3.0:3.4:0.4:8.2:9.5:0] [db:gtc-saccharomyces c
CONTIG4979	3990636_f2_5	5073	19176	732	244	YNL222W	544	1.5(10)-58	Saccharomyces cerevisiae	[ui:ynl222w] [pn:suppressor of cs mutant of sua7:ssu72 protein] [gn:ssu72;n1279] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG4979	2922250_f2_6	5074	19177	897	299	YNL221C	442	7.0(10)-41	Saccharomyces cerevisiae	[ui:ynl221c] [pn:protein component of ribonuclease p and ribonuclease mrp:pop1 protein] [gn:pop1;n1285] [gicfc:10.1:10.2:10.3:10.6] [keggfc:14.2] [sgdfc:4.2:0.4:5.0:9.5:0] [db:gtc-saccharomyces cerevisiae]

CONTIG2176	11844207_f1_1	5075	19178	723	241	YNL206C	220	1.3(10)-17	Saccharomyces cerevisiae	[ui:ynl206c] [pn:similarity to structure-specific recognition proteins:hypothetical 51.6 kd protein in ssp2-spx 18 intergenic region] [gn:n1346] [gtcfc:0.1:10.2] [keggfc:14.2] [sgdfc:9.5:0.9:6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4506	2007662_c3_16	5076	19179	1671	557	YNL189W	1978	1.5(10)-204	Saccharomyces cerevisiae	[ui:ynl189w] [pn:karyopherin-alpha or importin:importin alpha subunit:karyopherin alpha subunit:serine-rich rna polymerase i suppressor protein] [gn:srp1.kap60.n1606] [gtcfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8:0.8:1.0:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG3708	4688950_c2_8	5077	19180	1695	565	YNL172W	617	7.0(10)-79	Saccharomyces cerevisiae	[ui:ynl172w] [pn:subunit of anaphase-promoting complex:cyclosome:hypothetical 196.1 kd protein in rps-psd1 intergenic region] [gn:apc1:n1677] [gtcfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3902	23914011_f2_2	5078	19181	708	236	YNL167C	93	8.0(10)-5	Saccharomyces cerevisiae	[ui:ynl167c] [pn:cre-binding bzip protein:cre-binding bzip protein sh0] [gn:sh01.acr1:n1702] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2.9:5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4103	35303_f2_2	5079	19182	1611	537	YNL126W	583	1.6(10)-56	Saccharomyces cerevisiae	[ui:ynl126w] [pn:spindle pole body component:spindle pole body component spc98] [gn:spc98.n1222.n1879] [gicfc:10.1:10.2:11.1:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0.9.1.0.9.2.0.9.3.0.9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3467	325_c3_3	5080	19183	396	132	YNL112W	250	1.2(10)-20	Saccharomyces cerevisiae	[ui:ynl112w] [pn:atp-dependent mnhelicase of dead box family:p68-like protein] [gn:dbp2.n1945] [gicfc:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.2.0.9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4462	860660_c3_4	5081	19184	1377	459	YNL112W	1556	7.7(10)-160	Saccharomyces cerevisiae	[ui:ynl112w] [pn:atp-dependent mnhelicase of dead box family:p68-like protein] [gn:dbp2.n1945] [gicfc:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.2.0.9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG2968	10329700_c2_3	5082	19185	1374	458	YNL088W	1270	1.6(10)-129	Saccharomyces cerevisiae	[ui:ynl088w] [pn:atp-hydrolysing; dna topoisomerase ii] [gn:top2.tor3.n12244] [gicfc:10.1:10.2:10.8:14.1] [ec:5.99.1.3] [keggfc:14.1] [sgdfc:3.6.0.3.7.0.9.5.0] [db:gic-saccharomyces cerevisiae]

b3x14031.y	19962524_c1_2	5083	19186	486	162	YNL088W	506	3.2(10)-47	Saccharomyces cerevisiae	[ui:ynl088w] [pn:atp-hydrolysing-dna topoisomerase ii] [gn:top2.tor3.n2244]
CONTIG1244	953127_f2_2	5084	19187	999	333	YNL068C	429	3.3(10)-60	Saccharomyces cerevisiae	[gtfc:10.1:10.2:10.8:14.1] [ec:5.99.1.3] [keggc:14.1] [sgfc:3.6.0.3.7:0.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3621	18813_c3_5	5085	19188	1560	520	YNL061W	1727	5.9(10)-178	Saccharomyces cerevisiae	[ui:ynl061w] [pn:nucleolar protein.nucleolar protein nop2] [gn:nop2.yml.n2428.ynl2428w] [gtfc:10.1] [keggc:14.2] [sgfc:9.5.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5691	19723308_f2_11	5086	19189	363	121	YNL059C	111	1.8(10)-5	Saccharomyces cerevisiae	[ui:ynl059c] [pn:actin-related protein.hypothetical 87.6 kd protein in nop2-omp2 intergenic region] [gn:arp5.n2430.ynl2430c] [gtfc:10.1:10.2:12.16] [keggc:14.2] [sgfc:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5691	10335462_f3_18	5087	19190	1797	599	YNL059C	884	1.3(10)-88	Saccharomyces cerevisiae	[ui:ynl059c] [pn:actin-related protein.hypothetical 87.6 kd protein in nop2-omp2 intergenic region] [gn:arp5.n2430.ynl2430c] [gtfc:10.1:10.2:12.16] [keggc:14.2] [sgfc:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3388	13876567_f3_3	5088	19191	1929	643	YNL039W	507	1.1(10)-48	Saccharomyces cerevisiae	[ui:ynl039w] [pn:tflib subunit, 90 kd:transcription factor tflib b] [gn:ifc5;ifc7;n2682] [gicfc:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.1.0:4.4.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4101	22520752_o2_7	5089	19192	1431	477	YNL025C	593	3.6(10)-67	Saccharomyces cerevisiae	[ui:ynl025c] [pn:dna-directed rna polymerase ii holoenzyme and kornberg's mediator:srb subcomplex subunit, cyclin c homolog:rna polymerase ii holoenzyme cyclin-like subunit] [gn:ume3:ssn8:srb11:n2805] [gicfc:10.1:10.2:12.13:12.8] [keg]
CONTIG3012	6672175_c3_6	5090	19193	489	163	YNL016W	145	2.0(10)-9	Saccharomyces cerevisiae	[ui:ynl016w] [pn:major polyadenylated rna-binding protein of nucleus and cytoplasm:nuclear and cytoplasmic polyadenylated rna-binding protein pub1:ars consensus binding protein acbp-60:poly:u-binding protein:poly uridylate-binding pro
CONTIG5129	6642127_f3_6	5091	19194	1557	519	YNL016W	479	2.2(10)-76	Saccharomyces cerevisiae	[ui:ynl016w] [pn:major polyadenylated rna-binding protein of nucleus and cytoplasm:nuclear and cytoplasmic polyadenylated rna-binding protein pub1:ars consensus binding protein acbp-60:poly:u-binding protein:poly uridylate-binding pro

CONTIG3755	4532762_f2_4	5092	19195	1044	348	YNL007C	538	5.0(10)-87	Saccharomyces cerevisiae	[ui:ynl007c] [pn:heat shock protein:sis1 protein] [gn:sis1:n2879] [gtcfc:12.7:12.8] [keggfc:14.2] [sgdfc:3.8:0.5:2.0:9.2.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG2372	961003_f3_1	5093	19196	1341	447	YNR011C	1108	2.2(10)-112	Saccharomyces cerevisiae	[ui:ynr011c] [pn:ma-dependent splicing factor of dead box family:pre-mrna splicing factor rna helicase prp2] [gn:prp2:rnaz2:n2048] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.9:0.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4666	4190937_c1_11	5094	19197	327	109	YNR011C	96	0.00088	Saccharomyces cerevisiae	[ui:ynr011c] [pn:ma-dependent splicing factor of dead box family:pre-mrna splicing factor rna helicase prp2] [gn:prp2:rnaz2:n2048] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.9:0.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3881	4860936_c3_7	5095	19198	1314	438	YNR023W	196	2.1(10)-23	Saccharomyces cerevisiae	[ui:ynr023w] [pn:component of swi/snf global transcription activator complex:transcription regulatory protein swp73:swi/snf complex component swp73] [gn:snf12:swp73:n3224] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2.9:5.0] [db:gic-sa]
CONTIG1850	355782_c3_10	5096	19199	1281	427	YNR052C	64	4.0(10)-44	Saccharomyces cerevisiae	[ui:ynr052c] [pn:required for glucose derepression:pop2 protein] [gn:pop2:cafl:n3470] [gtcfc:0.1:10.2:12.13:12.15] [keggfc:4.2] [sgdfc:1.5:2.3:4.0:4.8:2.9:5.0] [db:gic-saccharomyces cerevisiae]

CONTIG585	24647191_f3_14	5097	19200	1485	495	YNR052C	469	1.2(10)-44	Saccharomyces cerevisiae	[ui:ym052c] [pn:required for glucose derepression;pop2 protein] [gn:pop2.cat1:n3470] [gtfc:10.1:10.2:12.13:12.15] [keggfc:14.2] [sgdgc:1.5.2:3.4.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3896	4020011_f2_3	5098	19201	1599	533	YOL148C	187	9.0(10)-26	Saccharomyces cerevisiae	[ui:yol148c] [pn:member of the tlp class of spt proteins that alter transcription site selection;transcription factor spl20] [gn:spf20:ada5] [gtfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG521	2822177_f1_3	5099	19202	1461	487	YOL123W	570	2.3(10)-55	Saccharomyces cerevisiae	[ui:yol123w] [pn:polyadenylated rna-binding protein] [gn:hrp1] [gtfc:10.1:10.2] [keggfc:14.2] [sgdgc:9.2.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4742	12676553_f3_6	5100	19203	408	136	YOL116W	130	6.0(10)-8	Saccharomyces cerevisiae	[ui:yol116w] [pn:transcriptional activator;msn1 protein;multicopy suppressor of snf1 protein 1] [gn:msn1:fup1:phd2:hrb382] [gtfc:10.1:10.2:12.13] [keggfc:14.2] [sgdgc:1.5.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5328	10947055_c3_16	5101	19204	1809	603	YOL116W	177	8.0(10)-11	Saccharomyces cerevisiae	[ui:yo116w] [pn:transcriptional activator:msn1 protein:multicopy suppressor of snf1 protein 1] [gn:msn1:fip1:phd2:hrb382] [gtcfc:10.1:10.2:12.13] [keggfc:14.2] [sgdfc:1.5.2:4.8:2.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5732	36367807_c2_29	5102	19205	1818	606	YOL115W	1140	9.4(10)-116	Saccharomyces cerevisiae	[ui:yo115w] [pn:topoisomerase i-related protein:topoisomerase i-related protein trf4] [gn:trf4.00716:hrc584] [gtcfc:10.1:10.2:10.8:12.8] [keggfc:14.2] [sgdfc:3.6.0:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5417	22064657_f3_7	5103	19206	987	329	YOL094C	1137	1.8(10)-115	Saccharomyces cerevisiae	[ui:yo094c] [pn:dna replication factor c, 37 kda subunit:activator 1, 37 kd subunit:replication factor c 37 kd subunit] [gn:rifc4.00923] [gtcfc:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.6.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5651	9960027_f1_1	5104	19207	2604	868	YOL090W	1279	8.1(10)-168	Saccharomyces cerevisiae	[ui:yo090w] [pn:dna mismatch repair protein:muis protein homolog 2] [gn:msh2.00935] [gtcfc:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3552	3939000_f1_1	5105	19208	1698	566	YOL089C	129	7.4(10)-7	Saccharomyces cerevisiae	[ui:yo089c] [pn:weak similarity to transcription factors] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5592	14275302_c3_8	5106	19209	2271	757	YOL089C	139	3.8(10)-11	Saccharomyces cerevisiae	[ui:yol089c] [pn:weak similarity to transcription factors] [gtfcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.29.5.0] [db:gtc-saccharomyces cerevisiae]
b2x16250.x	44824218_f1_1	5107	19210	747	249	YOL089C	91	0.34	Saccharomyces cerevisiae	[ui:yol089c] [pn:weak similarity to transcription factors] [gtfcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.29.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1152	\$65875_F2_3	5108	19211	204	68	YOL069W	90	0.00169	Saccharomyces cerevisiae	[ui:yol069w] [pn:spindle pole body protein:myosin-like protein:nuclear filament-containing protein 2:nuclear division protein nuf2] [gn:nuf2] [gtfcf:10.1:10.2:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0/9.3.0/9.5.0] [db:gtc-saccharomyces c
CONTIG1539	5911599_c1_3	5109	19212	954	318	YOL069W	198	1.7(10)-13	Saccharomyces cerevisiae	[ui:yol069w] [pn:spindle pole body protein:myosin-like protein:nuclear filament-containing protein 2:nuclear division protein nuf2] [gtfcf:10.1:10.2:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0/9.3.0/9.5.0] [db:gtc-saccharomyces c

CONTIG4978	14242151_f1_2	5110	19213	855	285	YOL067C	246	5.0(10)-21	Saccharomyces cerevisiae	[ui:yol067c] [pn:basic helix-loop-helix transcription factor that regulates cit2 gene expression:retrograde regulation protein 1] [gn:rtg1] [gicfc:10.1:10.2:12.13] [keggfc:14.2] [sgdfc:1.5:2:4.8:2:9.5:0] [db:gic-saccharomyces cerevisiae]
CONTIG411	9806442_f2_2	5111	19214	816	272	YOL051W	166	3.8(10)-11	Saccharomyces cerevisiae	[ui:yol051w] [pn:dna-directed dna polymerase ii holoenzyme and kornberg's mediator:srb subcomplex subunit:transcription regulatory protein gal11] [gn:gal11;spt13;ra3] [gicfc:10.1:10.2:12.13:12.15:12.9] [keggfc:14.2] [sgdfc:1.5:2:3.3]
CONTIG1537	25421931_c3_8	5112	19215	1317	439	YOL051W	108	7.5(10)-6	Saccharomyces cerevisiae	[ui:yol051w] [pn:dna-directed dna polymerase ii holoenzyme and kornberg's mediator:srb subcomplex subunit:transcription regulatory protein gal11] [gn:gal11;spt13;ra3] [gicfc:10.1:10.2:12.13:12.15:12.9] [keggfc:14.2] [sgdfc:1.5:2:3.3]
CONTIG1631	24023431_f1_2	5113	19216	1371	457	YOL006C	798	1.6(10)-79	Saccharomyces cerevisiae	[ui:yol006c] [pn:dna topoisomerase II] [gn:top1;mak1] [gicfc:10.1:10.2:10.8:14.1] [ec:5.99.1.2] [keggfc:14.1] [sgdfc:3.6:0.3:7.0:4.12:0.9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG1633	20484390_c3_3	5114	19217	306	102	YOL004W	336	4.7(10)-29	Saccharomyces cerevisiae	[ui:yo 004w] [pn:transcription regulatory protein:paired amphiphatic helix protein] [gn:sin3:sd1:ume4:rpdi:gam2] [gfcfc:10.1:10.2:12.15:12.8:12.9] [keggfc:13.1] [sgdfc:1.6.4.3.3.0.3.4.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1633	975750_f1_1	5115	19218	564	188	YOL004W	710	5.9(10)-69	Saccharomyces cerevisiae	[ui:yo 004w] [pn:transcription regulatory protein:paired amphiphatic helix protein] [gn:sin3:sd1:ume4:rpdi:gam2] [gfcfc:10.1:10.2:12.15:12.8:12.9] [keggfc:13.1] [sgdfc:1.6.4.3.3.0.3.4.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2942	14117288_f1_1	5116	19219	1086	362	YOL004W	581	3.6(10)-55	Saccharomyces cerevisiae	[ui:yo 004w] [pn:transcription regulatory protein:paired amphiphatic helix protein] [gn:sin3:sd1:ume4:rpdi:gam2] [gfcfc:10.1:10.2:12.15:12.8:12.9] [keggfc:13.1] [sgdfc:1.6.4.3.3.0.3.4.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2942	30080143_f2_3	5117	19220	738	246	YOL004W	225	3.2(10)-17	Saccharomyces cerevisiae	[ui:yo!004w] [pn:transcription regulatory protein:paired amphipathic helix protein] [gn:sin3:sd1:ume4:rpdi:gam2] [gicfc:10.1:10.2:12.15:12.8:12.9] [keggfc:13.1] [sgdfc:1.6.4.3.3.0.3.4.0:4.8:2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4369	13679061_c1_7	5118	19221	945	315	YOL004W	288	3.2(10)-41	Saccharomyces cerevisiae	[ui:yo!004w] [pn:transcription regulatory protein:paired amphipathic helix protein] [gn:sin3:sd1:ume4:rpdi:gam2] [gicfc:10.1:10.2:12.15:12.8:12.9] [keggfc:13.1] [sgdfc:1.6.4.3.3.0.3.4.0:4.8:2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4369	25866430_c2_10	5119	19222	585	195	YOL004W	173	1.1(10)-11	Saccharomyces cerevisiae	[ui:yo!004w] [pn:transcription regulatory protein:paired amphipathic helix protein] [gn:sin3:sd1:ume4:rpdi:gam2] [gicfc:10.1:10.2:12.15:12.8:12.9] [keggfc:13.1] [sgdfc:1.6.4.3.3.0.3.4.0:4.8:2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2417	35188800_3_2	5120	19223	771	257	YOL001W	288	1.8(10)-25	Saccharomyces cerevisiae	[ui:yo!001w] [pn:cyclin:phosphate system cyclin pho80] [gn:pho80:upp7:o2505:unb293] [gicfc:10.1:10.2:12.8:13.10] [keggfc:13.2][sgdfc:1.4:2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4252	23832562_c1_7	5121	19224	2676	892	YCR038C	631	1.3(10)-80	Saccharomyces cerevisiae	[ui:yor038c] [pn:histone transcription regulator:histone transcription regulator 2] [gn:hir2.or26] [gtfc:10.1:10.2] [keggc:1.4.2] [sgdc:4.8.2:9.5:0] [db:gic-saccharomyces cerevisiae]
CONTIG5125	817965_c2_13	5122	19225	321	107	YCR039W	135	6.5(10)-9	Saccharomyces cerevisiae	[ui:yor039w] [pn:casein kinase ii beta" chain cik ii] [gn:ckb2.or26] [gtfc:10.1:10.2:12.13] [ec:2.7.1.37] [keggfc:14.1] [sgdfc:4.7.0:9.5:0:15.0:0] [db:gic-saccharomyces cerevisiae]
CONTIG5125	16839061_c2_12	5123	19226	450	150	YOR039W	357	8.8(10)-33	Saccharomyces cerevisiae	[ui:yor039w] [pn:casein kinase ii beta" chain cik ii] [gn:ckb2.or26] [gtfc:10.1:10.2:12.13] [ec:2.7.1.37] [keggfc:14.1] [sgdfc:4.7.0:9.5:0:15.0:0] [db:gic-saccharomyces cerevisiae]
CONTIG1954	898453_c3_9	5124	19227	762	254	YOR048C	188	1.6(10)-13	Saccharomyces cerevisiae	[ui:yor048c] [pn:5"-3" exoribonuclease:ribonucleic acid trafficking protein 1] [gn:rat1.hke1:tap1] [gtfc:10.1:10.2:10.3:14.1] [ec:3.1.1.1] [keggfc:14.1] [sgdfc:4.2.0:8.1:0:9.5:0] [db:gic-saccharomyces cerevisiae]
CONTIG3145	17032156_c3_5	5125	19228	549	183	YOR048C	395	1.2(10)-35	Saccharomyces cerevisiae	[ui:yor048c] [pn:5"-3" exoribonuclease:ribonucleic acid trafficking protein 1] [gn:rat1.hke1:tap1] [gtfc:10.1:10.2:10.3:14.1] [ec:3.1.1.1] [keggfc:14.1] [sgdfc:4.2.0:8.1:0:9.5:0] [db:gic-saccharomyces cerevisiae]

CONTIG3505	191557_c1_4	5126	19229	513	171	YOR058C	130	2.1(10)-7	Saccharomyces cerevisiae	[ui:yor058c] [pn:microtubule-associated protein:nonmotor:anaphase spindle elongation protein] [gnase1] [gfcfc:10.1:10.2:12.16:12.8] [keggfc:14.2] [sgdfc:3.8:0.9:3.0:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG4199	6024011_f3_2	5127	19230	1869	623	YCR058C	313	8.3(10)-25	Saccharomyces cerevisiae	[ui:yor058c] [pn:microtubule-associated protein:nonmotor:anaphase spindle elongation protein] [gnase1] [gfcfc:10.1:10.2:12.16:12.8] [keggfc:14.2] [sgdfc:3.8:0.9:3.0:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG5406	6646925_c2_11	5128	19231	1002	334	YOR061W	1148	1.3(10)-116	Saccharomyces cerevisiae	[ui:yor061w] [pn:casein kinase ii "alpha" chain:casein kinase ii, alpha" chain:ck ii] [gfcfc:10.1:10.2:12.13:12.8] [ec:2.7.1.37] [keggfc:14.1] [sgdfc:3.8:0.4:7.0:9.5:0:15.0] [db:gic:saccharomyces cerevisiae]
CONTIG4701	23925327_c1_5	5129	19232	1974	658	YOR113W	477	1.5(10)-54	Saccharomyces cerevisiae	[ui:yor113w] [pn:asparagine-rich zinc finger protein:asparagine-rich zinc finger protein azf1] [gn:azf1_03244:yor3244w] [gfcfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.12:0.9:5.0] [db:gic-saccharomyces cerevisiae]

CONTIG3490	4140650_B3_3	5130	19233	2097	699	YOR140W	239	3.0(10)-22	Saccharomyces cerevisiae	[ui:yor140w] [pn:transcription factor:flocculation suppression protein:sfl1 protein] [gn:sfl1:yor3339w] [gicfc:10.1:10.2] [keggc:14.2] [sgdfc:4.8:2.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4557	9925880_c1_5	5131	19234	1086	362	YOR140W	195	1.2(10)-19	Saccharomyces cerevisiae	[ui:yor140w] [pn:transcription factor:flocculation suppression protein:sfl1 protein] [gn:sfl1:yor3339w] [gicfc:10.1:10.2] [keggc:14.2] [sgdfc:4.8:2.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG1476	1067693_f1_1	5132	19235	522	174	YOR194C	128	5.5(10)-8	Saccharomyces cerevisiae	[ui:yor194c] [pn:tfia subunit:transcription initiation factor, 32 kci:transcription initiation factor, 32 kci:iia large chain tfia 32 kd subunit] [gn:toa1] [gicfc:10.1:10.2] [keggc:14.2] [sgdfc:4.8:1.9:5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5758	14647127_c1_16	5133	19236	894	298	YOR194C	128	2.7(10)-18	Saccharomyces cerevisiae	[ui:yor194c] [pn:tfia subunit:transcription initiation factor, 32 kci:transcription initiation factor, 32 kci:iia large chain tfia 32 kd subunit] [gn:toa1] [gicfc:10.1:10.2] [keggc:14.2] [sgdfc:4.8:1.9:5.0] [db:gic-saccharomyces cerevisiae]

CONTIG5473	3947177_c1_7	5134	19237	222	74	YOR210W	313	4.0(10)-28	Saccharomyces cerevisiae	[ui:yor210w] [pn:dna-directed polymerase i, ii, iii 8.3 subunit:dna-directed dna polymerases i, ii, and iii 8.3 kd polypeptide:abc10-beta:abc8] [gn:rpb10] [gicfc:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.1:0.4:4.0:4.8:1.9.5.0] [db:gic-sa]
CONTIG4882	4867926_c2_9	5135	19238	1956	652	YOR217W	941	2.1(10)-128	Saccharomyces cerevisiae	[ui:yor217w] [pn:dna replication factor c, 95 kd subunit:activator 1 95 kd subunit:replication factor c 95 kd subunit:cell division control protein 44] [gn:rfl1:cdc44:yor50-7] [gicfc:10.1:0.2:10.8:12.8] [keggfc:14.2] [sgdfc:3.6:0.3.8]
CONTIG2108	26441302_f2_2	5136	19239	183	61	YOR257W	96	4.0(10)-5	Saccharomyces cerevisiae	[ui:yor257w] [pn:spindle pole body component, centrin:cell division control protein 3.11 [gn:cdc31:dsk1] [gicfc:10.1:0.2:12.8] [keggfc:14.2] [sgdfc:3.8:0.9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG1967	32440881_c3_2	5137	19240	1044	348	YOR290C	118	0.0011	Saccharomyces cerevisiae	[ui:yor290c] [pn:component of swi2:snf global transcription activator complex:transcription regulatory protein snf2:swi2/snf complex component snf2:regulatory protein swi2:regulatory protein gam1:transcription factor tye3] [gn:snf2:swi2:]

CONTIG4757	23672202_c3_7	5138	19241	861	287	YOR290C	313	1.6(10)-26	Saccharomyces cerevisiae	[ui:yor290c] [pn:component of swi/snf global transcription activator complex:transcription regulatory protein snf2:swi/snf complex component snf2:regulatory protein swi2:regulatory protein gam1 :transcription factor tye3] [gn:snf2:swi2:]
CONTIG5776	548153_f3_17	5139	19242	2940	980	YOR290C	1235	3.8(10)-129	Saccharomyces cerevisiae	[ui:yor290c] [pn:component of swi/snf global transcription activator complex:transcription regulatory protein snf2:swi/snf complex component snf2:regulatory protein swi2:regulatory protein gam1 :transcription factor tye3] [gn:snf2:swi2:]
CONTIG151	17037564_c1_1	5140	19243	588	196	YOR290C	745	1.3(10)-72	Saccharomyces cerevisiae	[ui:yor290c] [pn:component of swi/snf global transcription activator complex:transcription regulatory protein snf2:swi/snf complex component snf2:regulatory protein swi2:regulatory protein gam1 :transcription factor tye3] [gn:snf2:swi2:]

CONTIG1781	35283264_c1_3	5141	19244	678	226	YOR290C	659	2.1(10)-63	Saccharomyces cerevisiae	[ui:yor290c] [pn:component of swi/snf global transcription activator complex;transcription regulatory protein snf2:swi/snf complex component snf2:regulatory protein swi2:regulatory protein gam1:transcription factor tye3] [gn:snf2:swi2:
CONTIG3991	14095056_c2_9	5142	19245	807	269	YOR319W	393	1.3(10)-36	Saccharomyces cerevisiae	[ui:yor319w] [pn:similarity to human sap49 and ma-binding proteins] [gn:hsh49] [gicfc:10.1:10.2:10.9] [keggfc:14.2] [sgdfc:4.10.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG1988	5250758_c2_2	5143	19246	1767	589	YOR337W	187	3.2(10)-11	Saccharomyces cerevisiae	[ui:yor337w] [pn:ty1 enhancer activator] [gn:teal:06237] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3818	23866327_c3_3	5144	19247	1383	461	YOR337W	460	4.9(10)-51	Saccharomyces cerevisiae	[ui:yor337w] [pn:ty1 enhancer activator] [gn:teal:06237] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4425	4797183_c1_9	5145	19248	822	274	YOR344C	209	4.2(10)-17	Saccharomyces cerevisiae	[ui:yor344c] [pn:basic helix-loop-helix transcription factor;serine-rich protein tye7:basic-helix-loop-helix protein sgcl] [gn:tye7_sgcl:06233] [gicfc:10.1:10.2:12.13] [keggfc:1.4.2] [sgdfc:1.5.2:4.8.2:9.5.0] [db:gic-saccharomyces cere

CONTIG5154	33787535_c2_14	5146	19249	1164	388	YOR358W	403	1.2(10)-37	Saccharomyces cerevisiae	[ui:yor358w] [pn:ccat-binding factor subunit] [gn:hap5] [gtfc:10.1:10.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5815	12588150_f1_3	5147	19250	633	211	YPL248C	240	3.7(10)-19	Saccharomyces cerevisiae	[ui:yp1248c] [pn:transcription factor:regulatory protein] [gn:ga14] [gtfc:10.1:10.2:12.13] [keggfc:14.2] [sgdfc:1.5.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2382	31275181_f1_1	5148	19251	1464	488	YPL190C	244	1.1(10)-17	Saccharomyces cerevisiae	[ui:yp1190c] [pn:polyadenylated rna-binding protein:nuclear polyadenylated rna-binding protein] [gn:nab3] [gtfc:10.1:10.2:10.9] [keggfc:14.2] [sgdfc:4.10.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5737	15709528_f3_10	5149	19252	1086	362	YPL177C	191	4.7(10)-15	Saccharomyces cerevisiae	[ui:yp1177c] [pn:copper homeostasis protein:homeobox protein] [gn:cup9] [gtfc:10.1:10.2:12.6:12.8] [keggfc:13..1] [sgdfc: 1.8.1:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1448	1432316_f1_1	5150	19253	1518	506	YPL128C	265	8.4(10)-47	Saccharomyces cerevisiae	[ui:yp1128c] [pn:telomere ittaggg repeat-binding factor 1:tbfl 1:tbfl alpha] [gtfc:10.1:10.2] [keggfc:14.2] [sgdfc:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]

b1x18204.x	23484431_c1_3	5151	19254	786	262	YPL089C	240	9.5(10)-23	Saccharomyces cerevisiae	[ui:yp 089c] [pn:transcription factor of the mads box family] [gn:rlm1] [gicfc:10.1:10.2:12.13:12.8] [keggfc:14.2] [sgdfc:4.8.2:9.5.0:10.2.7] [db:gic-saccharomyces cerevisiae]
CONTIG3080	34072192_f3_1	5152	19255	693	231	YPL082C	313	1.8(10)-26	Saccharomyces cerevisiae	[ui:yp 082c] [pn:transcriptional accessory protein:probable helicase mot1] [gn:rnmt1:lpf4c] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3375	12689587_c2_5	5153	19256	1887	629	YPL082C	1301	2.5(10)-132	Saccharomyces cerevisiae	[ui:yp 082c] [pn:transcriptional accessory protein:probable helicase mot1] [gn:rnmt1:lpf4c] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG3509	31927007_f1_1	5154	19257	1662	554	YPL082C	1636	1.8(10)-179	Saccharomyces cerevisiae	[ui:yp 082c] [pn:transcriptional accessory protein:probable helicase mot1] [gn:rnmt1:lpf4c] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG800	19586568_f2_1	5155	19258	813	271	YPL082C	159	5.0(10)-9	Saccharomyces cerevisiae	[ui:yp 082c] [pn:transcriptional accessory protein:probable helicase mot1] [gn:rnmt1:lpf4c] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]

b2x17437.y	22928188_c2_4	5156	19259	633	211	YPL082C	570	7.7(10)-54	Saccharomyces cerevisiae	[ui:yp[082c] [pn:transcriptional accessory protein;probable helicase mot1] [gn:mot1:lpf4c] [gtfc:10.1:10.2] [keggfc:14.2] [sgfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4110	4017182_f3_3	5157	19260	2280	760	YPL043W	1153	2.2(10)-150	Saccharomyces cerevisiae	[ui:yp[043w] [pn:nucleolar protein;nucleolar protein nop77] [gn:nop4:nop77] [gtfc:10.1:10.2:10.3] [keggfc:14.2] [sgfc:4.2.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5317	9772711_c2_14	5158	19261	312	104	YPL022W	143	1.1(10)-8	Saccharomyces cerevisiae	[ui:yp[022w] [pn:component of the nucleotide excision repairosome:dna repair protein] [gn:rad1] [gtfc:10.1:10.10:10.2] [keggfc:14.2] [sgfc:9.5:0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5317	33789687_c2_13	5159	19262	2595	865	YPL022W	1059	3.6(10)-107	Saccharomyces cerevisiae	[ui:yp[022w] [pn:component of the nucleotide excision repairosome:dna repair protein] [gn:rad1] [gtfc:10.1:10.10:10.2] [keggfc:14.2] [sgfc:9.5:0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3345	25478402_c1_7	5160	19263	1557	519	YPL016W	164	4.2(10)-13	Saccharomyces cerevisiae	[ui:yp[016w] [pn:component of swi/snf global transcription regulatory protein adr6:swi/swi complex component adr6:regulatory protein swi:regulatory protein gam3] [gn:adr6:swi1:gam3] [gtfc:10.1:10.2:12.

CONTIG4649	4003906_c1_6	5161	19264	1470	490	YPL016W	186	7.0(10)-11	Saccharomyces cerevisiae	[ui:yp1016w] [pn:component of swi/snf global transcription activator complex:transcription regulatory protein adr6:swi/snf complex component adr6:regulatory protein swi1:regulatory protein gam3] [gn:adr6:swi1:gam3] [gicfc:10.1:10.2:12.
CONTIG4345	4710926_c2_9	5162	19265	813	271	YPL008W	277	4.0(10)-41	Saccharomyces cerevisiae	[ui:yp1008w] [pn:protein of the dead box family:ch11 protein] [gn:ch11:ctf1:yp8132] [gicfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4413	1054567_f2_1	5163	19266	1227	409	YPL008W	722	1.8(10)-71	Saccharomyces cerevisiae	[ui:yp1008w] [pn:protein of the dead box family:ch11 protein] [gn:ch11:ctf1:yp8132] [gicfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4413	26585900_f3_3	5164	19267	231	77	YPL008W	181	7.2(10)-13	Saccharomyces cerevisiae	[ui:yp1008w] [pn:protein of the dead box family:ch11 protein] [gn:ch11:ctf1:yp8132] [gicfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4413	23882316_f2_2	5165	19268	216	72	YPL008W	140	1.8(10)-8	Saccharomyces cerevisiae	[ui:yp1008w] [pn:protein of the dead box family:ch11 protein] [gn:ch11:ctf1:yp8132] [gicfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG5575	29495216_c1_11	5166	19269	1212	404	YPL001W	634	3.8(10)-62	Saccharomyces cerevisiae	[ui:yp1001w] [pn:histone acetyltransferase subunit] [gn:hat1] [gicfc:10.1:10.2:10.7] [keggfc:14.2] [sgdfc:6.3:0.9:2.0:9.5:0] [db:gic-saccharomyces cerevisiae]
CONTIG4598	4726387_f3_4	5167	19270	1125	375	YPR025C	466	2.5(10)-44	Saccharomyces cerevisiae	[ui:yp025c] [pn:tfifh subunit:transcription initiation factor, cyclin c component:cyclin ccl1] [gn:ccl1:yp024c:yp9367] [gicfc:10.1:10.10:10.2:12.8] [keggfc:14.2] [sgdfc:3.8:0.4:8.1:9.5:0:11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG1927	24406550_c3_8	5168	19271	276	92	YPR052C	245	6.5(10)-21	Saccharomyces cerevisiae	[ui:yp052c] [pn:nonhistone chromosomal protein related to mammalian hmg1:nonhistone chromosomal protein 6a] [gn:nhp6a:nhp49a:yp9499] [gicfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.1:0.3:2.0:9.5:0:9.6:0] [db:gic-saccharomyces cerevisiae]
CONTIG5403	31875_c2_7	5169	19272	765	255	YPR057W	109	0.001	Saccharomyces cerevisiae	[ui:yp057w] [pn:involved in snrnp biogenesis] [gn:brr] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.9:0.9:5.0] [db:gic-saccharomyces cerevisiae]

CONTIG5251	167182_c3_19	5170	19273	1857	619	YPR065W	258	2.7(10)-22	Saccharomyces cerevisiae	[ui:yp063w] [pn:heme-dependent transcriptional repressor of hoxic genes:rox1 repressor:hoxic function repressor:heme-dependent repression factor] [gn:rox1:yp9499] [gicfc:10.1:10.2:12.13:12.8] [keggfc:13.1] [sgdfc:1.7.3.4.8.2.9.5]
CONTIG5217	9960077_f3_8	5171	19274	426	142	YPR086W	339	7.0(10)-31	Saccharomyces cerevisiae	[ui:yp086w] [pn:tfiib subunit:transcription initiation factor, factor e:transcription initiation factor iib:tfiib:transcription factor e] [gn:sua7:p9513] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.1:9.5.0] [db:gic-saccharomyces cerev]
CONTIG5414	34187502_c3_9	5172	19275	564	188	YPR086W	316	1.8(10)-28	Saccharomyces cerevisiae	[ui:yp086w] [pn:tfiib subunit:transcription initiation factor, factor e:transcription initiation factor iib:tfiib:transcription factor e] [gn:sua7:p9513] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.1:9.5.0] [db:gic-saccharomyces cerev]
CONTIG5728	13705008_c2_18	5173	19276	1056	352	YPR086W	919	2.5(10)-92	Saccharomyces cerevisiae	[ui:yp086w] [pn:tfiib subunit:transcription initiation factor, factor e:transcription initiation factor iib:tfiib:transcription factor e] [gn:sua7:p9513] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.1:9.5.0] [db:gic-saccharomyces cerev]

CONTIG4832	34410427_f3_3	5174	19277	3018	1006	YPR104C	363	1.2(10)-50	Saccharomyces cerevisiae	[ui:yp104c] [pn:transcriptional activator of the forkhead/hnf3 family:pre-rna processing protein flh1] [gn:flh1:p8283]
CONTIG952	11893830_f1_1	5175	19278	825	275	YPR104C	365	1.7(10)-32	Saccharomyces cerevisiae	[ui:yp104c] [pn:transcriptional activator of the forkhead/hnf3 family:pre-rna processing protein flh1] [gn:flh1:p8283]
CONTIG5127	4382687_c3_9	5176	19279	2430	810	YPR135W	499	8.3(10)-75	Saccharomyces cerevisiae	[ui:yp135w] [pn:dna-directed dna polymerase alpha-binding protein:dnab polymerase alpha-binding protein chl15] [gn:pob1:chl15:p9659]
CONTIG5789	5917193_f2_7	5177	19280	1002	334	YPR141C	882	2.0(10)-88	Saccharomyces cerevisiae	[ui:yp141c] [pn:kinesin-related protein:kinesin-like protein kar3:nuclear fusion protein] [gn:kar3:p9659]

CONTIG3097	36047827_f3_1	5178	19281	513	171	YPR168W	306	2.2(10)-27	Saccharomyces cerevisiae	[ui:yp168w] [pn:negative regulator of ho endonuclease] [gr:nut2] [gtcfc:10.1:10.2:12.9] [keggfc:14.2] [sgdfc:3.3.0:4.8:2.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG393	23425906_c2_4	5179	19282	687	229	YPR162C	96	0.039	Saccharomyces cerevisiae	[ui:yp162c] [pn:origin recognition complex, 56 kd subunit.origin recognition complex protein, subunit 3:origin recognition complex protein 56 kd subunit] [gn:orc4,p9325] [gtcfc:10.1:10.2:10.8:12.8:12.9] [keggfc:13.2] [sgdfc:3.3.0:3.6] [sgdfc:4.9:6.4:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3767	26353552_c3_4	5180	19283	963	321	YPR178W	289	4.7(10)-45	Saccharomyces cerevisiae	[ui:yp178w] [pn:u4/u6 snmp 52 kd protein.u4/u6 small nuclear ribonucleoprotein prp4] [gn:prp4,rmad:p9705] [gtcfc:10.1:10.2:12.16] [keggfc:14.2] [sgdfc:4.9:6.4:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3767	22054712_c2_3	5181	19284	465	155	YPR178W	98	6.0(10)-8	Saccharomyces cerevisiae	[ui:yp178w] [pn:u4/u6 snmp 52 kd protein.u4/u6 small nuclear ribonucleoprotein prp4] [gn:prp4,rmad:p9705] [gtcfc:10.1:10.2:12.16] [keggfc:14.2] [sgdfc:4.9:6.4:0.9:5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG408	12671961_c1_4	5182	19285	378	126	YPR182W	215	9.8(10)-18	Saccharomyces cerevisiae	[ui:ypri182w] [pn:surna-associated protein of the sm family:small nuclear ribonucleoprotein like protein smx3] [gn:smx3;wp9705] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.9.0;9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2830	6672151_f1_1	5183	19286	396	132	YPR182W	136	2.2(10)-9	Saccharomyces cerevisiae	[ui:ypri182w] [pn:surna-associated protein of the sm family:small nuclear ribonucleoprotein like protein smx3] [gn:smx3;wp9705] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.9.0;9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2486	289003_c1_7	5184	19287	627	209	YPR186C	137	4.2(10)-14	Saccharomyces cerevisiae	[ui:ypri186c] [pn:transcription initiation factor:transcription factor iiiia;tfiiia] [gn:tfic2;pfzfl:tfiiia;p9677] [gtcfc:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.1.0;4.4.0;9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4935	21663962_c2_6	5185	19288	426	142	YPR186C	96	0.0014	Saccharomyces cerevisiae	[ui:ypri186c] [pn:transcription initiation factor:transcription factor iiiia;tfiiia] [gn:tfic2;pfzfl:tfiiia;p9677] [gtcfc:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.1.0;4.4.0;9.5.0] [db:gtc-saccharomyces cerevisiae]

b9x10d47.x	2557307_f2_1	5186	19289	462	154	YPR186C	357	8.8(10)-33	Saccharomyces cerevisiae	[ui:yp186c] [pn:transcription initiation factor:transcription factor iiiia:tfiiia] [gn:tfc2:pfzf1:tfiiia:p9677] [gicfc:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.1.0.4.4.0.9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG2145	25395386_f1_1	5187	19290	1092	364	YPR189W	94	0.28	Saccharomyces cerevisiae	[ui:yp189w] [pn:antiviral protein:superkiller 3 protein] [gn:ski3] [gicfc:10.1:10.2:12.14] [keggfc:14.2] [sgdfc:9.5.0:11.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG5354	14645010_c2_9	5188	19291	2262	754	YPR189W	688	5.0(10)-101	Saccharomyces cerevisiae	[ui:yp189w] [pn:antiviral protein:superkiller 3 protein] [gn:ski3] [gicfc:10.1:10.2:12.14] [keggfc:14.2] [sgdfc:9.5.0:11.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG4566	10642129_c1_3	5189	19292	1830	610	YPR189W	851	3.2(10)-84	Saccharomyces cerevisiae	[ui:yp189w] [pn:antiviral protein:superkiller 3 protein] [gn:ski3] [gicfc:10.1:10.2:12.14] [keggfc:14.2] [sgdfc:9.5.0:11.7.0] [db:gic-saccharomyces cerevisiae]
CONTIG1907	4484389_c1_2	5190	19293	1557	519	YPR196W	152	6.5(10)-8	Saccharomyces cerevisiae	[ui:yp196w] [pn:strong similarity to regulatory protein mal63 p:maltoose fermentation regulatory protein mal6r] [gn:mal6r:mal63] [gicfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG4799	35183443_c1_6	5191	19294	2370	790	YBL088C	131	2.1(10)-10	Saccharomyces cerevisiae	[uri:ybl088c] [pn:telomere length control protein:telomer length regulation protein tel1] [gn:tel1;ybl0706] [grcfc:10.1] [keggfc:14.2] [sgdfc:9.6.0] [db:gic-saccharomyces cerevisiae]
CONTIG4943	12594443_f3_1	5192	19295	2400	800	YBL088C	889	1.8(10)-87	Saccharomyces cerevisiae	[uri:ybl088c] [pn:telomere length control protein:telomer length regulation protein tel1] [gn:tel1;ybl0706] [grcfc:10.1] [keggfc:14.2] [sgdfc:9.6.0] [db:gic-saccharomyces cerevisiae]
CONTIG5480	19550937_f3_4	5193	19296	555	185	YBL088C	112	0.00209	Saccharomyces cerevisiae	[uri:ybl088c] [pn:telomere length control protein:telomer length regulation protein tel1] [gn:tel1;ybl0706] [grcfc:10.1] [keggfc:14.2] [sgdfc:9.6.0] [db:gic-saccharomyces cerevisiae]
CONTIG5480	10160093_f1_2	5194	19297	2844	948	YBL088C	108	0.00077	Saccharomyces cerevisiae	[uri:ybl088c] [pn:telomere length control protein:telomer length regulation protein tel1] [gn:tel1;ybl0706] [grcfc:10.1] [keggfc:14.2] [sgdfc:9.6.0] [db:gic-saccharomyces cerevisiae]
CONTIG5236	26564680_c1_8	5195	19298	1344	448	YBR195C	603	7.5(10)-59	Saccharomyces cerevisiae	[uri:ybr195c] [pn:chromatin assembly complex, subunit p50/msl protein:ira1 multicopy suppressor] [gn:msl1;yer1405] [grcfc:10.1;10.2;10.8;12.13;12.16] [keggfc:14.2] [sgdic:3.6.0;4.8.3;6.4.0;9.6.0;10.4.5] [db:gic-saccharomyces cerevisiae]

CONTIG5540	1368887_f3_11	5196	19299	525	175	YDL208W	481	6.4(10)-46	Saccharomyces cerevisiae	[ui:ydl208w] [pn:strong similarity to high mobility group-hmg family:high mobility group-like nuclear protein 2] [gn:nhp2:d1045] [lgcfc: 10.1:10.4] [keggc:14.2] [sgdfc:5.1:0.9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2920	32658177_f1_1	5197	19300	882	294	YDL002C	263	4.2(10)-30	Saccharomyces cerevisiae	[ui:ydl002c] [pn:non-histone protein] [gn:hmo2] [gtcfc:10.1] [keggfc:14.2] [sgdfc:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4371	10285206_c1_6	5198	19301	1203	401	YDR174W	141	8.5(10)-15	Saccharomyces cerevisiae	[ui:ydr174w] [pn:non-histone protein] [gn:hmo1] [gtcfc:10.1] [keggfc:14.2] [sgdfc:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5258	24242255_c3_12	5199	19302	402	134	YEL026W	505	1.8(10)-48	Saccharomyces cerevisiae	[ui:yel026w] [pn:strong similarity to high mobility group-like protein nhp2p:putative 60s ribosomal protein yel026w] [gtcfc:10.1:10.4] [keggfc:14.2] [sgdfc:5.1:0.9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1876	19531250_c1_3	5200	19303	618	206	YER159C	249	2.3(10)-21	Saccharomyces cerevisiae	[ui:yer159c] [pn:functional homolog of human n2alpha:hypothetical 15.5 kd protein in bem2-spi2 intergenic region] [gn:bun6] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2.9.6.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5754	9804627_f3_15	5201	19304	1734	578	YFR037C	614	3.2(10)-75	Saccharomyces cerevisiae	[ui:yft037c] [pn:subunit of the rsc complex:hypothetical 63.2 kd protein in cdc26-sap155 intergenic region] [gn:rsc8] [gtfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0:4.8.2:4.8.3:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4529	2775952_f1_3	5202	19305	1365	455	YGL194C	1506	1.5(10)-154	Saccharomyces cerevisiae	[ui:ygl194c] [pn:putative deacetylase:hypothetical 51.5 kd protein in gcn1-spo8 intergenic region] [gn:rtr1:g1330] [gtfc:10.1:10.2:10.7] [keggfc:14.2] [sgdfc:4.8.3:6.3.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5809	23834450_c1_16	5203	19306	1164	388	YGL194C	398	4.0(10)-37	Saccharomyces cerevisiae	[ui:ygl194c] [pn:putative deacetylase:hypothetical 51.5 kd protein in gcn1-spo8 intergenic region] [gn:rtr1:g1330] [gtfc:10.1:10.2:10.7] [keggfc:14.2] [sgdfc:4.8.3:6.3.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4405	23657050_c1_4	5204	19307	282	94	YGR187C	156	9.5(10)-11	Saccharomyces cerevisiae	[ui:ygr187c] [pn:weak similarity to human hmg1p and hmg2p:hgh1 protein] [gn:hgh1:g7538] [gtfc:0.1] [keggfc:14.2] [sgdfc:9.6.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5063	11765627_13_7	5205	19308	540	180	YGR187C	326	1.7(10)-29	Saccharomyces cerevisiae	[ui:ygr187c] [pn:weak similarity to human hmg1p and hmg2p:hgh1 protein] [gn:hgh1:gi:7538] [gicfc:10.1] [keggfc:14.2] [sgdfc:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2392	417703_c2_3	5206	19309	291	97	YGR218W	220	6.7(10)-17	Saccharomyces cerevisiae	[ui:ygr218w] [pn:chromosome region maintenance protein:chromosome region maintenance protein 1] [gn:crm1-g8514] [gicfc:10.1] [keggfc:14.2] [sgdfc:9.6.0] [db:gic-saccharomyces cerevisiae]
CONTIG2649	21535175_c3_7	5207	19310	1716	572	YGR218W	1870	4.0(10)-193	Saccharomyces cerevisiae	[ui:ygr218w] [pn:chromosome region maintenance protein:chromosome region maintenance protein 1] [gn:crm1-g8514] [gicfc:10.1] [keggfc:14.2] [sgdfc:9.6.0] [db:gic-saccharomyces cerevisiae]
CONTIG4726	26594678_c2_5	5208	19311	378	126	YGR218W	344	3.8(10)-30	Saccharomyces cerevisiae	[ui:ygr218w] [pn:chromosome region maintenance protein:chromosome region maintenance protein 1] [gn:crm1-g8514] [gicfc:10.1] [keggfc:14.2] [sgdfc:9.6.0] [db:gic-saccharomyces cerevisiae]
CONTIG2558	14554537_c3_4	5209	19312	1476	492	YJL074C	152	3.7(10)-7	Saccharomyces cerevisiae	[ui:yj074c] [pn:required for structural maintenance of chromosomes:hypothetical 141.3 kd protein in sep160-mpf18 intergenic region] [gn:smc3_jl049] [gicfc:10.1;12.8] [keggfc:14.2] [sgdfc:3.8.0;9.6.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5286	13953792_f1_1	5210	19313	3522	1174	YJL074C	1049	5.5(10)-171	Saccharomyces cerevisiae	[ui:yyj074c] [pn:required for structural maintenance of chromosomes: hypothetical 141.3 kd protein in scf160-mpf8 intergenic region] [gn:rsmc3;j:1049] [gtfc:10.1:12.8] [keggfc:14.2] [sgdfc:3.8.0.9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5470	22383430_c1_8	5211	19314	603	201	YKR048C	289	1.3(10)-25	Saccharomyces cerevisiae	[ui:ykf048c] [pn:nucleosome assembly protein i:nucleosome assembly protein] [gn:map1] [gtfc:10.1:12.16;12.8] [keggfc:14.2] [sgdfc:3.8.0.6.4.0.9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5416	21502177_c3_15	5212	19315	1080	360	YLR321C	314	3.2(10)-28	Saccharomyces cerevisiae	[ui:ylr321c] [pn:subunit of the rsc complex] [gn:sfn1] [gtfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0.4.8.2.4.8.3.9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5399	9851537_c1_11	5213	19316	1446	482	YML102W	578	3.3(10)-56	Saccharomyces cerevisiae	[ui:yml102w] [pn:chromatin assembly complex, subunit p60] [gn:cac2] [gtfc:10.1:10.2:10.8:12.16] [keggfc:14.2] [sgdfc:3.6.0.4.8.3.6.4.0.9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5164	15117178_c1_6	5214	19317	291	97	YOR213C	180	5.0(10)-14	Saccharomyces cerevisiae	[ui:yor213c] [pn:subunit of the rsc complex] [gtfc:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0.4.8.2.4.8.3.9.6.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5335	10553175_c1_7	5215	19318	597	199	YPL254W	94	0.00069	Saccharomyces cerevisiae	[ui:yp1254w] [pn:interacts functionally with histone h2a] [gn:hfi1] [gtcfc:10.1] [keggfc:14.2] [sgdfc:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4964	5901551_f1_3	5216	19319	447	149	YPL127C	144	6.0(10)-10	Saccharomyces cerevisiae	[ui:yp1127c] [pn:histone h1 protein:histone h1-like protein] [gn:hho1:ipi17c] [gtcfc:10.1:12.8] [keggfc:13.3] [sgdfc:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1370	16596905_c3_1	5217	19320	504	168	YPR018W	101	0.0051	Saccharomyces cerevisiae	[ui:yp018w] [pn:chromatin assembly complex, subunit p90] [gn:rif2] [gtcfc:10.1:10.2:10.8:12.16] [keggfc:14.2] [sgdfc:3.6.0:4.8.3:6.4.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3073	239062_c2_4	5218	19321	1266	422	YPR018W	188	2.8(10)-12	Saccharomyces cerevisiae	[ui:yp018w] [pn:chromatin assembly complex, subunit p90] [gn:rif2] [gtcfc:10.1:10.2:10.8:12.16] [keggfc:14.2] [sgdfc:3.6.0:4.8.3:6.4.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2829	23601500_c2_5	5219	19322	702	234	YDR002W	531	5.5(10)-61	Saccharomyces cerevisiae	[ui:ydr002w] [pn:ran-specific gtpase-activating protein:ran binding protein 1] [homolog:ranbp1]:perinuclear array-localised protein [gn:hn1:sfo1:yrb1:cst20:yd8119] [gtcfc:10.1:12.3] [keggfc:14.2] [sgdfc:4.11.0:8.1.0:9.2.0] [db:gtc-sacc

CONTIG1914	23524135_c1_6	5220	19323	258	86	YER110C	231	4.7(10)-18	Saccharomyces cerevisiae	[ui:yer110c] [pn:ran-binding protein:hypothetical 122.6 kd protein in nup157-swi4 intergenic region] [gn:kap123] [gicfc:10.1:12.3] [keggfc:14.2] [sgdfc:4.11.0] [db:gic-saccharomyces cerevisiae]
CONTIG5421	30081437_c1_8	5221	19324	630	210	YER110C	268	5.2(10)-22	Saccharomyces cerevisiae	[ui:yer110c] [pn:ran-binding protein:hypothetical 122.6 kd protein in nup157-swi4 intergenic region] [gn:kap123] [gicfc:10.1:12.3] [keggfc:14.2] [sgdfc:4.11.0] [db:gic-saccharomyces cerevisiae]
CONTIG5421	26595180_c2_11	5222	19325	2253	751	YER110C	1589	2.5(10)-163	Saccharomyces cerevisiae	[ui:yer110c] [pn:ran-binding protein:hypothetical 122.6 kd protein in nup157-swi4 intergenic region] [gn:kap123] [gicfc:10.1:12.3] [keggfc:14.2] [sgdfc:4.11.0] [db:gic-saccharomyces cerevisiae]
CONTIG3475	23438412_c2_6	5223	19326	615	205	YIR011C	140	3.3(10)-9	Saccharomyces cerevisiae	[ui:yir011c] [pn:required for transport of rna 5p from the cytoplasm to the nucleus:dbf8 protein] [gn:dbf8:ssi1:yib11c] [gicfc:12.3:10.1] [keggfc:14.2] [sgdfc:4.11.0:8.1.0] [db:gic-saccharomyces cerevisiae]

CONTIG384	4492217_c3_4	5224	19327	1062	354	YMR235C	603	7.5(10)-59	Saccharomyces cerevisiae	[ui:ymr235c] [pn:gipase activating protein:ran gipase activating protein 1.protein involved in rna production/processing] [gn:mal:ymr9959] [gtcfc:10.1:10.3:10.6:12.3] [keggfc:14.2] [sgdgc:4.2.0:4.5.0:4.11.0:9.2.0] [db:gtc-saccharomyce]
CONTIG3429	24317187_c2_4	5225	19328	2217	739	YCR160W	1317	1.6(10)-134	Saccharomyces cerevisiae	[ui:yor160w] [pn:involved in rna transport] [gn:mir10] [gtcfc:12.3:10.1] [keggfc:14.2] [sgdgc:4.11.0:8.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4250	11115780_f2_2	5226	19329	564	188	YAL005C	329	4.7(10)-29	Saccharomyces cerevisiae	[ui:yal005c] [pn:heat shock protein of hsp70 family, cytosolic:heat shock protein:heat shock protein yg100] [gn:ssal] [gtcfc:12.7:10.7:13.2] [keggfc:14.2] [sgdgc:6.1.0:6.2.0:8.1.0:9.1.0:9.2.0:1.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3363	5110625_c2_24	5227	19330	1101	367	YBR017C	431	1.3(10)-39	Saccharomyces cerevisiae	[ui:ybr017c] [pn:karyopherin:hypothetical 103.7 kd protein in tip1-gal7 intergenic region] [gn:kap104:ybr017w:ybr0224] [gtcfc:10.1] [keggfc:14.2] [sgdgc:8.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5363	5281253_c1_18	5228	19331	1668	556	YBR017C	423	3.1(10)-66	Saccharomyces cerevisiae	[ui:ybr017c] [pn:karyopherin:hypothetical 103.7 kd protein in ttp1-gal7 intergenic region] [gn:kap 04:ybr017w:ybr0224] [gicfc:0.1] [keggfc:14.2] [sgdfc:8.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1592	30506930_c1_1	5229	19332	741	247	YBR170C	786	3.1(10)-78	Saccharomyces cerevisiae	[ui:ybr170c] [pn:nuclear protein localization factor and er translocation component:pl4 protein] [gn:opl4:ybr1231] [gicfc:0.1:10.7:11.1:12.16] [keggfc:14.2] [sgdfc:6.2.0:8.1.0:8.8.0] [db:gtc-saccharomyces cerevisiae]
b3x18484_y	15642686_c2_1	5230	19333	387	129	YER009W	542	2.2(10)-52	Saccharomyces cerevisiae	[ui:yer009w] [pn:nuclear transport factor:nuclear transport factor 2:ntf-2:nuclear transport factor p10] [gn:ntf2] [gicfc:10.1:12.6] [keggfc:14.2] [sgdfc:8.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3257	3022780_f1_1	5231	19334	1128	376	YIL063C	190	3.5(10)-13	Saccharomyces cerevisiae	[ui:yil063c] [pn:similarity to s.pombe brefeidin a resistance protein and yrb1:p:hypothetical 36.1 kd protein in rnf3-snp1 intergenic region] [gn:yrb2] [gicfc:10.1:11.1] [keggfc:14.2] [sgdfc:8.1.0:9.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2639	25410253_c3_7	5232	19335	243	81	YLR347C	215	1.7(10)-16	Saccharomyces cerevisiae	[ui:ylr347c] [pn:karyopherin-beta] [gn:kap95] [gicfc:10.1:0.7:11.1] [keggfc:14.2] [sgdfc:6.2:0.8:1.0] [db:gic-saccharomyces cerevisiae]
CONTIG2639	7160212_c3_6	5233	19336	261	87	YLR347C	202	4.0(10)-15	Saccharomyces cerevisiae	[ui:ylr347c] [pn:karyopherin-beta] [gn:kap95] [gicfc:10.1:0.7:11.1] [keggfc:14.2] [sgdfc:6.2:0.8:1.0] [db:gic-saccharomyces cerevisiae]
CONTIG5020	37500_c2_10	5234	19337	1239	413	YLR347C	1012	3.3(10)-102	Saccharomyces cerevisiae	[ui:ylr347c] [pn:karyopherin-beta] [gn:kap95] [gicfc:10.1:0.7:11.1] [keggfc:14.2] [sgdfc:6.2:0.8:1.0] [db:gic-saccharomyces cerevisiae]
CONTIG3033	4179755_f1_1	5235	19338	1314	438	YPL174C	188	9.6(10)-16	Saccharomyces cerevisiae	[ui:ypl174c] [pn:nuclear import protein:protein] [gn:nip80] [gicfc:10.1] [keggfc:14.2] [sgdfc:8.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG5689	23484437_f1_2	5236	19339	2472	824	YBR073W	1073	2.6(10)-121	Saccharomyces cerevisiae	[ui:ybr073w] [pn:required for meiosis:hypothetical 108.0 kd helicase in hsp26-secl8 intergenic region] [gn:rdh54:ybr0715] [gicfc:10.10:0.8:12.8] [keggfc:14.2] [sgdfc:3.5.0.3.7.0:11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG3226	13759687_f3_5	5237	19340	1782	594	YDL088C	184	3.2(10)-18	Saccharomyces cerevisiae	[ui:ydl088c] [pn:suppressor of temperature-sensitive mutations in pol3p] [gn:asm4] [gicfc:10.10] [keggfc:14.2] [sgdfc:11.2.1] [db:gic-saccharomyces cerevisiae]

CONTIG2898	10719562_f2_1	5238	19341	576	192	YDR061W	285	1.7(10)-24	Saccharomyces cerevisiae	[ui:ydr061w] [pn:similarity to e.coli modf and photorepair protein phra] [gfcfc:10.10] [keggc:14.2] [sgdfc:11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG3624	4773567_f3_2	5239	19342	918	306	YDR061W	309	3.8(10)-27	Saccharomyces cerevisiae	[ui:ydr061w] [pn:similarity to e.coli modf and photorepair protein phra] [gfcfc:10.10] [keggc:14.2] [sgdfc:11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG1861	24804700_q2_4	5240	19343	633	211	YDR460W	123	2.5(10)-7	Saccharomyces cerevisiae	[ui:ydr460w] [pn:tfih subunit:transcription/repair factor] [gn:tfhb] [gfcfc:10.10:10.2:12.16] [keggfc:14.2] [sgdfc:4.8.1:6.4.0:11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG1861	22275312_c1_3	5241	19344	387	129	YDR460W	391	2.2(10)-36	Saccharomyces cerevisiae	[ui:ydr460w] [pn:tfih subunit:transcription/repair factor] [gn:tfhb] [gfcfc:10.10:10.2:12.16] [keggfc:14.2] [sgdfc:4.8.1:6.4.0:11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG5225	22464786_f2_3	5242	19345	832	284	YEL019C	169	1.6(10)-12	Saccharomyces cerevisiae	[ui:yel019c] [pn:dna repair protein] [gn:mms21] [gfcfc:10.10:10.8] [keggfc:14.2] [sgdfc:3.7:0:11.2.1] [db:gic-saccharomyces cerevisiae]

CONTIG580	179661_f1_2	5243	19346	618	206	YER176W	350	9.4(10)-31	Saccharomyces cerevisiae	[ui:yer176w] [pn: dna dependent atpase/dna helicase b:hypothetical 127.0 kd protein in rad24-bmh1 intergenic region] [gn:sygp-orf61] [gfc:10.10;10.8] [keggc:14.2] [sgdfc:3.6;0.3;7.0;11.2.1] [db:gic- saccharomyces cerevisiae]
CONTIG580	34102067_f1_3	5244	19347	2754	918	YER176W	1340	6.0(10)-137	Saccharomyces cerevisiae	[ui:yer176w] [pn: dna dependent atpase/dna helicase b:hypothetical 127.0 kd protein in rad24-bmh1 intergenic region] [gn:sygp-orf61] [gfc:10.10;10.8] [keggc:14.2] [sgdfc:3.6;0.3;7.0;11.2.1] [db:gic- saccharomyces cerevisiae]
CONTIG55	10198760_f3_1	5245	19348	609	203	YFR038W	589	2.2(10)-57	Saccharomyces cerevisiae	[ui:yfr038w] [pn:strong similarity to mouse lymphocyte specific helicase:hypothetical 88.7 kd helicase in cdc26-sap155 intergenic region] [gfc:10.10] [keggc:14.2] [sgdfc:11.2.1] [db:gic- saccharomyces cerevisiae]
CONTIG440	22273389_c1_2	5246	19349	1224	408	YFR038W	465	1.3(10)-43	Saccharomyces cerevisiae	[ui:yfr038w] [pn:strong similarity to mouse lymphocyte specific helicase:hypothetical 88.7 kd helicase in cdc26-sap155 intergenic region] [gfc:10.10] [keggc:14.2] [sgdfc:11.2.1] [db:gic- saccharomyces cerevisiae]

CONTIG3831	25443877_c3_3	5247	19350	2007	669	YIL128W	498	6.0(10)-53	Saccharomyces cerevisiae	[ui:yil128w] [pn:involved in ncr repair and nra polymerase ii transcription:hypothetical 117.9 kd protein in fkh1-sh1 intergenic region] [gn:met18] [gtcfc:10.10:10.2] [keggfc:14.2] [sgdfc:4.8.1:11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG5589	26439630_c2_16	5248	19351	1602	534	YLR005W	651	1.1(10)-103	Saccharomyces cerevisiae	[ui:ylr005w] [pn:tfih subunit:transcription initiation factor, factor b:suppressor of stem-loop protein 1] [gn:ssl1] [gtcfc:10.10:10.2:10.7] [keggfc:14.2] [sgdfc:4.8.1:5.2.0:11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG1262	984453_c1_6	5249	19352	696	232	YLR288C	124	7.5(10)-9	Saccharomyces cerevisiae	[ui:ylr288c] [pn:g2-specific checkpoint protein] [gn:mec3] [gtcfc:10.10:10.8:12.8] [keggfc:14.2] [sgdfc:3.7.0:3.8:0:11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG1590	24409805_f2_3	5250	19353	915	305	YOL043C	486	1.8(10)-46	Saccharomyces cerevisiae	[ui:yol043c] [pn:endonuclease iii-like glycosylase 2] [gn:nng2] [gtcfc:10.10] [keggfc:14.2] [sgdfc:11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG2962	14641943_c2_4	5251	19354	852	284	YOR206W	809	1.1(10)-80	Saccharomyces cerevisiae	[ui:yor206w] [pn:strong similarity to rad4p:hypothetical 84.4 kd protein in rpe2/ret1 3' region] [gn:yox001] [gtcfc:10.10] [keggfc:14.2] [sgdfc:11.2.1] [db:gic-saccharomyces cerevisiae]

CONTIG5003	13750026_f2_5	5252	19355	915	305	YOR206W	368	3.7(10)-33	Saccharomyces cerevisiae	[ui:yor206w] [pn:strong similarity to rad4p;hypothetical 84.4 kd protein in rpc2/ret1 3'region] [gn:yox001] [gtcfc: 0.10] [keggfc: 14.2] [sgdgc: 11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG5003	12140763_f3_6	5253	19356	567	189	YOR206W	493	4.2(10)-47	Saccharomyces cerevisiae	[ui:yor206w] [pn:strong similarity to rad4p;hypothetical 84.4 kd protein in rpc2/ret1 3'region] [gn:yox001] [gtcfc: 10.10] [keggfc: 14.2] [sgdgc: 11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG5606	6054715_c3_50	5254	19357	1146	382	YOR368W	301	7.5(10)-27	Saccharomyces cerevisiae	[ui:yor368w] [pn:dna damage checkpoint control protein] [gn:rad17] [gtcfc: 10.10;12.8] [keggfc: 14.2] [sgdgc: 3.5.0;3.8.0;11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG5807	860175_c3_23	5255	19358	1524	508	YPL122C	683	2.7(10)-123	Saccharomyces cerevisiae	[ui:ypf122c] [pn:tfih subunit:transcription/repair factor] [gn:tfb2] [gtcfc: 10.10;0.2] [keggfc: 14.2] [sgdgc: 4.8.1;11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG4935	24610337_f3_3	5256	19359	1128	376	YPR056W	453	1.8(10)-64	Saccharomyces cerevisiae	[ui:ypf056w] [pn:component of rna polymerase transcription initiation tfih factor] [gn:tfi1] [gtcfc: 10.10;10.2] [keggfc: 14.2] [sgdgc: 4.8.1;11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG5522	36360905_f1_3	5257	19360	789	263	YGL213C	243	2.1(10)-20	Saccharomyces cerevisiae	[ui:ygl213c] [pn:antiviral protein of the beta-transducin:wd-40 repeat family:antiviral protein] [gn:ski8] [gtcfc: 10.10;12.14] [keggfc: 14.2] [sgdgc: 11.6.0] [db:gic-saccharomyces cerevisiae]

CONTIG5522	4897306_f2_7	5258	19361	495	165	YGL213C	358	6.9(10)-33	Saccharomyces cerevisiae	[ui:ygl213c] [pn:antiviral protein of the beta-transducin:wd-40 repeat family antiviral protein] [gn:ski8] [gcfc:10.10.12.14] [keggfc:14.2] [sgfc:11.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1373	11909444_c2_2	5259	19362	666	222	YBL041W	916	5.0(10)-92	Saccharomyces cerevisiae	[ui:ybl041w] [pn:multicatalytic endopeptidase complex subunit c5] [gn:pr3;pre7;pis1;ybl0407] [gcfc:10.11.14.1] [ec:3.4.99.46] [keggfc:14.1] [sgfc:6.5.1;]
CONTIG643	30350813_f2_1	5260	19363	597	199	YBR058C	382	1.7(10)-34	Saccharomyces cerevisiae	[ui:ybr058c] [pn:ubiquitin specific protease:ubiquitin carboxyl-terminal hydrolase 14;ubiquitin thioesterase 14:ubiquitin-specific processing protease 14;deubiquinating enzyme 14] [gn:ubp14;ybr0515] [gcfc:10.11] [ec:3.12.15] [keg]
CONTIG2277	24492311_c2_4	5261	19364	678	226	YBR058C	271	1.5(10)-22	Saccharomyces cerevisiae	[ui:ybr058c] [pn:ubiquitin specific protease:ubiquitin carboxyl-terminal hydrolase 14;ubiquitin thioesterase 14:ubiquitin-specific processing protease 14;deubiquinating enzyme 14] [gn:ubp14;ybr0515] [gcfc:10.11] [ec:3.12.15] [keg]

b2x12892.y	13835917_c1_2	5262	19365	438	146	YBR082C	699	5.0(10)-69	Saccharomyces cerevisiae	[ui:ybr082c] [pn:ubiquitin-conjugating enzyme:ubiquitin-conjugating enzyme e2-16 kd:ubiquitin-protein ligase:ubiquitin carrier protein] [gn:ube4:ybr0745] [gicfc:10.11:12.9:13.2:14.1] [ec:6.3.2.19] [keggfc:14.1] [sgdfc:3.3.0:6.5.1:9.2]
CONTIG5492	24412517_c3_15	5263	19366	3246	1082	YDL190C	1724	1.2(10)-177	Saccharomyces cerevisiae	[ui:ycl1190c] [pn:ubiquitin fusion degradation protein:ub fusion degradation protein 2] [gn:ufd2:d1255] [gicfc:10.11] [keggfc:14.2] [sgdfc:6.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG1035	10634680_c3_2	5264	19367	720	240	YDL132W	612	8.4(10)-60	Saccharomyces cerevisiae	[ui:ycl1132w] [pn:controls g1/s transition] [gn:cdc53] [gicfc:10.11:12.8] [keggfc:13.3] [sgdfc:3.8.0:6.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG2950	992030_c3_5	5265	19368	1866	622	YDL132W	140	1.0(10)-14	Saccharomyces cerevisiae	[ui:ycl1132w] [pn:controls g1/s transition] [gn:cdc53] [gicfc:10.11:12.8] [keggfc:13.3] [sgdfc:3.8.0:6.5.1] [db:gic-saccharomyces cerevisiae]
b9x12j03.y	271937_c1_1	5266	19369	630	210	YDL132W	199	8.0(10)-15	Saccharomyces cerevisiae	[ui:ycl1132w] [pn:controls g1/s transition] [gn:cdc53] [gicfc:10.11:12.8] [keggfc:13.3] [sgdfc:3.8.0:6.5.1] [db:gic-saccharomyces cerevisiae]

CONTIG1905	12601703_f3_4	5267	19370	342	114	YDL126C	290	1.5(10)-24	Saccharomyces cerevisiae	[ui:ydl126c] [pn:microsomal protein of /pas l/sec l8 family of atpas:cell division control protein 48] [gn:cdc48] [gtcfc:10.11:12.8] [keggfc:14.2] [sgdfc:3.8:0:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5516	6500_f3_6	5268	19371	2529	843	YDL126C	3106	0	Saccharomyces cerevisiae	[ui:ydl126c] [pn:microsomal protein of /pas l/sec l8 family of atpas:cell division control protein 48] [gn:cdc48] [gtcfc:10.11:12.8] [keggfc:14.2] [sgdfc:3.8:0:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5084	4095180_c2_11	5269	19372	918	306	YDL122W	240	6.0(10)-22	Saccharomyces cerevisiae	[ui:ydl122w] [pn:ubiquitin-specific protease:ubiquitin carboxyl-terminal hydrolase 1:ubiquitin thioesterase 1:ubiquitin-specific processing enzyme 1:deubiquitinating enzyme 1][gn:ubp1] [gtcfc:10.11] [ec:3.1.2.15] [keggfc:1.1] [sg]
CONTIG5129	5081556_f2_4	5270	19373	696	232	YDL122W	157	2.5(10)-10	Saccharomyces cerevisiae	[ui:ydl122w] [pn:ubiquitin-specific protease:ubiquitin carboxyl-terminal hydrolase 1:ubiquitin thioesterase 1:ubiquitin-specific processing enzyme 1:deubiquitinating enzyme 1][gn:ubp1] [gtcfc:10.11] [ec:3.1.2.15] [keggfc:1.4.1] [sg]

CONTIG5129	13859438_f2_5	5271	19374	588	196	YDL122W	227	7.9(10)-18	Saccharomyces cerevisiae	[ui:yd1122w] [pn:ubiquitin-specific protease:ubiquitin carboxyl-terminal hydrolase 1:ubiquitin thiolesterase 1:ubiquitin-specific processing protease 1:deubiquitinating enzyme 1] [gn:ubp1] [gtcfc:10.11] [ec:3.1.2.15] [keggfc:14.1] [sg
CONTIG5760	26602260_f1_3	5272	19375	666	222	YDL064W	596	4.2(10)-58	Saccharomyces cerevisiae	[ui:yd1064w] [pn:ubiquitin-conjugating enzyme e2-18 kd:ubiquitin-protein ligase:ubiquitin carrier protein] [gn:ubc9] [gtcfc:10.11:10.7:12.8] [ec:6.3.2.19] [keggfc:14.1] [sgdfc:3.8:0.6:3:0.6:5.1] [db:gic-saccharomyces cerevisiae]
CONTIG4273	26850002_c2_9	5273	19376	702	234	YDL007W	849	6.4(10)-85	Saccharomyces cerevisiae	[ui:yd1007w] [pn:probable component of 26s proteasome complex:26s protease regulatory subunit 4 homologtat-binding homolog 5] [gn:yta5:yhs4:d2920] [gtcfc:10.11] [keggfc:14.2] [sgdfc:6.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG5610	14644806_c2_15	5274	19377	873	291	YDL007W	681	4.0(10)-67	Saccharomyces cerevisiae	[ui:yd1007w] [pn:probable component of 26s proteasome complex:26s protease regulatory subunit 4 homologtat-binding homolog 5] [gn:yta5:yhs4:d2920] [gtcfc:10.11] [keggfc:14.2] [sgdfc:6.5.1] [db:gic-saccharomyces cerevisiae]

CONTIG3149	29464092_c3_3	5275	19378	1614	538	YDR069C	681	4.0(10)-67	Saccharomyces cerevisiae	[ui:yd:069c] [pn:ubiquitin-specific protease;ubiquitin carboxyl-terminal hydrolase 4;ubiquitin thioesterase 4;ubiquitin-specific processing protease 4;deubiquitinating enzyme 4;vacuole biogenesis protein ssv7] [gn:ubp4;doa4:ssv7;yd960]
CONTIG5815	14552002_f3_21	5276	19379	567	189	YDR092W	104	1.1(10)-12	Saccharomyces cerevisiae	[ui:yd:092w] [pn:ubiquitin-conjugating enzyme;ubiquitin-conjugating enzyme e2-17.5] [kd:ubiquitin-protein ligase;ubiquitin carrier protein] [gn:ubc13;yd6652] [gtfc:10.11:10.7] [ec:6.3.2.19] [keggfc:14.1] [sgdfc:6.3.0.6.5.1] [db:gtc-sac]
CONTIG894	24414010_c1_2	5277	19380	264	88	YDR177W	237	4.5(10)-20	Saccharomyces cerevisiae	[ui:yd:177w] [pn:ubiquitin-conjugating enzyme;ubiquitin-conjugating enzyme e2-24] [kd:ubiquitin- protein ligase;ubiquitin carrier protein] [gn:ubc1;yd9395] [gtfc:10.11:10.7:12.15:14.1] [ec:6.3.2.19] [keggfc:14.1] [sgdfc:3.4.0:6.3.0:6.5]

CONTIG965	22454057_f1_2	5278	19381	207	69	YDR177W	162	4.0(10)-12	Saccharomyces cerevisiae	[ui:ycl177w] [pn:ubiquitin conjugating enzyme:ubiquitin-conjugating enzyme e2-24 kd:ubiquitin- protein ligase:ubiquitin carrier protein] [gn:ubc1.yd9395] [gctc:10.11:10.7:12.15:14.1] [ec:6.3.2.19] [keggfc:14.1] [sgdfc:3.4:6.3:0.6.5]
CONTIG2882	26384713_c2_4	5279	19382	1119	373	YDR394W	1368	6.5(10)-140	Saccharomyces cerevisiae	[ui:yd394w] [pn:26s proteasome subunit:26s protease regulatory subunit 6 homolog:ynt1 protein:tail-binding homolog 2] [gn:yta2.ynt1.yd95091][gctc:10.11] [keggfc:4.2] [sgdfc:6.5.1] [db:gctc:saccharomyces cerevisiae]
CONTIG523	3922777_c1_17	5280	19383	621	207	YER012W	738	3.7(10)-73	Saccharomyces cerevisiae	[ui:yer012w] [pn:26s proteasome subunit c11:proteasome component c11:macropain subunit c11:proteinase yscE subunit c11:multicatalytic endopeptidase complex subunit c11] [gn:pre11] [gctc:10.11] [ec:3.4.99.46] [keggfc:4.1] [sgdfc:6.5.1:]
CONTIG5728	11218942_f2_7	5281	19384	1290	430	YER021W	779	1.7(10)-77	Saccharomyces cerevisiae	[ui:yer021w] [pn:26s proteasome subunit:proteasome component] [gn:sun21][gctc:10.11] [keggfc:14.2] [sgdfc:6.5.1] [db:gctc:saccharomyces cerevisiae]

CONTIG4785	10972161_f1_1	5282	19385	627	209	YER094C	815	2.6(10)-81	Saccharomyces cerevisiae	[ui:yer094c] [pn:26s proteasome subunit:proteasome component:macropain subunit:multicatalytic endopeptidase complex subunit pup3] [gn:pup3] [grcfc:10.11] [ec:3.4.99.46] [keggfc:14.1] [sgdfe:6.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG2102	22457535_c2_5	5283	19386	942	314	YER098W	165	9.8(10)-20	Saccharomyces cerevisiae	[ui:yer098w] [pn:ubiquitin carboxyl-terminal hydrolase:ubiquitin carboxyl-terminal hydrolase 9:ubiquitin thioesterase 9:ubiquitin-specific processing protease 9:deubiquitinating enzyme 9] [gn:ubp9] [grcfc:10.11] [ec:3.1.2.15] [keggfc]
b2x17720.x	22470307_c3_5	5284	19387	735	245	YER098W	221	3.1(10)-17	Saccharomyces cerevisiae	[ui:yer098w] [pn:ubiquitin carboxyl-terminal hydrolase:ubiquitin carboxyl-terminal hydrolase 9:ubiquitin thioesterase 9:ubiquitin-specific processing protease 9:deubiquitinating enzyme 9] [gn:ubp9] [grcfc:10.11] [ec:3.1.2.15] [keggfc]

CONTIG4175	10584432_f3_3	5285	19388	777	259	YER100W	609	1.7(10)-59	Saccharomyces cerevisiae	[ui:yer100w] [pn:ubiquitin-conjugating enzyme:ubiquitin-conjugating enzyme e2-28.4 kd:ubiquitin-protein ligase:ubiquitin carrier protein] [gn:ubc6;doa2] [gicfc:10.11;10.7;12.16;12.9] [ec:6.3.2.19] [keggfc:14.1] [sgdfc:3.3.0;6.3.0;5.5]
CONTIG1561	12773437_c3_7	5286	19389	1044	348	YER151C	140	2.8(10)-10	Saccharomyces cerevisiae	[ui:yer151c] [pn:ubiquitin-specific proteinase:ubiquitin carboxyl-terminal hydrolase 3:ubiquitin thioesterase 3:ubiquitin-specific processing protease 3:deubiquitinating enzyme 3] [gn:ubp3] [gicfc:10.11] [ec:3.1.2.15] [keggfc:14.1][
b9x11r65.x	3010967_f2_1	5287	19390	276	92	YER151C	217	1.1(10)-16	Saccharomyces cerevisiae	[ui:yer151c] [pn:ubiquitin-specific proteinase:ubiquitin carboxyl-terminal hydrolase 3:ubiquitin thioesterase 3:ubiquitin-specific processing protease 3:deubiquitinating enzyme 3] [gn:ubp3] [gicfc:10.11] [ec:3.1.2.15] [keggfc:14.1][
CONTIG2463	34272812_f1_1	5288	19391	864	288	YFR050C	752	1.2(10)-74	Saccharomyces cerevisiae	[ui:yfr050c] [pn:26s proteasome subunit:proteasome component:macropain subunit:proteinase yscE subunit pre4:multicatalytic endopeptidase complex subunit pre4] [gicfc:10.11] [ec:3.4.99.46] [keggfc:14.1] [sgdfc:6.5.1;9.2.0] [d]

CONTIG4163	24398262_F2_2	5289	19392	888	296	YFR052W	403	1.2(10)-37	Saccharomyces cerevisiae	[ui:yf052w] [pn:26s proteasome regulatory subunit:nuclear integrity protein 1] [gn:nin1] [gicfc:10.11:12.8:13.2] [keggfc:4.2] [sgdgc:3.8.0:6.5.1:9.2.0:11.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG2706	19532125_c2_4	5290	19393	450	150	YGL087C	428	2.6(10)-40	Saccharomyces cerevisiae	[ui:yg1087c] [pn:similarity to ubiquitin--protein ligase:hypothetical 15.5 kd protein in mfa12-mad1 intergenic region] [gicfc:10.11:10.7] [keggfc:14.2] [sgdgc:6.3.0:6.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG1103	12282626_F2_3	5291	19394	417	139	YGL048C	335	1.8(10)-30	Saccharomyces cerevisiae	[ui:yg1048c] [pn:26s proteasome subunit:26s protease regulatory subunit 8 homolog:sug1 protein:cim3 protein:tat-binding protein thy1] [gn:sug1:thy1:tbpy:cim3:crl3] [gicfc:10.11:12.8] [keggfc:14.2] [sgdgc:3.8.0:6.5.1] [db:gic-saccharom]
CONTIG2002	12282626_F3_3	5292	19395	957	319	YGL048C	1184	2.0(10)-120	Saccharomyces cerevisiae	[ui:yg1048c] [pn:26s proteasome subunit:26s protease regulatory subunit 8 homolog:sug1 protein:cim3 protein:tat-binding protein thy1] [gn:sug1:thy1:tbpy:cim3:crl3] [gicfc:10.11:12.8] [keggfc:14.2] [sgdgc:3.8.0:6.5.1] [db:gic-saccharom]

CONTIG783	4116567_f2_1	5293	19396	249	83	YGL048C	355	1.3(10)-32	Saccharomyces cerevisiae	[ui:yg[048c] [pn:26s proteasome subunit:26s protease regulatory subunit 8 homolog:sugl protein:cim3 protein:tat-binding protein thy]] [gn:sug1:thy]:bpy:cim3:cr[3] [gicfc:10.11]:12.8] [keggfc:14.2] [sgdgc:3.8.0:6.5.1] [db:gic-saccharom]
CONTIG4529	20009682_c2_9	5294	19397	732	244	YGL011C	784	5.0(10)-78	Saccharomyces cerevisiae	[ui:yg[011c] [pn:26s proteasome subunit yc7alpha:y8:proteasome component:c7-alpha:macropain subunit c7-alpha:proteinase ysec subunit 7:multicatalytic endopeptidase complex c7:component y8:scl1 suppressor protein] [gn:prs2:prc2:scl1] [g
CONTIG4962	789628_f2_4	5295	19398	1059	353	YGR048W	771	1.2(10)-76	Saccharomyces cerevisiae	[ui:yg[048w] [pn:ubiquitin fusion degradation:protein:ub fusion degradation:protein II [gn:ufd1] [gicfc:10.11] [keggfc:4.2] [sgdgc:6.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG5108	5960292_f1_1	5296	19399	234	78	YGR048W	151	2.7(10)-10	Saccharomyces cerevisiae	[ui:yg[048w] [pn:ubiquitin fusion degradation:protein:ub fusion degradation:protein II [gn:ufd1] [gicfc:10.11] [keggfc:4.2] [sgdgc:6.5.1] [db:gic-saccharomyces cerevisiae]

CONTIG5107	20414682_02_9	5297	19400	771	257	YGR135W	788	1.8(10)-78	Saccharomyces cerevisiae	[ui:ygr135w] [pn:26s proteasome subunit y13:proteasome component y13:macropain subunit y13:proteinase yscc subunit y13:multicatalytic endopeptidase complex subunit y13]
CONTIG1129	25572906_c2_2	5298	19401	1305	435	YGR184C	178	6.0(10)-10	Saccharomyces cerevisiae	[ui:ygr184c] [pn:ubiquitin-protein ligase:n-end-recognizing protein:ubiquitin-protein ligase e3 component:n-recognition [gn:ubrl:g7168] [gicfc:10.11] [keggfc:14.21][sgdsc:6.5.1.9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG4544	32619157_f2_1	5299	19402	2454	818	YGR184C	165	4.7(10)-13	Saccharomyces cerevisiae	[ui:ygr184c] [pn:ubiquitin-protein ligase:n-end-recognizing protein:ubiquitin-protein ligase e3 component:n-recognition [gn:ubrl:g7168] [gicfc:10.11] [keggfc:14.21][sgdsc:6.5.1.9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG4837	594792_f3_2	5300	19403	1896	632	YGR184C	728	1.2(10)-70	Saccharomyces cerevisiae	[ui:ygr184c] [pn:ubiquitin-protein ligase:n-end-recognizing protein:ubiquitin-protein ligase e3 component:n-recognition [gn:ubrl:g7168] [gicfc:10.11] [keggfc:14.21][sgdsc:6.5.1.9.2.0] [db:gic-saccharomyces cerevisiae]

CONTIG4837	12503175_f1_1	5301	19404	1488	496	YGR184C	104	0.096	Saccharomyces cerevisiae	[ui:ygr184c] [pn:ubiquitin-protein ligase:n-end-recognition component:n-recognin] [gn:ubr1.g7168] [gtcfc:10.11] [keggfc:14.2] [sgdfc:6.5.1.9.2.0] [db:gtc-saccharomyces_cerevisiae]
CONTIG3090	26298260_c1_2	5302	19405	303	101	YGR253C	267	3.0(10)-23	Saccharomyces cerevisiae	[ui:ygr253c] [pn:26s proteasome subunit:proteasome component pup2:macropain subunit pup2:proteinase ysce subunit pup2:multicatalytic endopeptidase complex subunit pup2] [gn:pup2:dna5] [gtcfc:10.11:12.8] [ec:3.4.99.46] [keggfc:14.1] [s]
CONTIG355	1204657_c3_5	5303	19406	315	105	YGR253C	395	8.3(10)-37	Saccharomyces cerevisiae	[ui:ygr253c] [pn:26s proteasome subunit:proteasome component pup2:macropain subunit pup2:proteinase ysce subunit pup2:multicatalytic endopeptidase complex subunit pup2] [gn:pup2:dna5] [gtcfc:10.11:12.8] [ec:3.4.99.46] [keggfc:14.1] [s]
CONTIG3713	4882176_f3_6	5304	19407	1227	409	YGR270W	200	2.0(10)-13	Saccharomyces cerevisiae	[ui:ygr270w] [pn:26s proteasome subunit:tat-binding homolog 7] [gn:ya7] [gtcfc:10.11] [keggfc:14.2] [sgdfc:6.5.1] [db:gtc-saccharomyces_cerevisiae]
CONTIG5713	40677_f1_3	5305	19408	2760	920	YGR270W	1743	3.2(10)-186	Saccharomyces cerevisiae	[ui:ygr270w] [pn:26s proteasome subunit:tat-binding homolog 7] [gn:ya7] [gtcfc:10.11] [keggfc:14.2] [sgdfc:6.5.1] [db:gtc-saccharomyces_cerevisiae]

CONTIG1924	1907192_f1_1	5306	19409	660	220	YHR027C	511	3.7(10)-48	Saccharomyces cerevisiae	[ui:yhr027c] [pn:subunit of the 26s proteasome:hypothetical 109.5 kd protein in ppa1-dap2 intergenic region] [gn:hrd2] [gicfc:10.11] [keggfc:14.2] [sgdfc:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2755	24665942_f1_1	5307	19410	468	156	YHR027C	479	1.1(10)-44	Saccharomyces cerevisiae	[ui:yhr027c] [pn:subunit of the 26s proteasome:hypothetical 109.5 kd protein in ppa1-dap2 intergenic region] [gn:hrd2] [gicfc:10.11] [keggfc:14.2] [sgdfc:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2755	6835138_f1_2	5308	19411	249	83	YHR027C	256	8.5(10)-21	Saccharomyces cerevisiae	[ui:yhr027c] [pn:subunit of the 26s proteasome:hypothetical 109.5 kd protein in ppa1-dap2 intergenic region] [gn:hrd2] [gicfc:10.11] [keggfc:14.2] [sgdfc:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2755	25581512_f1_3	5309	19412	978	326	YHR027C	430	2.0(10)-39	Saccharomyces cerevisiae	[ui:yhr027c] [pn:subunit of the 26s proteasome:hypothetical 109.5 kd protein in ppa1-dap2 intergenic region] [gn:hrd2] [gicfc:10.11] [keggfc:14.2] [sgdfc:6.5.1] [db:gtc-saccharomyces cerevisiae]
b3x12710_x	24414075_f2_2	5310	19413	213	71	YHR027C	106	8.9(10)-5	Saccharomyces cerevisiae	[ui:yhr027c] [pn:subunit of the 26s proteasome:hypothetical 109.5 kd protein in ppa1-dap2 intergenic region] [gn:hrd2] [gicfc:10.11] [keggfc:14.2] [sgdfc:6.5.1] [db:gtc-saccharomyces cerevisiae]

CONTIG2548	20881662_f3_2	5311	19414	741	247	YHR200W	514	2.0(10)-49	Saccharomyces cerevisiae	[ui:yi200w] [pn:26s proteasome subunit:26s proteasome regulatory subunit] [gn:sun1] [gtcfc:0.11] [keggfc:1.4.2] [sgdfc:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5430	34078136_c3_19	5312	19415	2886	962	YIL156W	471	4.7(10)-63	Saccharomyces cerevisiae	[ui:yi156w] [pn:ubiquitin carboxy terminal hydrolase:ubiquitin carboxyl-terminal hydrolase] [7:ubiquitin thiolesterase 7:ubiquitin-specific processing protease 7:deubiquitinating enzyme 7] [gn:ubp7] [gtcfc:0.11] [ec:3.1.2.15] [keggfc:1.4.2]
CONTIG2488	12925375_c3_8	5313	19416	543	181	YIL075C	304	. 5.7(10)-26	Saccharomyces cerevisiae	[ui:yi075c] [pn:26s proteasome regulatory subunit:trna-processing protein] [gn:sen3] [gtcfc:10.11:10.6] [keggfc:1.4.2] [sgdfc:4.5.0:6.5.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4919	915882_f3_6	5314	19417	2079	693	YIL075C	1728	4.5(10)-178	Saccharomyces cerevisiae	[ui:yi075c] [pn:26s proteasome regulatory subunit:trna-processing protein] [gn:sen3] [gtcfc:10.11:10.6] [keggfc:1.4.2] [sgdfc:4.5.0:6.5.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5716	10723752_f2_6	5315	19418	963	321	YJL197W	263	2.2(10)-21	Saccharomyces cerevisiae	[ui:yi197w] [pn:ubiquitin c-terminal hydrolase:ubiquitin carboxyl-terminal hydrolase] [12:ubiquitin-specific processing protease 12:deubiquitinating enzyme 12] [gn:ubp12:j0340] [gtcfc:10.11] [ec:3.1.2.15] [keggfc:1.4.2]

CONTIG5716	24728462_f1_2	5316	19419	2142	714	YJL197W	620	6.4(10)-98	Saccharomyces cerevisiae	[ui:yj1197w] [pn:ubiquitin c-terminal hydrolase:ubiquitin carboxyl-terminal hydrolase 12:ubiquitin thiolesterase 12:ubiquitin-specific processing protease 12:deubiquitinating enzyme 12] [gn:ubp12;jo340] [gicfc:10.11] [ec:3.1.2.15] [ke]
CONTIG4322	24647805_f1_1	5317	19420	345	115	YJL001W	299	1.2(10)-26	Saccharomyces cerevisiae	[ui:yj001w] [pn:multicatalytic endopeptidase complex subunit:proteasome component pre3 precursor:macropain subunit pre3:proteinase yscE subunit pre3:multicatalytic endopeptidase complex subunit pre3] [gn:pre3;j1407] [gicfc:10.11;12.8]
CONTIG2332	959380_f2_1	5318	19421	80	270	YJR099W	280	1.3(10)-24	Saccharomyces cerevisiae	[ui:yj099w] [pn:ubiquitin-specific protease:ubiquitin carboxyl-terminal hydrolase yuh1:ubiquitin thiolesterase] [gn:yuh1;j194] [gicfc: 0.11] [ec:3.1.2.15] [keggfc: 14.1] [sgdic:6.3.0;6.5.1;9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG336	3907128_f3_3	5319	19422	867	289	YKL213C	493	4.7(10)-47	Saccharomyces cerevisiae	[ui:yk1213c] [pn:involved in ubiquitin-dependent proteolysis:protein] [gn:doa1] [gicfc:10.11] [keggfc:14.2] [sgdic: 6.5.1] [db:gic-saccharomyces cerevisiae]

CONTIG5139	13792203_c2_7	5320	19423	1530	510	YKL213C	512	3.8(10)-58	Saccharomyces cerevisiae	[ui:yk1213c] [pn:involved in ubiquitin-dependent proteolysis;protein] [gn:doa1] [gicfc:10.11] [keggfc:14.2] [sgdfc:6.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG5615	3907128_f1_4	5321	19424	357	119	YKL213C	120	1.8(10)-6	Saccharomyces cerevisiae	[ui:yk1213c] [pn:involved in ubiquitin-dependent proteolysis;protein] [gn:doa1] [gicfc:10.11] [keggfc:14.2] [sgdfc:6.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG1706	1197311_f3_1	5322	19425	1269	423	YKL145W	1401	3.7(10)-176	Saccharomyces cerevisiae	[ui:yk145w] [pn:26s proteasome subunit;26s protease regulatory subunit 7 homolog;cim5 protein;tat-binding homolog 3] [gr:cim5:ya3] [gicfc:10.11:12.8] [keggfc:14.2] [sgdfc:3.8:0.6.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG1540	25554760_f2_2	5323	19426	1002	334	YKL010C	165	5.5(10)-9	Saccharomyces cerevisiae	[ui:yk1010c] [pn:similarity to rat ubiquitin ligase nedd4:hypothetical 167.8 kd protein cce l-cap1 intergenic region] [gn:ufd4:yk1162] [gicfc:10.11] [keggfc:14.2] [sgdfc:6.5.1:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG3231	36331255_f3_3	5324	19427	915	305	YKL010C	397	1.3(10)-35	Saccharomyces cerevisiae	[ui:yk1010c] [pn:similarity to rat ubiquitin ligase nedd4:hypothetical 167.8 kd protein cce l-cap1 intergenic region] [gn:ufd4:yk1162] [gicfc:10.11] [keggfc:14.2] [sgdfc:6.5.1:9.2.0] [db:gic-saccharomyces cerevisiae]

CONTIG4051	21734385_c1_4	5325	19428	411	137	YKL010C	449	4.0(10)-41	Saccharomyces cerevisiae	[ui:yk010c] [pn:similarity to rat ubiquitin ligase nedd4;hypothetical 167.8 kd protein cce1-cap1 intergenic region] [gn:ufid4;yk1162] [gtfc:10.11] [keggfc:14.2] [sgdfc:6.5.1.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4051	19644012_c3_5	5326	19429	1323	441	YKL010C	528	1.5(10)-65	Saccharomyces cerevisiae	[ui:yk010c] [pn:similarity to rat ubiquitin ligase nedd4;hypothetical 167.8 kd protein cce1-cap1 intergenic region] [gn:ufid4;yk1162] [gtfc:10.11] [keggfc:14.2] [sgdfc:6.5.1.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5676	24397906_f1_1	5327	19430	621	207	YLR167W	545	1.1(10)-52	Saccharomyces cerevisiae	[ui:ylr167w] [pn:ubiquitin/ribosomal protein s27a:ubiquitin] [gn:ubi3;19470] [gtfc:10.11 :10.4] [keggfc:14.2] [sgdfc:5.1.0;6.5.1.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5781	3990936_c2_24	5328	19431	606	202	YLR306W	417	3.8(10)-39	Saccharomyces cerevisiae	[ui:ylr306w] [pn:ubiquitin-conjugating enzyme:ubiquitin-conjugating enzyme e2-21.2 kd:ubiquitin-protein ligase:ubiquitin carrier protein] [gn:ubc12;12142] [gtfc:10.11:10.7] [keggfc:14.1] [sgdfc:6.3.0;6.5.1] [db:gtc-sacc]

CONTIG1979	9953462_f2_1	5329	19432	1368	456	YLR452C	285	4.7(10)-52	Saccharomyces cerevisiae	[ui:ylr452c] [pn:involved in desensitization to alpha-factor pheromone:protein] [gn:ss12] [gicfc:10.11:11.1:12.8:2.9] [keggfc:14.2] [sgdic:3.3.0:6.5.1:9.1:0.10.1.6] [db:gtc-saccharomyces cerevisiae]
CONTIG5416	32501382_f1_1	5330	19433	1407	469	YML111W	95	0.34	Saccharomyces cerevisiae	[ui:yml111w] [pn:strong similarity to ubiquitination protein bullp] [gicfc:10.11:10.7] [keggfc:14.2] [sgdfc:6.3.0:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5738	986261_c3_21	5331	19434	1158	386	YML111W	309	1.6(10)-26	Saccharomyces cerevisiae	[ui:yml111w] [pn:strong similarity to ubiquitination protein bullp] [gicfc:10.11:10.7] [keggfc:14.2] [sgdfc:6.3.0:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3334	15735437_c1_3	5332	19435	273	91	YML092C	278	2.1(10)-24	Saccharomyces cerevisiae	[ui:yml092c] [pn:26s proteasome subunit y7:proteasome component y7:macropain subunit y7:proteinase y7:multicatalytic endopeptidase complex subunit y7] [gn:prs4:pr8] [gicfc:10.11:12.8] [ec:3.4.99.46] [keggfc:14.1] [sgdfc:6
CONTIG5642	4771952_f2_4	5333	19436	501	167	YML092C	543	1.7(10)-52	Saccharomyces cerevisiae	[ui:yml092c] [pn:26s proteasome subunit y7:proteasome component y7:macropain subunit y7:proteinase y7:multicatalytic endopeptidase complex subunit y7] [gn:prs4:pr8] [gicfc:10.11:12.8] [ec:3.4.99.46] [keggfc:14.1] [sgdfc:6

CONTIG5642	22051285_f3_5	5334	19437	534	178	YMR022W	637	1.8(10)-62	Saccharomyces cerevisiae	[ui:ymr022w] [pn:ubiquitin-conjugation enzyme:ubiquitin-conjugating enzyme e2-18-kd:ubiquitin-protein ligase:ubiquitin-carrier protein] [gn:ubc7:qrib8:ym9711] [gtfc:10.11:10.7:12.16:12.9:13.2] [ec:6.3.2.19] [keggc:14.1] [sgdfc:3.3.0]
CONTIG2798	35367187_f3_3	5335	19438	1212	404	YMR223W	236	3.2(10)-44	Saccharomyces cerevisiae	[ui:ymr223w] [pn:similarity to human putative ubiquitin carboxyl-terminal hydrolase:putative ubiquitin carboxyl-terminal hydrolase ymr223w:ubiquitin thioesterase:ubiquitin-specific processing protease:deubiquitinating enzyme] [gn:ym99]
CONTIG2798	4882180_f3_4	5336	19439	255	85	YMR223W	178	5.5(10)-13	Saccharomyces cerevisiae	[ui:ymr223w] [pn:similarity to human putative ubiquitin carboxyl-terminal hydrolase:putative ubiquitin carboxyl-terminal hydrolase ymr223w:ubiquitin thioesterase:ubiquitin-specific processing protease:deubiquitinating enzyme] [gn:ym99]

CONTIG916	22067010_c1_1	5337	19440	978	326	YMR223W	236	1.0(10)-35	Saccharomyces cerevisiae	[ui:ymr223w] [pn:similarity to human putative ubiquitin carboxyl-terminal hydrolase;putative ubiquitin carboxyl-terminal hydrolase ymr223w;ubiquitin thioesterase;ubiquitin-specific processing protease;deubiquitinating enzyme] [gn:ym99]
CONTIG8	12312660_f3_1	5338	19441	570	190	YMR275C	95	0.04399	Saccharomyces cerevisiae	[ui:ymr275c] [pn:ubiquitination pathway protein:ubiquitination pathway protein bul1,respiration deficiency suppressor] [gn:bul1:dag1:rds1:ym8021] [gicfc:10.11:10.7] [keggfc:14.2] [sgdfc:6.3.0:6.5.1] [db:gicsaccharomyces cerevisiae]
CONTIG1692	35798416_c2_1	5339	19442	1215	405	YMR275C	384	1.7(10)-34	Saccharomyces cerevisiae	[ui:ymr275c] [pn:ubiquitination pathway protein:ubiquitination pathway protein bul1,respiration deficiency suppressor] [gn:bul1:dag1:rds1:ym8021] [gicfc:10.11:10.7] [keggfc:14.2] [sgdfc:6.3.0:6.5.1] [db:gicsaccharomyces cerevisiae]
CONTIG4859	2158338_c3_13	5340	19443	1173	391	YMR275C	289	2.5(10)-24	Saccharomyces cerevisiae	[ui:ymr275c] [pn:ubiquitination pathway protein:ubiquitination pathway protein bul1,respiration deficiency suppressor] [gn:bul1:dag1:rds1:ym8021] [gicfc:10.11:10.7] [keggfc:14.2] [sgdfc:6.3.0:6.5.1] [db:gicsaccharomyces cerevisiae]

CONTIG5472	24641625_f1_1	5341	19444	1008	336	YMR275C	272	1.6(10)-22	Saccharomyces cerevisiae	[ui:ymr275c] [pn:ubiquitination pathway protein:ubiquitination pathway protein bull:respiration deficiency suppressor] [gn:bull:dag:ids1:ym8021] [gtcfc:0.11:10.7] [keggfc:14.2] [sgdc:6.3.0:6.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG5200	33212758_f3_8	5342	19445	855	285	YMR314W	733	1.3(10)-72	Saccharomyces cerevisiae	[ui:ymr314w] [pn:26s proteasome subunit, alpha-type:proteasome component pre5:macropain subunit pre5:proteinase yscE subunit pre5:multicatalytic endopeptidase complex subunit pre5] [gn:pre5:ym9924] [gtcfc:10.11:12.8] [ec:3.4.99.46] [keggfc:14.1]
CONTIG5810	5083552_f1_5	5343	19446	1614	538	YNL239W	902	1.6(10)-90	Saccharomyces cerevisiae	[ui:ynl239w] [pn:aminopeptidase of cysteine protease family:cysteine proteinase 1:y3:bleomycin hydrolase:blm hydrolase] [gn:blhl1:ycpl1:lap3:gal6:n1118] [gtcfc:10.11:5.5] [ec:3.4.22.-] [keggfc:14.1] [sgdc:6.5.1:9.2.0] [db:gic-saccharom
CONTIG4281	20914068_c2_5	5344	19447	735	245	YOL038W	806	2.2(10)-80	Saccharomyces cerevisiae	[ui:yol038w] [pn:multicatalytic endopeptidase complex chain:proteasome component:macropain subunit:proteinase yscE subunit pre6:multicatalytic endopeptidase complex subunit pre6] [gn:pre6] [gtcfc:10.11:12.8] [ec:3.4.99.46] [keggfc:14.

CONTIG1575	25807938_f1_1	5345	19448	969	323	YOR117W	1160	7.0(10)-118	Saccharomyces cerevisiae	[ui:yor117w] [pn:26s proteasome subunit;probable 26s protease subunit tbp-1:tat-binding protein homolog 1] [gn:ytal:03258:yor3258w] [gicfc:10.11] [keggfc:14.2] [sgdfc:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3560	954776_f1_1	5346	19449	1908	636	YOR124C	837	5.5(10)-120	Saccharomyces cerevisiae	[ui:yor124c] [pn:ubiquitin-specific proteinase;ubiquitin carboxyl-terminal hydrolase 2:ubiquitin thiolesterase 2:ubiquitin-specific processing protease 2:deubiquitinating enzyme 2] [gn:ubp2:03281:yor3281c] [gicfc:10.11] [ec:3.1.2.15]
CONTIG4291	5115900_c3_9	5347	19450	1896	632	YOR124C	190	4.5(10)-19	Saccharomyces cerevisiae	[ui:yor124c] [pn:ubiquitin-specific proteinase;ubiquitin carboxyl-terminal hydrolase 2:ubiquitin thiolesterase 2:ubiquitin-specific processing protease 2:deubiquitinating enzyme 2] [gn:ubp2:03281:yor3281c] [gicfc:10.11] [ec:3.1.2.15]
CONTIG4662	34656251_f1_2	5348	19451	465	155	YOR157C	504	2.2(10)-48	Saccharomyces cerevisiae	[ui:yor157c] [pn:26s proteasome subunit;proteasome component precursor;macropain subunit;proteinase yscE subunit pup1:multicatalytic endopeptidase complex subunit pup1] [gn:pup1] [gicfc:10.11:12.8] [ec:3.4.99.46] [keggfc:14.1] [sgdfc:

CONTIG4662	29410912_f2_3	5349	19452	483	161	YOR157C	537	7.4(10)-52	Saccharomyces cerevisiae	[ui:yor157c] [pn:26s proteasome subunit:proteasome component precursor:macropain subunit:proteinase ysce subunit pup1:multicatalytic endopeptidase complex subunit pup1] [gn:pup1] [gtcfc:10.11:12.8] [ec:3.4.99.46] [keggfc:14.1] [sgdfc:14.1]
CONTIG3491	12540827_c2_7	5350	19453	1197	399	YOR259C	1574	9.5(10)-162	Saccharomyces cerevisiae	[ui:yor259c] [pn:26s proteasome subunit:probable 26s protease subunit sug2] [gn:crl13_sug2:crl13_of_yor259c] [gtcfc:10.11:10.2] [keggfc:14.2] [sgdfc:4.8.26.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5559	20423437_f1_4	5351	19454	1029	343	YOR261C	854	1.8(10)-85	Saccharomyces cerevisiae	[ui:yor261c] [pn:strong similarity to human 26s proteasome regulatory chain, p40] [gtcfc:10.11] [keggfc:14.2] [sgdfc:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5711	26204426_f1_4	5352	19455	243	81	YOR362C	307	1.7(10)-27	Saccharomyces cerevisiae	[ui:yor362c] [pn:26s proteasome subunit c1:proteasome component c1:macropain subunit c1:proteinase ysce subunit 1:multicatalytic endopeptidase complex subunit c1] [gn:prsl:prc1:pre10] [gtcfc:10.11:12.8] [ec:3.4.99.46] [keggfc:14.1] [s]

CONTIG5711	867015_f1_5	5353	19456	516	172	YOR362C	448	2.0(10)-42	Saccharomyces cerevisiae	[ui:yor362c] [pn:26s proteasome subunit c1:proteasome component c1:macropain subunit c1:proteinase ysce subunit1:multicatalytic endopeptidase complex subunit c1] [gn:prs1:prc1:pre10] [gicfc: 10.11:12.8] [ec:3.4.99.46] [keggfc:14.1] [s]
CONTIG4364	23626263_c3_8	5354	19457	252	84	YPL074W	244	1.1(10)-19	Saccharomyces cerevisiae	[ui:yp1074w] [pn:similarity to vps4p and yta4p:probable 26s protease subunit:taf-binding homolog 6] [gn:ytal6] [gicfc:10.11] [keggfc:14.2] [sgdfc:6.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG4774	40662_f1_2	5355	19458	537	179	YPL074W	440	6.5(10)-41	Saccharomyces cerevisiae	[ui:yp1074w] [pn:similarity to vps4p and yta4p:probable 26s protease subunit:taf-binding homolog 6] [gn:ytal6] [gicfc:10.11] [keggfc:14.2] [sgdfc:6.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG3898	37900_c1_3	5356	19459	840	280	YPL003W	286	6.5(10)-25	Saccharomyces cerevisiae	[ui:yp1003w] [pn:similarity to ubiquitin-activating enzymes] [gicfc:10.11:10.7] [keggfc:14.2] [sgdfc:6.3.0:6.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG5726	20345018_c2_23	5357	19460	1047	349	YPR066W	564	1.0(10)-54	Saccharomyces cerevisiae	[ui:yp1066w] [pn:strong similarity to ubiquitin-activating enzymes] [gicfc:10.11:10.7] [keggfc:14.2] [sgdfc:6.3.0:6.5.1] [db:gic-saccharomyces cerevisiae]

CONTIG5036	21679002_c3_13	5358	19461	942	314	YPR103W	1144	3.5(10)-116	Saccharomyces cerevisiae	[ui:yp103w] [pn:26s proteasome subunit;proteasome component pre2 precursor:macropain subunit pre2:proteinase ysee subunit pre2:multicatalytic endopeptidase complex subunit pre2] [gn:pre2;prg1:doa3;prg2:83] [gtcfc:10.11:12.8] [ec:3.4.99]
CONTIG2014	23631875_f1_1	5359	19462	912	304	YPR180W	236	5.7(10)-20	Saccharomyces cerevisiae	[ui:yp180w] [pn:similarity to ubiquitin-activating enzymes] [gtcfc:10.11:10.7] [keggfc:14.2] [sgdgc:6.3.0:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5485	31672080_f3_5	5360	19463	315	105	YPR180W	181	1.2(10)-13	Saccharomyces cerevisiae	[ui:yp180w] [pn:similarity to ubiquitin-activating enzymes] [gtcfc:10.11:10.7] [keggfc:14.2] [sgdgc:6.3.0:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4098	32609638_c2_4	5361	19464	2112	704	YDL077C	283	3.2(10)-21	Saccharomyces cerevisiae	[ui:ydl077c] [pn:vacuolar carboxypeptidase Y] [gn:vam6] [gtcfc:10.11:12.16] [keggfc:14.2] [sgdgc:6.5.2:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2363	23627260_c3_5	5362	19465	183	61	YEL060C	144	4.2(10)-9	Saccharomyces cerevisiae	[ui:yel060c] [pn:protease b, vacuolar:cerevisin precursor:vacuolar protease b:proteinase yscb] [gn:prb1] [gtcfc:10.11:12.16] [ec:3.4.21.48] [keggfc:14.1] [sgdgc:6.3.0:6.5.2:9.10.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4372	24429712_f1_3	5363	19466	1068	356	YEL060C	818	1.2(10)-81	Saccharomyces cerevisiae	[ui:ye 060c] [pn:protease b, vacuolar:cerevisin precursor:vacuolar protease b:proteinase yscb] [gn:prb1] [gicfc:10.11:12.16] [ec:3.4.21.48]	[Keggfc: 14..1]	[sgdfc:6.3.0:6.5.2:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5557	4105375_c1_15	5364	19467	1041	347	YEL060C	482	5.0(10)-46	Saccharomyces cerevisiae	[ui:ye 060c] [pn:protease b, vacuolar:cerevisin precursor:vacuolar protease b:proteinase yscb] [gn:prb1] [gicfc:10.11:12.16] [ec:3.4.21.48]	[Keggfc: 14..1]	[sgdfc:6.3.0:6.5.2:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5557	5256575_c3_19	5365	19468	1209	403	YEL060C	479	1.0(10)-45	Saccharomyces cerevisiae	[ui:ye 060c] [pn:protease b, vacuolar:cerevisin precursor:vacuolar protease b:proteinase yscb] [gn:prb1] [gicfc:10.11:12.16] [ec:3.4.21.48]	[Keggfc: 14..1]	[sgdfc:6.3.0:6.5.2:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG809	36047562_f3_2	5366	19469	519	173	YEL060C	501	4.7(10)-48	Saccharomyces cerevisiae	[ui:ye 060c] [pn:protease b, vacuolar:cerevisin precursor:vacuolar protease b:proteinase yscb] [gn:prb1] [gicfc:10.11:12.16] [ec:3.4.21.48]	[Keggfc: 14..1]	[sgdfc:6.3.0:6.5.2:9.10.0] [db:gtc-saccharomyces cerevisiae]

CONTIG934	9877305_c2_4	5367	19470	243	81	YEL060C	284	3.6(10)-24	Saccharomyces cerevisiae	[ui:ye060c] [pn:protease b, vacuolar;cerevisin precursor:vacuolar protease b;proteinasesycb1 [gn:prb1] [gicfc:10.11:12.16] [ec:3.4.21.48] [keggfc:14.1] [sgdfc:6.3.0:6.5.2:9.10.0] [db:gic-saccharomyces cerevisiae]
CONTIG3501	14878552_f1_1	5368	19471	837	279	YHR028C	336	1.6(10)-29	Saccharomyces cerevisiae	[ui:yhr028c] [pn:dipeptidyl aminopeptidase b;dpap b;yscv] [gn:dap2] [gicfc:10.11:12.16] [ec:3.4.14.-] [keggfc:14.1] [sgdfc:6.5.2:9.10.0] [db:gic-saccharomyces cerevisiae]
CONTIG4805	26692808_c2_4	5369	19472	1485	495	YHR028C	1154	3.1(10)-117	Saccharomyces cerevisiae	[ui:yhr028c] [pn:dipeptidyl aminopeptidase b;dpap b;yscv] [gn:dap2] [gicfc:10.11:12.16] [ec:3.4.14.-] [keggfc:4.1] [sgdfc:6.5.2:9.10.0] [db:gic-saccharomyces cerevisiae]
CONTIG3410	9844200_c1_9	5370	19473	876	292	YKL103C	964	4.2(10)-97	Saccharomyces cerevisiae	[ui:ykl103c] [pn:aminopeptidase ysci precursor, vacuolar;vacuolar aminopeptidase i precursor:polypeptidase:leucine aminopeptidase:aminopeptidase iii:aminopeptidase ysci/lapiv] [gn:ape1;lap4:ykl455] [gicfc:10.11:12.16] [ec:3.4.11.1] [k

CONTIG3410	36523442_c2_10	5371	19474	876	292	YKL103C	549	4.0(10)-53	Saccharomyces cerevisiae	[ui:ykl103c] [pn:aminopeptidase ysci precursor, vacuolar aminopeptidase i precursor:polypeptidase:leucine aminopeptidase:aminopeptidase iii:aminopeptidase ysci:lapiv] [gn:ape1:lap4:ykl455] [gtcfc:10.11:12.16] [ec:3.4.11.1][k]
CONTIG4002	36353158_c1_6	5372	19475	954	318	YKL103C	459	1.3(10)-43	Saccharomyces cerevisiae	[ui:ykl103c] [pn:aminopeptidase ysci precursor, vacuolar aminopeptidase i precursor:polypeptidase:leucine aminopeptidase:aminopeptidase iii:aminopeptidase ysci:lapiv] [gn:ape1:lap4:ykl455] [gtcfc:10.11:12.16] [ec:3.4.11.1][k]
CONTIG4002	11141300_c3_8	5373	19476	852	284	YKL103C	277	1.1(10)-23	Saccharomyces cerevisiae	[ui:ykl103c] [pn:aminopeptidase ysci precursor, vacuolar aminopeptidase i precursor:polypeptidase:leucine aminopeptidase:aminopeptidase iii:aminopeptidase ysci:lapiv] [gn:ape1:lap4:ykl455] [gtcfc:10.11:12.16] [ec:3.4.11.1][k]
CONTIG5022	24491408_c2_7	5374	19477	1737	579	YMR297W	1588	3.1(10)-163	Saccharomyces cerevisiae	[ui:ymr297w] [pn:carboxypeptidase y, serine-type protease:carboxypeptidase y precursor:carboxypeptidase yscy] [gn:prc1] [gtcfc:10.11:12.16] [Kegg:fc:14.1] [sgd:fc:6.5:2:9.10.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5684	4878376_f3_11	5375	19478	1599	533	YMR297W	989	9.4(10)-100	Saccharomyces cerevisiae	[ui:ymr297w] [pn:carboxypeptidase Y, serine-type protease;carboxypeptidase yscy] [gn:prc1] [gicfc:10.11:12.16] [keggfc:14.1] [sgdfc:6.5:2.9:10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5790	22695252_f1_5	5376	19479	1659	553	YMR297W	1348	8.5(10)-138	Saccharomyces cerevisiae	[ui:ymr297w] [pn:carboxypeptidase Y, serine-type protease;carboxypeptidase yscy] [gn:prc1] [gicfc:10.11:12.16] [keggfc:14.1] [sgdfc:6.5:2.9:10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4471	10970285_c3_11	5377	19480	1008	336	YNR007C	293	5.5(10)-61	Saccharomyces cerevisiae	[ui:ynr007cl] [pn:essential for autophagy/cytosis;hypothetical 35.9 kd protein in vps27-cse2 intergenic region] [gn:aut1:n2040] [gicfc:10.11:12.13] [keggfc:14.2] [sgdic:6.5:2.8.5:0][db:gtc-saccharomyces cerevisiae]
CONTIG2749	16075_c3_7	5378	19481	1146	382	YPL154C	146	2.2(10)-7	Saccharomyces cerevisiae	[ui:ypl154cl] [pn:aspartyl protease;sacharopepsin precursor:aspartate protease;proteinase a;proteinase yscal] [gn:pep4-pho9-pral:p2585] [gicfc:10.11:5.2:7.2] [ec:3.4.23.25] [keggfc:14.1] [sgdfc:6.3:0.6.5:2.9:10.0][db:gtc-saccharomyces]

CONTIG5808	24003930_f2_13	5379	19482	1011	337	YPL154C	1342	3.7(10)-137	Saccharomyces cerevisiae	[ui:yp1154c] [pn:aspartyl protease;saccharopepsin precursor;aspartate protease;proteinase a;proteinase yscal] [gn:ppp4:pho9:pra1:p2:385] [gicfc:10.11:5.2:7.2] [ec:3.4.23.25] [keggfc:14.1] [sgdfc:6.3.0:6.5.2:9.10.0] [db:gic-saccharomyces cerevisiae]
CONTIG436	14941251_f1_1	5380	19483	726	242	YCL057W	592	1.1(10)-57	Saccharomyces cerevisiae	[ui:ycl057w] [pn:saccharatolysin protease d;proteinase ysed:oligopeptidase ysed] [gn:pid1:ycl57w] [gicfc:10.11:7.2] [ec:3.4.24.37] [keggfc:14.1] [sgdfc:6.5.3] [db:gic-saccharomyces cerevisiae]
CONTIG436	3015887_f2_2	5381	19484	204	68	YCL057W	152	7.0(10)-10	Saccharomyces cerevisiae	[ui:ycl057w] [pn:saccharatolysin protease d;proteinase ysed:oligopeptidase ysed] [gn:pid1:ycl57w] [gicfc:10.11:7.2] [ec:3.4.24.37] [keggfc:14.1] [sgdfc:6.5.3] [db:gic-saccharomyces cerevisiae]
CONTIG2081	10631932_c2_8	5382	19485	1455	485	YDR144C	192	4.7(10)-12	Saccharomyces cerevisiae	[ui:ydr144c] [pn:aspartyl protease of the periplasmic space;aspartic proteinase mkc7 precursor] [gn:mkc7:yd8338] [gicfc:10.11:11.15.2] [ec:3.4.23.-] [keggfc:14.1] [sgdfc:6.5.3:9.1.0] [db:gic-saccharomyces cerevisiae]

CONTIG3875	23943801_c3_4	5383	19486	675	225	YHR113W	508	8.8(10)-49	Saccharomyces cerevisiae	[ui:yht113w] [pn:similarity to vacuolar aminopeptidase ape1p:hypothetical 54.2 kd protein in cdc12-orc6 intergenic region] [gicfc:10.11] [keggfc:14.2] [sgdfc:6.5.3] [db:gic-saccharomyces cerevisiae]
CONTIG651	25429661_c2_3	5384	19487	750	250	YHR113W	796	2.7(10)-79	Saccharomyces cerevisiae	[ui:yht113w] [pn:similarity to vacuolar aminopeptidase ape1p:hypothetical 54.2 kd protein in cdc12-orc6 intergenic region] [gicfc:10.11] [keggfc:14.2] [sgdfc:6.5.3] [db:gic-saccharomyces cerevisiae]
CONTIG3699	26594376_c3_8	5385	19488	870	290	YIL015W	265	3.3(10)-22	Saccharomyces cerevisiae	[ui:yil015w] [pn:barriopepsin precursor:extracellular] [gn:barl:ssi] [gicfc:10.11:12.9] [ec:3.4.23.35] [keggfc:14.1] [sgdfc:3.3.0:6.5.3] [db:gic-saccharomyces cerevisiae]
CONTIG5353	5111011_B_8	5386	19489	564	188	YDL104C	302	5.9(10)-27	Saccharomyces cerevisiae	[ui:yd104c] [pn:similarity to h.influenzae sialoglycoprotease:gcp:putative protease qrl7] [gn:qrl7:d2366] [gicfc:10.11] [ec:3.4.24.-] [keggfc:14.1] [sgdfc:6.6.0] [db:gic-saccharomyces cerevisiae]
b1x10133.x	24658450_c3_2	5387	19490	546	182	YDL104C	155	1.3(10)-10	Saccharomyces cerevisiae	[ui:yd104c] [pn:similarity to h.influenzae sialoglycoprotease:gcp:putative protease qrl7] [gn:qrl7:d2366] [gicfc:10.11] [ec:3.4.24.-] [keggfc:14.1] [sgdfc:6.6.0] [db:gic-saccharomyces cerevisiae]

CONTIG5255	15897912_c3_8	5388	19491	513	171	YDR415C	478	1.3(10)-45	Saccharomyces cerevisiae	[uiydr415c] [pn:strong similarity to bacterial leucyl aminopeptidase] [gtcfc:10.11] [keggfc:14.2] [sgdfc:6.6.0] [db:gic-saccharomyces cerevisiae]
CONTIG5738	21595160_f2_4	5389	19492	1293	431	YLR299W	575	7.0(10)-56	Saccharomyces cerevisiae	[uiylr299w] [pn:gamma-glutamyltransferase, involved in glutathione synthesis] [gn:cis2] [gtcfc:10.2;12.8] [keggfc:14.2] [sgdfc:1.1.2;3.8.0] [db:gic-saccharomyces cerevisiae]
CONTIG5738	24417207_f3_6	5390	19493	672	224	YLR299W	469	1.2(10)-44	Saccharomyces cerevisiae	[uiylr299w] [pn:gamma-glutamyltransferase, involved in glutathione synthesis] [gn:cis2] [gtcfc:10.2;12.8] [keggfc:14.2] [sgdfc:1.1.2;3.8.0] [db:gic-saccharomyces cerevisiae]
CONTIG3001	24022812_f3_4	5391	19494	660	220	YMR116C	647	1.6(10)-63	Saccharomyces cerevisiae	[uiymr116c] [pn:strong similarity to n.crassa opc2 protein:guanine nucleotide-binding protein beta subunit-like protein] [gn:ym9718] [gtcfc:10.2] [keggfc:14.2] [sgdfc:1.1.2] [db:gic-saccharomyces cerevisiae]
CONTIG3001	605055_f1_2	5392	19495	426	142	YMR116C	472	5.7(10)-45	Saccharomyces cerevisiae	[uiymr116c] [pn:strong similarity to n.crassa opc2 protein:guanine nucleotide-binding protein beta subunit-like protein] [gn:ym9718] [gtcfc:10.2] [keggfc:14.2] [sgdfc:1.1.2] [db:gic-saccharomyces cerevisiae]

CONTIG1120	30484717_c3_3	5393	19496	843	281	YBR142W	288	2.1(10)-24	Saccharomyces cerevisiae	[ui:ybr142w] [pn:atp-dependent ma helicase:atp-dependent rna helicase mak5][gn:rnak5:ybr1119] [gicfc:10.2:10.3] [keggfc:14.2] [sgdfc:4.2.0:4.9.0] [db:gic-saccharomyces cerevisiae]
CONTIG5583	24353432_f1_1	5394	19497	1098	366	YBR142W	627	2.2(10)-61	Saccharomyces cerevisiae	[ui:ybr142w] [pn:atp-dependent ma helicase:atp-dependent rna helicase mak5][gn:rnak5:ybr1119] [gicfc:10.2:10.3] [keggfc:14.2] [sgdfc:4.2.0:4.9.0] [db:gic-saccharomyces cerevisiae]
CONTIG5583	990677_f1_2	5395	19498	1209	403	YBR142W	629	1.3(10)-61	Saccharomyces cerevisiae	[ui:ybr142w] [pn:atp-dependent ma helicase:atp-dependent rna helicase mak5][gn:rnak5:ybr1119] [gicfc:10.2:10.3] [keggfc:14.2] [sgdfc:4.2.0:4.9.0] [db:gic-saccharomyces cerevisiae]
CONTIG2054	24250007_c1_1	5396	19499	336	112	YGL120C	262	1.3(10)-21	Saccharomyces cerevisiae	[ui:ygl120c] [pn:strong similarity to prp22p:putative atp-dependent rna helicase ygl120c] [gicfc:10.2] [keggfc:14.2][sgdfc:4.9.0] [db:gic-saccharomyces cerevisiae]
CONTIG902	35792152_f1_1	5397	19500	765	255	YGL120C	1057	5.7(10)-107	Saccharomyces cerevisiae	[ui:ygl120c] [pn:strong similarity to prp22p:putative atp-dependent rna helicase ygl120c] [gicfc:10.2] [keggfc:14.2][sgdfc:4.9.0] [db:gic-saccharomyces cerevisiae]
b3x13229_y	6134452_c1_1	5398	19501	513	171	YGL120C	537	8.6(10)-52	Saccharomyces cerevisiae	[ui:ygl120c] [pn:strong similarity to prp22p:putative atp-dependent rna helicase ygl120c] [gicfc:10.2] [keggfc:14.2][sgdfc:4.9.0] [db:gic-saccharomyces cerevisiae]

CONTIG5788	23538311_c3_27	5399	19502	1407	469	YHR086W	285	1.0(10)-43	Saccharomyces cerevisiae	[ui:yh086w] [pn:meiotic recombination protein,nam8 protein] [gn:nam8:mre2] [kgfc:10.2:10.8:12.8] [keggc:14.2] [sgfc:3.5:0.3:7.0:4.9:0] [db:gtc-saccharomyces cerevisiae]
CONTIG5094	19728952_c2_12	5400	19503	1488	496	YKL078W	1172	3.7(10)-119	Saccharomyces cerevisiae	[ui:yk078w] [pn:strong similarity to atp-dependent rna helicases;putative atp-dependent rna helicase ykl078w] [gn:ykl408] [kgfc:10.2] [keggc:14.2] [sgfc:4.9:0] [db:gtc-saccharomyces cerevisiae]
CONTIG5094	16598182_c1_10	5401	19504	1128	376	YKL078W	560	2.7(10)-54	Saccharomyces cerevisiae	[ui:yk078w] [pn:strong similarity to atp-dependent rna helicases;putative atp-dependent rna helicase ykl078w] [gn:ykl408] [kgfc:10.2] [keggc:14.2] [sgfc:4.9:0] [db:gtc-saccharomyces cerevisiae]
CONTIG1718	5116262_f1_1	5402	19505	936	312	YKL012W	239	2.2(10)-19	Saccharomyces cerevisiae	[ui:yk012w] [pn:splicing factor:hypothetical 69.1 kd protein in put3-cce] [intergenic region] [gn:prp40:ykl1165] [kgfc:10.2] [keggc:14.2] [sgfc:4.9:0] [db:gtc-saccharomyces cerevisiae]
CONTIG3526	23634591_f2_2	5403	19506	594	198	YKL012W	132	1.3(10)-16	Saccharomyces cerevisiae	[ui:yk012w] [pn:splicing factor:hypothetical 69.1 kd protein in put3-cce] [intergenic region] [gn:prp40:ykl1165] [kgfc:10.2] [keggc:14.2] [sgfc:4.9:0] [db:gtc-saccharomyces cerevisiae]

CONTIG4950	10351387_f3_5	5404	19507	864	288	YKR024C	509	1.1(10)-48	Saccharomyces cerevisiae	[ui:yr024c] [pn:similarity to pre-mrna processing protein prp5p:hypothetical 83.3 kd protein in ypt52-gcn3 intergenic region] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.9.0] [db:gic-saccharomyces cerevisiae]
CONTIG4950	31818950_f1_3	5405	19508	240	80	YKR024C	142	8.8(10)-9	Saccharomyces cerevisiae	[ui:yr024c] [pn:similarity to pre-mrna processing protein prp5p:hypothetical 83.3 kd protein in ypt52-gcn3 intergenic region] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.9.0] [db:gic-saccharomyces cerevisiae]
CONTIG4950	11757627_f2_4	5406	19509	681	227	YKR024C	275	4.7(10)-23	Saccharomyces cerevisiae	[ui:yr024c] [pn:similarity to pre-mrna processing protein prp5p:hypothetical 83.3 kd protein in ypt52-gcn3 intergenic region] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.9.0] [db:gic-saccharomyces cerevisiae]
CONTIG5796	33992218_c3_20	5407	19510	462	154	YKR024C	355	1.1(10)-31	Saccharomyces cerevisiae	[ui:yr024c] [pn:similarity to pre-mrna processing protein prp5p:hypothetical 83.3 kd protein in ypt52-gcn3 intergenic region] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.9.0] [db:gic-saccharomyces cerevisiae]
CONTIG421	2844376_f1_1	5408	19511	819	273	YNL286W	203	1.8(10)-16	Saccharomyces cerevisiae	[ui:ynl286w] [pn:cold sensitive u2 smna suppressor:hypothetical 32.3 kd protein in sec21-mp110 intergenic region] [gn:us2.n0549] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.9.0] [db:gic-saccharomyces cerevisiae]

CONTIG5467	94017_f1_3	5409	19512	276	92	YOR159C	204	1.3(10)-16	Saccharomyces cerevisiae	[ui:yor159c] [pn:strong similarity to human small nuclear ribonucleoprotein e] [gn:sme1]
CONTIG5618	24038438_c1_18	5410	19513	1905	635	YOR204W	1703	2.1(10)-175	Saccharomyces cerevisiae	[ui:yor204w] [pn:atp-dependent rna helicase;putative atp-dependent rna helicase ded1] [gn:ded1] [sp:SP81]
CONTIG254	13085062_c2_2	5411	19514	1206	402	YPL060W	517	1.5(10)-54	Saccharomyces cerevisiae	[ui:ypl060w] [pn:strong similarity to mrs2p] [gtcfc:10.2]
CONTIG5566	34258256_c1_19	5412	19515	393	131	YDR045C	464	4.0(10)-44	Saccharomyces cerevisiae	[ui:ydr045c] [pn:strong similarity to s.acidocaldarius transcription elongation factor tfs] [gtcfc:10.2]
CONTIG4966	22070192_c1_7	5413	19516	1185	395	YDR145W	494	2.7(10)-47	Saccharomyces cerevisiae	[ui:ydr145w] [pn:tfid subunit:tp-associated factor] [gn:taf61]
CONTIG5705	9978402_c1_14	5414	19517	1551	517	YDR145W	338	2.2(10)-30	Saccharomyces cerevisiae	[ui:ydr145w] [pn:tfid subunit:tp-associated factor] [gn:taf61]

CONTIG2805	23631531_c2_6	5415	19518	726	242	YDR167W	419	2.3(10)-39	Saccharomyces cerevisiae	[ui:dr167w] [pn:tfid subunit:tbp-associated factor, 23 kd] [gn:taf23] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.8.1] [db:gic-saccharomyces cerevisiae]
CONTIG1627	4096062_c3_4	5416	19519	501	167	YGL244W	197	4.5(10)-15	Saccharomyces cerevisiae	[ui:yg1244w] [pn:involved in tata site selection by tbp hypothetical 54.6 kd protein in pde1-cse1 intergenic region] [gn:rfl:hra458] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.8.1] [db:gic-saccharomyces cerevisiae]
CONTIG3430	25478412_c2_4	5417	19520	1281	427	YGL244W	250	4.5(10)-26	Saccharomyces cerevisiae	[ui:yg1244w] [pn:involved in tata site selection by tbp hypothetical 54.6 kd protein in pde1-cse1 intergenic region] [gn:rfl:hra458] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.8.1] [db:gic-saccharomyces cerevisiae]
CONTIG4359	29428312_f2_4	5418	19521	1005	335	YML015C	128	4.2(10)-11	Saccharomyces cerevisiae	[ui:yml015c] [pn:tfid subunit:tbp-associated factor, 40 kd] [gn:taf40] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.8.1] [db:gic-saccharomyces cerevisiae]
CONTIG3736	4062655_f2_3	5419	19522	1320	440	YMR227C	99	0.07199	Saccharomyces cerevisiae	[ui:ymr227c] [pn:tfid subunit:tbp-associated factor, 67 kd] [gn:taf67] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.8.1] [db:gic-saccharomyces cerevisiae]
CONTIG5817	9929701_c2_50	5420	19523	1248	416	YMR227C	91	0.00018	Saccharomyces cerevisiae	[ui:ymr227c] [pn:tfid subunit:tbp-associated factor, 67 kd] [gn:taf67] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.8.1] [db:gic-saccharomyces cerevisiae]

CONTIG5817	24313753_c3_58	5421	19524	201	67	YNMR227C	106	4.7(10)-5	Saccharomyces cerevisiae	[ui:ymr227c] [pn:tfid subunit:ibp-associated factor, 67 kd] [gn:taf67] [gicfc: 0.2] [keggfc:14.2] [sgdfc:4.8.] [db:gic-saccharomyces cerevisiae]
CONTIG3717	1257677_f1_2	5422	19525	339	113	YPL046C	159	8.4(10)-12	Saccharomyces cerevisiae	[ui:yp046c] [pn:strong similarity to human dna-directed rna polymerase ii elongation factor sii p15 subunit] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.8.] [db:gic-saccharomyces cerevisiae]
CONTIG4645	5079530_c3_8	5423	19526	1356	452	YAR003W	522	6.0(10)-80	Saccharomyces cerevisiae	[ui:yar003w] [pn:similarity to human rb protein binding protein,hypothetical trp-asp repeats containing protein in tfc3-rfa1 intergenic region] [gn:fun16] [gicfc: 0.2;12.8] [keggfc:14.2] [sgdfc:3.8.0;4.8.2] [db:gic-saccharomyces cerev]
CONTIG3762	241637_f3_3	5424	19527	1026	342	YBL066C	141	1.3(10)-9	Saccharomyces cerevisiae	[ui:ybl066c] [pn:putative transcription factor;putative 118.2 kd transcriptional regulatory protein in ubp13-kip1 intergenic region] [gn:sefl,ybl0501,ybl0526] [gicfc: 10.2;12.15] [keggfc:14.2] [sgdfc:3.4.0;4.8.2] [db:gic-saccharomyces]
CONTIG4782	353392050_c3_12	5425	19528	1626	542	YBL066C	652	5.2(10)-90	Saccharomyces cerevisiae	[ui:ybl066c] [pn:putative transcription factor;putative 118.2 kd transcriptional regulatory protein in ubp13-kip1 intergenic region] [gn:sefl,ybl0501,ybl0526] [gicfc: 10.2;12.15] [keggfc:14.2] [sgdfc:3.4.0;4.8.2] [db:gic-saccharomyces]

b9x11s19.x	21517807_c2_2	5426	19529	531	177	YBL066C	481	7.7(10)-45	Saccharomyces cerevisiae	[ui:ybl066c] [pn:putative transcription factor:putative 118.2 kd transcriptional regulatory protein in upb13-kip1 intergenic region] [gn:sef1:ybl0501:ybl0526] [gtcfc: 0.2:12.15] [keggfc: 14.2] [sgdfc:3.4:0.4:8.2] [db:gic-saccharomyces]
CONTIG5117	24015900_c1_7	5427	19530	2202	734	YBL052C	877	6.9(10)-88	Saccharomyces cerevisiae	[ui:ybl052c] [pn:silencing protein:hypothetical 97.6 kd protein in ptc3-sec17 intergenic region] [gn:sas3:ybl0515:ybl0507] [gtcfc:10.2:12.9] [keggfc: 14.2] [sgdfc: 3.3:0.4:8.2] [db:gic-saccharomyces cerevisiae]
CONTIG5690	5313390_c2_22	5428	19531	2916	972	YBR033W	99	0.25	Saccharomyces cerevisiae	[ui:ybr033w] [pn:weak similarity to transcription factors:putative 103.4 kd transcriptional regulatory protein in p12-odp1 intergenic region] [gn:ybr03118] [gtcfc: 10.2] [keggfc: 14.2] [sgdfc:4.8:2] [db:gic-saccharomyces cerevisiae]
CONTIG5253	23645200_f1_1	5429	19532	948	316	YBR061C	929	2.1(10)-93	Saccharomyces cerevisiae	[ui:ybr061c] [pn:similarity to e.coli ftsj protein:hypothetical 34.7 kd protein in orc2-tp1 intergenic region] [gn:ybr0527] [gtcfc: 10.2] [keggfc: 14.2] [sgdfc:4.8:2] [db:gic-saccharomyces cerevisiae]

CONTIG4558	34239382_f3_7	5430	19533	447	149	YBR215W	154	3.5(10)-10	Saccharomyces cerevisiae	[ui:ybr215w] [pn:cell cycle regulatory protein:histone promoter control 2 protein] [gn:hpc2:ybr1503] [gtcfc:10.2:12.8] [keggfc:14.2] [sgdfc:3.8:0:4.8:2] [db:gic:saccharomyces cerevisiae]
CONTIG4332	30251343_c1_8	5431	19534	1452	484	YBR245C	1761	1.5(10)-181	Saccharomyces cerevisiae	[ui:ybr245c] [pn:strong similarity to snf2/swi2 dna binding regulatory protein:hypothetical 132.7 kd helicase in alg7-emp1 intergenic region] [gn:ybr1633] [gtcfc:10.2] [keggfc: 14.2] [sgdfc:4.8:2] [db:gic-saccharomyces cerevisiae]
CONTIG4332	21642001_c1_7	5432	19535	330	110	YBR245C	146	5.7(10)-9	Saccharomyces cerevisiae	[ui:ybr245c] [pn:strong similarity to snf2/swi2 dna binding regulatory protein:hypothetical 132.7 kd helicase in alg7-emp1 intergenic region] [gn:ybr1633] [gtcfc:10.2] [keggfc: 14.2] [sgdfc:4.8:2] [db:gic-saccharomyces cerevisiae]
CONTIG4551	26384826_f2_2	5433	19536	838	286	YBR245C	490	1.0(10)-45	Saccharomyces cerevisiae	[ui:ybr245c] [pn:strong similarity to snf2/swi2 dna binding regulatory protein:hypothetical 132.7 kd helicase in alg7-emp1 intergenic region] [gn:ybr1633] [gtcfc:10.2] [keggfc: 14.2] [sgdfc:4.8:2] [db:gic-saccharomyces cerevisiae]

CONTIG5642	10188800_c2_19	5434	19537	669	223	YCR020C	185	2.1(10)-21	Saccharomyces cerevisiae	[ui:ycr020c] [pn:similarity to regulatory protein:pet18 protein] [gn:pet18;ycr20c] [gtfc:10.2] [keggc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG2578	10657875_c2_5	5435	19538	1395	465	YDL153C	381	5.7(10)-64	Saccharomyces cerevisiae	[ui:ydr153c] [pn:involved in silencing] [gn:sas10] [gtfc:10.2] [keggc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4067	26210886_f3_4	5436	19539	963	321	YDR017C	430	6.4(10)-51	Saccharomyces cerevisiae	[ui:ydr017c] [pn:potential transcription factor of the bzip type] [gn:kes1] [gtfc:10.2] [keggc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5453	4329067_c2_23	5437	19540	1476	492	YDR026C	273	1.0(10)-25	Saccharomyces cerevisiae	[ui:ydr026c] [pn:strong similarity to dna-binding protein rbf1p] [gtfc:10.2] [keggc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG2433	21972625_c3_4	5438	19541	705	235	YDR334W	627	4.2(10)-60	Saccharomyces cerevisiae	[ui:ydr334w] [pn:similarity to nuclear st1p, snf2p and related proteins] [gtfc:10.2] [keggc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4520	1458582_c3_7	5439	19542	2697	899	YDR334W	1462	1.3(10)-178	Saccharomyces cerevisiae	[ui:ydr334w] [pn:similarity to nuclear st1p, snf2p and related proteins] [gtfc:10.2] [keggc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5708	4787512_c2_24	5440	19543	3969	1323	YDR464W	122	0.0023	Saccharomyces cerevisiae	[ui:ydr464w] [pn:negative regulator of prp3 and prp4 gene expression:protein] [gn:spp4] [gtfc:10.2] [keggc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]

CONTIG3037	547083_f2_2	5441	19544	1215	405	YEL056W	473	2.7(10)-65	Saccharomyces cerevisiae	[ui:yei056w] [pn:subunit of the major yeast histone acetyltransferase:hypothetical trp-aspartate repeats containing protein in pcm1-rpl15b intergenic region] [gn:hat2] [gtcfc:10.2:0.7] [keggfc: 14.2] [sgdfc:4.8.2;6.3.0;9.2.0] [db:gtc-saccha-
CONTIG5752	13751312_f2_9	5442	19545	1497	499	YEL056W	494	2.7(10)-47	Saccharomyces cerevisiae	[ui:yei056w] [pn:subunit of the major yeast histone acetyltransferase:hypothetical trp-aspartate repeats containing protein in pcm1-rpl15b intergenic region] [gn:hat2] [gtcfc:10.2:10.7] [keggfc: 14.2] [sgdfc:4.8.2;6.3.0;9.2.0] [db:gtc-saccha-
CONTIG5770	14459375_f3_15	5443	19546	1278	426	YER027C	472	7.7(10)-78	Saccharomyces cerevisiae	[ui:yer027c] [pn:glucose repression protein:glucose repression protein gal83;spm1] [protein] [gn:gal83;spm1] [gtcfc:10.2:12.13] [keggfc: 14.2] [sgdfc: 1.5.2;4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG1916	24006261_f1_1	5444	19547	1332	444	YER164W	1651	6.5(10)-170	Saccharomyces cerevisiae	[ui:yer164w] [pn:hypothetical 168.2 kd protein in rad4-pab1 intergenic region] [gn:chd1 :sygp-orf4] [gtcfc:10.2] [keggfc: 14.2] [sgdfc: 4.8.2] [db:gtc-saccharomyces cerevisiae]

CONTIG241	1204413_c3_2	5445	19548	642	214	YER164W	803	5.5(10)-79	Saccharomyces cerevisiae	[ui:yer164w] [pn:transcriptional regulator:hypothetical 168.2 kd protein in rad4-pab1 intergenic region] [gn:chd1:sygp-orf4] [gicfc: 10.2] [keggfc: 14.2] [sgdfc: 4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG3287	31942_c3_7	5446	19549	1254	418	YER164W	365	3.6(10)-56	Saccharomyces cerevisiae	[ui:yer164w] [pn:transcriptional regulator:hypothetical 168.2 kd protein in rad4-pab1 intergenic region] [gn:chd1:sygp-orf4] [gicfc: 10.2] [keggfc: 14.2] [sgdfc: 4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG3940	19571965_c3_15	5447	19550	1053	351	YER169W	336	1.5(10)-29	Saccharomyces cerevisiae	[ui:yer169w] [pn:similarity to human retinoblastoma binding protein 2;putative 90.2 kd zinc finger protein in cca1-adk2 intergenic region] [gicfc: 10.2] [keggfc: 14.2] [sgdfc: 4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG2457	24016507_B_3	5448	19551	243	81	YGL221C	142	1.5(10)-9	Saccharomyces cerevisiae	[ui:ygl221c] [pn:nmg] [p:interacting factor 3:hypothetical 31.9 kd protein in gog5-clg1 intergenic region] [gn:nif3] [gicfc: 10.2] [keggfc: 14.2] [sgdfc: 4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG3428	24016507_c1_3	5449	19552	222	74	YGL221C	139	3.2(10)-9	Saccharomyces cerevisiae	[ui:ygl221c] [pn:nmg] [p:interacting factor 3:hypothetical 31.9 kd protein in gog5-clg1 intergenic region] [gn:nif3] [gicfc: 10.2] [keggfc: 14.2] [sgdfc: 4.8.2] [db:gic-saccharomyces cerevisiae]

b1x12535.y	638431_c3_5	5450	19553	306	102	YGL221C	178	1.1(10)-13	Saccharomyces cerevisiae	[ui:yg1221c] [pn:neg] p-interacting factor 3:hypothetical 31.9 kd protein in gog5-clg1 intergenic region [gn:nif3] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]
b3x19292.x	19625262_c1_3	5451	19554	699	233	YGL181W	404	9.1(10)-38	Saccharomyces cerevisiae	[ui:yg1181w] [pn:transcription factor of the ges1p/glo3p/sps18p family:gis1 protein:isrl protein] [gn:gis1:isrl] [gicfc:10.2:12.8:13.2] [keggfc:14.2] [sgdfc:3.2:0.3:8.0:4.8:2:11.0] [db:gic-saccharomyces cerevisiae]
CONTIG5777	4694055_c3_26	5452	19555	4185	1395	YGL150C	1758	1.3(10)-261	Saccharomyces cerevisiae	[ui:yg1150c] [pn:similarity to snf2p and human snf2alpha:hypothetical 171.5 kd helicase in lys5-aro2 intergenic region] [gn:gi1880] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG3283	1954656_c3_3	5453	19556	1707	569	YGL073W	415	2.5(10)-52	Saccharomyces cerevisiae	[ui:yg1073w] [pn:heat shock factor protein:hsf:heat shock transcription factor:hsf] [gn:hsf] [gicfc:12.7:10.2:13.2] [keggfc:14.2] [sgdfc:4.8.2:11.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG4623	24350010_c2_9	5454	19557	1491	497	YGL073W	93	0.46	Saccharomyces cerevisiae	[ui:yg1073w] [pn:heat shock factor protein:hsf:heat shock transcription factor:hsf] [gn:hsf] [gicfc:12.7:10.2:13.2] [keggfc:14.2] [sgdfc:4.8.2:11.1.0] [db:gic-saccharomyces cerevisiae]

CONTIG489	787510_c3_3	5455	19558	624	208	YGR097W	90	0.37	Saccharomyces cerevisiae	[uri:ygr097w] [pn:involved in skn7p-dependent transcription protein] [gn:ask10] [gtcfc:10.2] [keggfc:4.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4474	21698426_c3_8	5456	19559	1149	383	YGR100W	586	2.2(10)-56	Saccharomyces cerevisiae	[uri:ygr100w] [pn:mac1p interacting protein:mic1 protein] [gn:mic1:g5717] [gtcfc:10.2:13.2] [keggfc:14.2] [sgdfc:4.8.2:11.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4474	11223943_c2_6	5457	19560	1083	361	YGR100W	1222	1.8(10)-124	Saccharomyces cerevisiae	[uri:ygr100w] [pn:mac1p interacting protein:mic1 protein] [gn:mic1:g5717] [gtcfc:10.2:13.2] [keggfc:14.2] [sgdfc:4.8.2:11.1.0] [db:gtc-saccharomyces cerevisiae]
b9x13m30.y	4407157_f2_1	5458	19561	297	99	YGR100W	110	3.2(10)-5	Saccharomyces cerevisiae	[uri:ygr100w] [pn:mac1p interacting protein:mic1 protein] [gn:mic1:g5717] [gtcfc:10.2:13.2] [keggfc:14.2] [sgdfc:4.8.2:11.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4300	6145055_c3_12	5459	19562	1908	636	YHR178W	836	3.6(10)-88	Saccharomyces cerevisiae	[uri:yhr178w] [pn:sin3 binding protein:putative 83.5 kd transcriptional regulatory protein in eno2-oye2 intergenic region] [gn:stb5] [gtcfc:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4379	9845317_f1_1	5460	19563	2016	672	YHR178W	91	0.65	Saccharomyces cerevisiae	[uri:yhr178w] [pn:sin3 binding protein:putative 83.5 kd transcriptional regulatory protein in eno2-oye2 intergenic region] [gn:stb5] [gtcfc:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]

CONTIG5812	13759657_f3_18	5461	19564	711	237	YHR178W	103	0.0071	Saccharomyces cerevisiae	[ui:yhr178w] [pn:sin3 binding protein;putative 83.5 kd transcriptional regulatory protein in eno2-oye2 intergenic region] [gn:stb5] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG1667	34385005_f2_1	5462	19565	1227	409	YIL130W	99	0.063	Saccharomyces cerevisiae	[ui:yil130w] [pn:similarity to put3p and to hypothetical protein yjl206c;putative 108.8 kd transcriptional regulatory protein in fkh1-sth1 intergenic region] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG2486	190937_f1_1	5463	19566	588	196	YIL130W	99	0.016	Saccharomyces cerevisiae	[ui:yil130w] [pn:similarity to put3p and to hypothetical protein yjl206c;putative 108.8 kd transcriptional regulatory protein in fkh1-sth1 intergenic region] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG3929	26615877_c1_1	5464	19567	2190	730	YIL130W	171	3.7(10)-9	Saccharomyces cerevisiae	[ui:yil130w] [pn:similarity to put3p and to hypothetical protein yjl206c;putative 108.8 kd transcriptional regulatory protein in fkh1-sth1 intergenic region] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]

CONTIG4508	11718875_02_3	5465	19568	1605	535	YIL130W	130	6.0(10)-5	Saccharomyces cerevisiae	[uiyil130w] [pn:similarity to put3p and to hypothetical protein yjl206c;putative 108.8 kd transcriptional regulatory protein in fkh1-sth1 intergenic region] [gicfc:10.2] [keggfc:14.2] [sgdgc:4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG4575	10172526_01_7	5466	19569	792	264	YIL130W	205	2.2(10)-15	Saccharomyces cerevisiae	[uiyil130w] [pn:similarity to put3p and to hypothetical protein yjl206c;putative 108.8 kd transcriptional regulatory protein in fkh1-sth1 intergenic region] [gicfc:10.2] [keggfc:14.2] [sgdgc:4.8.2] [db:gic-saccharomyces cerevisiae]
b3x17449_y	24412675_03_4	5467	19570	327	109	YIL130W	132	1.3(10)-7	Saccharomyces cerevisiae	[uiyil130w] [pn:similarity to put3p and to hypothetical protein yjl206c;putative 108.8 kd transcriptional regulatory protein in fkh1-sth1 intergenic region] [gicfc:10.2] [keggfc:14.2] [sgdgc:4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG4784	32229813_F2_6	5468	19571	792	264	YIL050W	223	9.3(10)-34	Saccharomyces cerevisiae	[uiyil050w] [pn:similarity to ncrassa regulatory protein preg+;hypothetical 32.0 kd protein in gpp1-sygl intergenic region] [gicfc:10.2] [keggfc:14.2] [sgdgc:4.8.2] [db:gic-saccharomyces cerevisiae]

CONTIG2883	10579552_f3_4	5469	19572	321	107	YJL115W	277	2.6(10)-24	Saccharomyces cerevisiae	[ui:yjl115w] [pn:anti-silencing protein.anti-silencing protein 1] [gn:asfl_j0755] [gtcfc:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4945	25665938_f2_1	5470	19573	1578	526	YJL115W	113	0.00059	Saccharomyces cerevisiae	[ui:yjl115w] [pn:anti-silencing protein.anti-silencing protein 1] [gn:asfl_j0755] [gtcfc:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG1122	7320285_c2_2	5471	19574	723	241	YJR032W	547	6.5(10)-53	Saccharomyces cerevisiae	[ui:yjr032w] [pn:member of the cyclophilin family:peptidyl-prolyl cis-trans isomerase cyp7:ppiaser:rotamase] [gn:cpr7_jl585] [gtcfc:10.2:10.5:10.7:12.7:12.8] [ec:5.2.1.8] [keggfc:14.1] [sgdfc:3.1.0.4.8.2.6.1.0] [db:gtc-saccharomyces ce]
CONTIG5620	7893_f1_2	5472	19575	1221	407	YJR032W	599	2.2(10)-72	Saccharomyces cerevisiae	[ui:yjr032w] [pn:member of the cyclophilin family:peptidyl-prolyl cis-trans isomerase cyp7:ppiaser:rotamase] [gn:cpr7_jl585] [gtcfc:10.2:10.5:10.7:12.7:12.8] [ec:5.2.1.8] [keggfc:14.1] [sgdfc:3.1.0.4.8.2.6.1.0] [db:gtc-saccharomyces ce]
CONTIG3852	36382953_f3_1	5473	19576	1524	508	YJR119C	132	2.7(10)-12	Saccharomyces cerevisiae	[ui:yjr119c] [pn:similarity to human retinoblastoma binding protein 2:hypothetical 85.0 kd protein in nmfl-atp2 intergenic region] [gn:j2035] [gtcfc:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]

CONTIG5804	20343762_f2_19	5474	19577	393	131	YJR119C	172	5.2(10)-12	Saccharomyces cerevisiae	[ui:yjr119c] [pn:similarity to human retinoblastoma binding protein 2:hypothetical 85.0 kd protein in nnfl -atp2 intergenic region] [gn:J20351][gtcfc:10.2] [keggfc: 14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG5804	20704760_f2_20	5475	19578	1800	600	YJR119C	806	2.2(10)-80	Saccharomyces cerevisiae	[ui:yjr119c] [pn:similarity to human retinoblastoma binding protein 2:hypothetical 85.0 kd protein in nnfl -atp2 intergenic region] [gn:J20351][gtcfc:10.2] [keggfc: 14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG5322	24228466_f2_4	5476	19579	660	220	YKL185W	295	1.8(10)-25	Saccharomyces cerevisiae	[ui:ykl185w] [pn:negative regulator of ho expression:hypothetical 65.7 kd protein in mtr2-ord1 intergenic region] [gn:gnash1][gtcfc: 10.2:12.9] [keggfc: 14.2] [sgdfc:3.3.0:4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG1694	33484567_c1_4	5477	19580	984	328	YKL072W	90	0.5	Saccharomyces cerevisiae	[ui:ykl072w] [pn:sin3 binding protein:hypothetical 88.8 kd protein in lhs1-nup100 intergenic region] [gn:stb6.yk1352][gtcfc: 0.2] [keggfc: 14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]

b3x13540_y	1116379_cl_2	5478	19581	444	148	YKL070W	213	1.6(10)-17	Saccharomyces cerevisiae	[ui:ykl070w] [pn:similarity to b.subtilis transcriptional regulatory protein:hypothetical 19.8 kd protein in lls1-nup100 intergenic region] [gn:ykl1343] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG1623	4490650_f2_2	5479	19582	798	266	YKR036C	129	1.5(10)-5	Saccharomyces cerevisiae	[ui:ykr036c] [pn:ccr4 associated factor:hypothetical trp-asp repeats containing protein in dal80-gap1 intergenic region] [gn:caf4] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG2785	1203385_f2_3	5480	19583	648	216	YKR036C	129	6.0(10)-6	Saccharomyces cerevisiae	[ui:ykr036c] [pn:ccr4 associated factor:hypothetical trp-asp repeats containing protein in dal80-gap1 intergenic region] [gn:caf4] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG3407	35580275_f2_2	5481	19584	312	104	YKR064W	104	0.00012	Saccharomyces cerevisiae	[ui:ykr064w] [pn:weak similarity to transcription factors:putative 101.8 kd transcriptional regulatory protein in las1-cpl1 intergenic region] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]

CONTIG4938	25596942_f3_4	5482	19585	528	176	YLR136C	239	2.7(10)-20	Saccharomyces cerevisiae	[uiylr136c] [pn:member of the inducible coch zinc-finger family:zinc finger protein cth2:yts11 protein] [gn:cth2:yts11:19606] [gtfcfc:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG4311	23681561_f3_5	5483	19586	1224	408	YLR216C	943	7.0(10)-95	Saccharomyces cerevisiae	[uiylr216c] [pn:member of the cyclophilin family:peptidyl-prolyl cis-trans isomerase] [gn:cpr6:18.67] [gtfcfc:10.2:10.5:10.7:12.7:14.1] [ec:5.2.1.8] [keggfc:14.1] [sgdfc:4.8.2:6.1.0:9.2.0] [db:gic-saccharomyces ce]
CONTIG3802	266942_c1_8	5484	19587	759	253	YLR228C	204	2.2(10)-15	Saccharomyces cerevisiae	[uiylr228c] [pn:strong similarity to ydr213w, weak similarity to lys14p] [gtfcfc:0.2] [keggfc: 14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG4763	6370753_f2_3	5485	19588	1212	404	YLR228C	917	4.0(10)-92	Saccharomyces cerevisiae	[uiylr228c] [pn:strong similarity to ydr213w, weak similarity to lys14p] [gtfcfc:10.2] [keggfc: 14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG4218	21517037_f3_2	5486	19589	1152	384	YML081W	280	3.2(10)-23	Saccharomyces cerevisiae	[uiyml081w] [pn:strong similarity to zms1 protein] [gtfcfc:10.2] [keggfc: 14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]

CONTIG4755	25978317_f3_2	5487	19590	2022	674	YML081W	373	4.9(10)-31	Saccharomyces cerevisiae	[ui:yml081w] [pn:strong similarity to zms1 protein] [gtcfc: 10.2] [keggfc: 14.2] [sgdfc: 4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG2923	34406717_f3_4	5488	19591	1263	421	YMR019W	183	1.5(10)-19	Saccharomyces cerevisiae	[ui:ymr019w] [pn:sin3 binding protein] putative 109.8 kd transcriptional regulatory protein in sok2-fms1 intergenic region [gn:stb4:ymr971] [gtcfc: 10.2] [keggfc: 14.2] [sgdfc: 4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4039	3164050_c2_7	5489	19592	1110	370	YMR019W	111	0.00359	Saccharomyces cerevisiae	[ui:ymr019w] [pn:sin3 binding protein] putative 109.8 kd transcriptional regulatory protein in sok2-fms1 intergenic region [gn:stb4:ymr971] [gtcfc: 10.2] [keggfc: 14.2] [sgdfc: 4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4390	26378336_c3_10	5490	19593	939	313	YMR019W	126	3.0(10)-5	Saccharomyces cerevisiae	[ui:ymr019w] [pn:sin3 binding protein] putative 109.8 kd transcriptional regulatory protein in sok2-fms1 intergenic region [gn:stb4:ymr971] [gtcfc: 10.2] [keggfc: 14.2] [sgdfc: 4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4765	4163211_c3_8	5491	19594	789	263	YMR019W	194	3.3(10)-14	Saccharomyces cerevisiae	[ui:ymr019w] [pn:sin3 binding protein] putative 109.8 kd transcriptional regulatory protein in sok2-fms1 intergenic region [gn:stb4:ymr971] [gtcfc: 10.2] [keggfc: 14.2] [sgdfc: 4.8.2] [db:gtc-saccharomyces cerevisiae]

b9x13233.x	20806887_c3_1	5492	19595	621	207	YMR053C	165	3.7(10)-11	Saccharomyces cerevisiae	[ui:ymr053c] [pn:sin3p binding protein:stb2 protein] [gn:stb2;ymr979c] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG5814	34173260_c1_36	5493	19596	1077	359	YNR127C	524	2.3(10)-58	Saccharomyces cerevisiae	[ui:ymr127c] [pn:involved in silencing at fmr:sas2 protein] [gn:sas2;ymr9553] [gicfc:10.2;12.8;12.9] [keggfc:14.2] [sgdfc:3.3.0;3.8.0;4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG5741	10634655_f3_8	5494	19597	768	256	YNL107W	282	7.5(10)-38	Saccharomyces cerevisiae	[ui:ynl107w] [pn:similarity to human af-9 protein:hypothetical 26.0 kd protein in cyb5-leu4 intergenic region] [gn:nl1966] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG5142	956251_c2_6	5495	19598	357	119	YOL133W	388	4.5(10)-36	Saccharomyces cerevisiae	[ui:yol133w] [pn:similarity to human ring-finger protein] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG3634	21678177_c1_7	5496	19599	1020	340	YOL068C	631	5.5(10)-94	Saccharomyces cerevisiae	[ui:yol068c] [pn:silencing protein:protein] [gn:hts1] [gicfc:10.2;12.9] [keggfc:14.2] [sgdfc:3.3.0;4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG5551	962637_f1_3	5497	19600	1644	548	YOL055C	462	9.0(10)-55	Saccharomyces cerevisiae	[ui:yol055c] [pn:weak similarity to bacterial transcription factors] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]

CONTIG4179	2775332_f2_1	5498	19601	1467	489	YOR025W	838	9.4(10)-84	Saccharomyces cerevisiae	[ui:yor025w] [pn:silencing protein:hst3 protein] [gr:hst3.or26] [gtcfc:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG3722	14642938_f3_2	5499	19602	1827	609	YOR304W	1781	1.1(10)-183	Saccharomyces cerevisiae	[ui:yor304w] [pn:strong similarity to human snf2p homolog] [gtcfc:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG4332	22285135_c2_10	5500	19603	237	79	YOR304W	155	6.0(10)-10	Saccharomyces cerevisiae	[ui:yor304w] [pn:strong similarity to human snf2p homolog] [gtcfc:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG5389	9960258_c2_17	5501	19604	276	92	YOR304W	225	2.1(10)-17	Saccharomyces cerevisiae	[ui:yor304w] [pn:strong similarity to human snf2p homolog] [gtcfc:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG389	1302_c2_16	5502	19605	273	91	YOR304W	142	1.5(10)-8	Saccharomyces cerevisiae	[ui:yor304w] [pn:strong similarity to human snf2p homolog] [gtcfc:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG3787	34087807_c2_8	5503	19606	852	284	YPL015C	663	3.2(10)-65	Saccharomyces cerevisiae	[ui:ypl015c] [pn:similarity to hst1p and sir2p:hst2 protein] [gr:hst2:p2a2] [gtcfc:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]

CONTIG5531	34462782_f3_20	5504	19607	795	265	YPR115W	118	4.2(10)-9	Saccharomyces cerevisiae	[ui:ypf115w] [pn:similarity to probable transcription factor ask10p, and to hypothetical proteins ynl047c and yil105cl] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG5531	24844186_f2_14	5505	19608	1182	394	YPR115W	136	9.0(10)-6	Saccharomyces cerevisiae	[ui:ypf115w] [pn:similarity to probable transcription factor ask10p, and to hypothetical proteins ynl047c and yil105cl] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gic-saccharomyces cerevisiae]
CONTIG5468	3943927_c1_15	5506	19609	1476	492	YAL013W	159	4.2(10)-9	Saccharomyces cerevisiae	[ui:yaf013w] [pn:regulator of phospholipid metabolism:dep1 protein] [gn:dep1.fun54] [gicfc:10.2] [keggfc:14.2] [sgdfc: 1.6.4:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG2498	3937516_c2_4	5507	19610	852	284	YGL162W	108	0.00046	Saccharomyces cerevisiae	[ui:ygl162w] [pn:hypoxic protein involved in sterol uptake:probable sterol carrier] [gn:sut1.g1828] [gicfc:10.2] [keggfc:14.2] [sgdfc: 1.6.4] [db:gic-saccharomyces cerevisiae]
CONTIG5619	875463_f2_5	5508	19611	513	171	YJL096W	220	2.8(10)-18	Saccharomyces cerevisiae	[ui:yj096w] [pn:putative regulator of purine and/or pyrimidine biosynthesis:hypothetical 25.4 kd protein in sap185-bck1 intergenic region] [gn:j0904] [gicfc:10.2] [keggfc:14.2] [sgdfc:1.3.5] [db:gic-saccharomyces cerevisiae]

CONTIG5357	20895052_c1_14	5509	19612	702	234	YOL110W	152	2.5(10)-10	Saccharomyces cerevisiae	[ui:yol110w] [pn:ras suppressor:ras modification protein sh5] [gn:sh5:hr0237] [gtcfc:10.2:12.13:12.8:13.2] [keggfc:14.2] [sgdfc: 1.3.5:1.5.2:3.10.0:10.4.8] [db:gtc-saccharomyces cerevisiae]
CONTIG1003	24251676_c2_1	5510	19613	798	266	YOR101W	550	3.1(10)-53	Saccharomyces cerevisiae	[ui:yor101w] [pn:gtp-binding protein:ras-like protein 1] [gn:ras]:yor3205w [gtcfc:10.2:11.1:12.13:12.8] [keggfc:13.1] [sgdfc: 1.3.5:1.5.2:3.10.0:9.1.0:10.4.4:11.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3766	3908311_f1_1	5511	19614	996	332	YOR101W	221	1.1(10)-17	Saccharomyces cerevisiae	[ui:yor101w] [pn:gtp-binding protein:ras-like protein 1] [gn:ras]:yor3205w [gtcfc:10.2:11.1:12.13:12.8] [keggfc:13.1] [sgdfc: 1.3.5:1.5.2:3.10.0:9.1.0:10.4.4:11.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5802	4803441_f2_17	5512	19615	567	189	YOR101W	352	3.0(10)-32	Saccharomyces cerevisiae	[ui:yor101w] [pn:gtp-binding protein:ras-like protein 1] [gn:ras]:yor3205w [gtcfc:10.2:11.1:12.13:12.8] [keggfc:13.1] [sgdfc: 1.3.5:1.5.2:3.10.0:9.1.0:10.4.4:11.5.0] [db:gtc-saccharomyces cerevisiae]

b9x11m02.x	14068917_c2_5	5513	19616	711	237	YOR101W	437	2.8(10)-41	Saccharomyces cerevisiae	[ui.yor101w] [pn:gtp-binding protein;ras-like protein 1] [gn:ras1:yor3205w] [gtfc:10.2:11.1:12.13:12.8] [keggc:13.1] [sgfc:1.3.5:1.5:2.3.10.0:9.1.0:10.4. 4:11.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1745	24001542_c3_6	5514	19617	648	216	YFR004W	220	2.8(10)-18	Saccharomyces cerevisiae	[ui.yfr004w] [pn:strong similarity to s.pombe pad1 protein:protein] [gn:mpr1] [gtfc:10.2:10.6] [keggc:14.2] [sgfc:4.4:0:4.5.0] [db:gtc-saccharomyces cerevisiae]
b2x19164.x	33385_c1_6	5515	19618	783	261	YFR004W	894	1.1(10)-89	Saccharomyces cerevisiae	[ui.yfr004w] [pn:strong similarity to s.pombe pad1 protein:protein] [gn:mpr1] [gtfc:10.2:10.6] [keggc:14.2] [sgfc:4.4:0:4.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5668	163188_f1_1	5516	19619	1893	631	YBR238C	438	2.0(10)-39	Saccharomyces cerevisiae	[ui.ybr238c] [pn:strong similarity to general chromatin factor spt16p:hypothetical 83.7 kd protein in pnp5-alg7 intergenic region] [gn:ybr1608] [gtfc:10.2:12.8] [keggc:14.2] [sgfc:3.8:0:4.8.3] [db:gtc-saccharomyces cerevisiae]
CONTIG4750	15134650_c2_7	5517	19620	2280	760	YBR212W	470	4.2(10)-79	Saccharomyces cerevisiae	[ui.ybr212w] [pn:glucose-repressible rna-binding protein:negative growth regulatory protein ngr1:ma- binding protein rbp1] [gn:ngr1:rbp1:ybr1459] [gtfc:10.2:12.8] [keggc:14.2] [sgfc:3.1.0:4.12.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2397	9939050_c2_3	5518	19621	894	298	YBR233W	195	5.7(10)-15	Saccharomyces cerevisiae	[ui:ybr233w] [pn:similarity to human hnmp-e] protein:hypothetical 45.8 kd protein in pes60-abd1 intergenic region] [gn:ybr153] [gicfc: 10.2] [keggfc: 14.2] [sgdfc: 4.12.0] [db:gic-saccharomyces cerevisiae]
CONTIG5481	22479187_c1_12	5519	19622	966	322	YBR233W	347	1.0(10)-31	Saccharomyces cerevisiae	[ui:ybr233w] [pn:similarity to human hnmp-e] protein:hypothetical 45.8 kd protein in pes60-abd1 intergenic region] [gn:ybr153] [gicfc: 10.2] [keggfc: 14.2] [sgdfc: 4.12.0] [db:gic-saccharomyces cerevisiae]
CONTIG4607	10737577_f3_6	5520	19623	435	145	YCL033C	310	8.4(10)-28	Saccharomyces cerevisiae	[ui:yc1033c] [pn:similarity to m.capricolum transcription repressor:hypothetical 19.3 kd protein in ste50 5"region] [gn:yc133c] [gicfc: 10.2] [keggfc: 14.2] [sgdfc: 4.12.0] [db:gic-saccharomyces cerevisiae]
CONTIG2363	13710252_q3_7	5521	19624	477	159	YCR004C	504	2.2(10)-48	Saccharomyces cerevisiae	[ui:ycr004c] [pn:strong similarity to s.pombe protein obr1:hypothetical 26.4 kd protein in cdc10-cit2 intergenic region] [gn:yp4:yer4c:yer042] [gicfc: 10.2] [keggfc: 14.2] [sgdfc: 4.12.0] [db:gic-saccharomyces cerevisiae]

CONTIG434	22712776_c2_2	5522	19625	813	271	YCR004C	598	2.5(10)-58	Saccharomyces cerevisiae	[ui:ycr004c] [pn:strong similarity to s. pombe protein obr1:hypothetical 26.4 kd protein in cdc10-cit2 intergenic region] [gn:yp4:ycrc4:ycr042] [gtcfc:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5438	21956281_c2_18	5523	19626	681	227	YCR004C	610	1.3(10)-59	Saccharomyces cerevisiae	[ui:ycr004c] [pn:strong similarity to s. pombe protein obr1:hypothetical 26.4 kd protein in cdc10-cit2 intergenic region] [gn:yp4:ycrc4:ycr042] [gtcfc:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5438	20509375_f3_10	5524	19627	768	256	YCR004C	566	6.2(10)-55	Saccharomyces cerevisiae	[ui:ycr004c] [pn:strong similarity to s. pombe protein obr1:hypothetical 26.4 kd protein in cdc10-cit2 intergenic region] [gn:yp4:ycrc4:ycr042] [gtcfc:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5343	6735005_c2_16	5525	19628	420	140	YCR087C-A	243	1.1(10)-20	Saccharomyces cerevisiae	[ui:ycr087c-a] [pn:nucleic acid-binding protein:hypothetical 17.7 kd protein in abp1 5' region] [gn:ycrx16c] [gtcfc:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4385	24617258_f1_1	5526	19629	843	281	YDL051W	167	1.7(10)-12	Saccharomyces cerevisiae	[ui:ydl051w] [pn:rna binding protein:a protein homolog] [gn:lah1:lhpl:yal1] [gtcfc:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3713	22307888_c3_10	5527	19630	1146	382	YDL031W	923	9.3(10)-93	Saccharomyces cerevisiae	[ui:yd1031w] [pn:similarity to ma helicases] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gic-saccharomyces cerevisiae]
CONTIG405	25430337_f3_2	5528	19631	810	270	YDL031W	776	3.5(10)-77	Saccharomyces cerevisiae	[ui:yd1031w] [pn:similarity to ma helicases] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gic-saccharomyces cerevisiae]
b2x12979.x	5331552_f1_1	5529	19632	561	187	YDL031W	400	3.2(10)-36	Saccharomyces cerevisiae	[ui:yd1031w] [pn:similarity to ma helicases] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gic-saccharomyces cerevisiae]
CONTIG571	3947692_f1_1	5530	19633	411	137	YDR043C	233	1.2(10)-19	Saccharomyces cerevisiae	[ui:yd43c] [pn:weak similarity to k.marxianus mig1 and other regulatory proteins] [gicfc:0.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gic-saccharomyces cerevisiae]
CONTIG5754	23550337_c1_24	5531	19634	900	300	YDR429C	479	1.0(10)-45	Saccharomyces cerevisiae	[ui:yd429c] [pn:similarity to nuclear ma binding proteins] [gicfc:0.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gic-saccharomyces cerevisiae]
CONTIG4050	1204390_c3_6	5532	19635	1002	334	YGL171W	453	5.9(10)-43	Saccharomyces cerevisiae	[ui:yg171w] [pn:atp-dependent ma helicase;atp-dependent ma helicase rok1] [gn:rok1:g16511] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gic-saccharomyces cerevisiae]
b1x13309.x	3020816_f1_1	5533	19636	609	203	YGL171W	706	9.1(10)-70	Saccharomyces cerevisiae	[ui:yg171w] [pn:atp-dependent ma helicase;atp-dependent ma helicase rok1] [gn:rok1:g16511] [gicfc:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gic-saccharomyces cerevisiae]

CONTIG2561	34179687_c3_3	5534	19637	510	170	YGL127C	185	1.5(10)-14	Saccharomyces cerevisiae	[ui:ygl127c] [pn:allows hpr1 null mutant to grow at 37 deg;soh1 protein] [gn:soh1_g2864] [gtfc:10.2:10.8] [keggfc:14.2] [sgdfc:3.7.0:4.12.0] [db:gic-saccharomyces cerevisiae]
CONTIG2747	2151131_c2_3	5535	19638	1170	390	YGL014W	356	6.2(10)-49	Saccharomyces cerevisiae	[ui:ygl14w] [pn:similarity to drosophila pumilio protein and mpt5p protein;hypothetical regulatory protein in pdr6-pdr1 intergenic region] [gn:ygl023] [gtfc:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gic-saccharomyces cerevisiae]
CONTIG5525	4329575_f1_3	5536	19639	1749	583	YGL014W	476	1.6(10)-44	Saccharomyces cerevisiae	[ui:ygl14w] [pn:similarity to drosophila pumilio protein and mpt5p protein;hypothetical regulatory protein in pdr6-pdr1 intergenic region] [gn:ygl023] [gtfc:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gic-saccharomyces cerevisiae]
CONTIG3729	16829030_c1_4	5537	19640	1311	437	YGR067C	231	4.5(10)-17	Saccharomyces cerevisiae	[ui:ygr067c] [pn:weak similarity to transcription factors;putative 91.0 kd zinc finger protein in spf4-rom1 intergenic region] [gtfc:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gic-saccharomyces cerevisiae]
CONTIG2764	22055252_c2_11	5538	19641	1104	368	YHR169W	1072	1.5(10)-108	Saccharomyces cerevisiae	[ui:yhr169w] [pn:strong similarity to dead box rna helicase;putative aip-dependent rna helicase yhr169w] [gtfc:0.2] [keggfc:4.2] [sgdfc:4.12.0] [db:gic-saccharomyces cerevisiae]

CONTIG5584	15017211_o3_13	5539	19642	228	76	YHR169W	181	2.2(10)-13	Saccharomyces cerevisiae	[ui:yhr169w] [pn:strong similarity to dead box ma helicases:putative atp-dependent ma helicase yhr169w] [gicfc:10.2] [Keggfc:14.2] [sgdfc:4.12.0] [db:gic-saccharomyces cerevisiae]
CONTIG3603	34179556_o2_6	5540	19643	1665	555	YHR170W	1516	1.3(10)-155	Saccharomyces cerevisiae	[ui:yhr170w] [pn:nonsense-mediated mrna decay protein:nonsense-mediated mrna decay protein 3] [gn:nmd3] [gicfc:0.2] [keggfc:4.2] [sgdfc:4.12.0] [db:gic-saccharomyces cerevisiae]
CONTIG5333	30719437_f2_2	5541	19644	480	160	YHR170W	141	6.7(10)-9	Saccharomyces cerevisiae	[ui:yhr170w] [pn:nonsense-mediated mrna decay protein:nonsense-mediated mrna decay protein 3] [gn:nmd3] [gicfc:0.2] [keggfc:4.2] [sgdfc:4.12.0] [db:gic-saccharomyces cerevisiae]
CONTIG5757	21509380_f2_3	5542	19645	2139	713	YIL105C	507	1.1(10)-48	Saccharomyces cerevisiae	[ui:yil105c] [pn:weak similarity to probable transcription factor ask10p:hypothetical 78.0 kd protein in pR26-sga1 intergenic region] [gicfc:0.2] [keggfc:4.2] [sgdfc:4.12.0] [db:gic-saccharomyces cerevisiae]
CONTIG5722	1375400_f2_7	5543	19646	3651	1217	YIL030C	577	1.1(10)-86	Saccharomyces cerevisiae	[ui:yil030c] [pn:involved in mma turnover:ssm4 protein] [gn:ssm4:yi3299] [gicfc:10.2] [Keggfc:14.2] [sgdfc:4.12.0] [db:gic-saccharomyces cerevisiae]

CONTIG3532	26369157_c2_10	5544	19647	771	257	YIR001C	216	7.7(10)-18	Saccharomyces cerevisiae	[uri:yir001c] [pn:similarity to d.melanogaster rna binding protein;hypothetical 29.0 kd protein in bet1-pan1 intergenic region] [gn:yib1c] [grfc:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3773	26370316_f2_3	5545	19648	513	171	YIR001C	238	3.6(10)-20	Saccharomyces cerevisiae	[uri:yir001c] [pn:similarity to d.melanogaster rna binding protein;hypothetical 29.0 kd protein in bet1-pan1 intergenic region] [gn:yib1c] [grfc:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5223	3917563_c3_14	5546	19649	1071	357	YIR005W	255	5.7(10)-22	Saccharomyces cerevisiae	[uri:yir005w] [pn:similarity to man-binding proteins;hypothetical 17.1 kd protein in bet1-pan1 intergenic region] [gn:yib5w] [grfc:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5594	31298426_c1_12	5547	19650	297	99	YJL124C	134	3.7(10)-9	Saccharomyces cerevisiae	[uri:yjl124c] [pn:weak similarity to human sm protein g;hypothetical 20.3 kd protein in gcd14-pos18 intergenic region] [gn:j0714] [grfc:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4617	15626338_f2_2	5548	19651	2289	763	YML017W	156	3.0(10)-11	Saccharomyces cerevisiae	[uri:yml017w] [pn:suppressor of dha polymerase alpha mutation;psp2 protein] [gn:psp2;ym9571] [grfc: 10.2] [keggfc: 14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5315	24300255_f2_4	5549	19652	873	291	YMR213W	359	1.7(10)-32	Saccharomyces cerevisiae	[uiymr213w] [pn:similarity to s.pombe putative transcription factor cdc5:hypothetical 67.7 kd protein in rar1-scl1 intergenic region] [gn:yjm9646] [gtcfc:10.2] [keggc:14.2] [sgdgc:4.12.0] [db:gic-saccharomyces cerevisiae]
CONTIG1236	15761316_c2_5	5550	19633	531	177	YNL255C	398	4.0(10)-37	Saccharomyces cerevisiae	[uiyml255c] [pn:strong similarity to nucleic acid-binding proteins:hypothetical 17.1 kd protein in rpl3-mrp130 intergenic region] [gn:n0852] [gtcfc:10.2] [keggc:14.2] [sgdgc:4.12.0] [db:gic-saccharomyces cerevisiae]
CONTIG5079	6054138_c2_8	5551	19634	1233	411	YNL175C	583	9.9(10)-57	Saccharomyces cerevisiae	[uiyml175c] [pn:similarity to s.pombe rpl24p:hypothetical 45.7 kd protein in rps3-psd1 intergenic region] [gn:n1665] [gtcfc:10.2] [keggc:14.2] [sgdgc:4.12.0] [db:gic-saccharomyces cerevisiae]
CONTIG4233	23489151_c3_4	5552	19655	330	110	YNL027W	259	2.1(10)-21	Saccharomyces cerevisiae	[uiyml027w] [pn:similarity to zinc-finger proteins:hypothetical 76.3 kd zinc finger protein in hhf2-ume3 intergenic region] [gn:n2760] [gtcfc:10.2] [keggc:14.2] [sgdgc:4.12.0] [db:gic-saccharomyces cerevisiae]
CONTIG4828	2150313_c1_7	5553	19656	1245	415	YNL027W	188	8.0(10)-12	Saccharomyces cerevisiae	[uiyml027w] [pn:similarity to zinc-finger proteins:hypothetical 76.3 kd zinc finger protein in hhf2-ume3 intergenic region] [gn:n2760] [gtcfc:10.2] [keggc:14.2] [sgdgc:4.12.0] [db:gic-saccharomyces cerevisiae]

CONTIG5723	4119002_c3_35	5554	19657	288	96	YNR063W	135	3.7(10)-8	Saccharomyces cerevisiae	[ui:ymr063w] [pn:weak similarity to cyc1/cyp3 transcription activator;putative transcriptional regulatory protein in b03-hxt17 intergenic region] [gn:n3531] [keggc:10.2] [keggc:14.2] [sgdgc:4.12.0] [db:gic-saccharomyces cerevisiae]
CONTIG5781	16831535_c3_32	5555	19658	1632	544	YCR244W	1180	7.0(10)-132	Saccharomyces cerevisiae	[ui:yor244w] [pn:similarity to sas2p and sas3p] [gtcfc:10.2] [keggc:14.2] [sgdgc:4.12.0] [db:gic-saccharomyces cerevisiae]
CONTIG3139	9773376_c3_12	5556	19659	795	265	YPL230W	271	1.1(10)-23	Saccharomyces cerevisiae	[ui:yp1230w] [pn:similarity to transcription factors] [gtcfc:10.2] [keggc:14.2] [sgdgc:4.12.0] [db:gic-saccharomyces cerevisiae]
CONTIG2137	13759635_f2_1	5557	19660	402	134	YPL133C	138	1.1(10)-8	Saccharomyces cerevisiae	[ui:yp1133c] [pn:weak similarity to transcription factors;putative transcriptional regulatory protein in mkk2-cox11 intergenic region] [gn:ipi12c] [gtcfc:10.2] [keggc:14.2] [sgdgc:4.12.0] [db:gic-saccharomyces cerevisiae]
CONTIG2962	9852266_f3_3	5558	19661	1185	395	YPL133C	873	6.2(10)-97	Saccharomyces cerevisiae	[ui:yp1133c] [pn:weak similarity to transcription factors;putative transcriptional regulatory protein in mkk2-cox11 intergenic region] [gn:ipi12c] [gtcfc:10.2] [keggc:14.2] [sgdgc:4.12.0] [db:gic-saccharomyces cerevisiae]
CONTIG3967	47885_f2_2	5559	19662	1143	381	YPR013C	187	2.2(10)-13	Saccharomyces cerevisiae	[ui:ypr013c] [pn:similarity to transcription factors] [gtcfc:10.2] [keggc:14.2] [sgdgc:4.12.0] [db:gic-saccharomyces cerevisiae]

CONTIG2677	34663912_c2_8	5560	19663	2001	667	YPR031W	833	2.7(10)-92	Saccharomyces cerevisiae	[ui:ypr031w] [pn:similarity to human zinc-finger protein br140] [gicfc: 10.2] [keggfc: 14.2] [sgdfc: 4.12.0] [db:gic-saccharomyces cerevisiae]
CONTIG2941	4569427_f1_1	5561	19664	774	258	YPR031W	117	0.00038	Saccharomyces cerevisiae	[ui:ypr031w] [pn:similarity to human zinc-finger protein br140] [gicfc: 10.2] [keggfc: 14.2] [sgdfc: 4.12.0] [db:gic-saccharomyces cerevisiae]
CONTIG5797	4476387_c3_36	5562	19665	657	219	YPR107C	655	2.2(10)-64	Saccharomyces cerevisiae	[ui:ypr107c] [pn:strong similarity to d.melanogaster zinc finger protein] [gicfc: 10.2] [keggfc: 14.2] [sgdfc: 4.12.0] [db:gic-saccharomyces cerevisiae]
CONTIG4909	7827_f1_1	5563	19666	1620	540	YHR065C	1309	1.2(10)-133	Saccharomyces cerevisiae	[ui:yhr065c] [pn:required for maturation of the 35s primary transcript atp-dependent rna helicase] [gn:rtp3] [gicfc: 10.3] [keggfc: 14.2] [sgdfc: 4.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG3377	2737785_c2_7	5564	19667	648	216	YJL033W	214	1.8(10)-16	Saccharomyces cerevisiae	[ui:yj033w] [pn:can suppress the u14 snorna rna processing function:probable atp-dependent rna helicase ca4] [gn:hca4:j1250] [gicfc: 10.3] [keggfc: 14.2] [sgdfc: 4.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG3717	1253_f2_1	5565	19668	2430	810	YJL033W	1949	1.8(10)-201	Saccharomyces cerevisiae	[ui:yj033w] [pn:can suppress the u14 snorna rna processing function:probable atp-dependent rna helicase ca4] [gn:hca4:j1250] [gicfc: 10.3] [keggfc: 14.2] [sgdfc: 4.2.0] [db:gic-saccharomyces cerevisiae]

CONTIG5118	1213187_f1_2	5566	19669	564	188	YLR059C	353	2.2(10)-32	Saccharomyces cerevisiae	[ui:yl059c] [pn:suppressor of mal2/yme2/ymt20 protein] [gn:ymt20 121 59] [gfc:10.3]
b2x13585.y	6561_c3_2	5567	19670	297	99	YBL092W	377	6.7(10)-35	Saccharomyces cerevisiae	[keggc:14.2] [sgfc:4.2.0] [db:gic-saccharomyces cerevisiae] [ui:yl092w] [pn:ribosomal protein I32.e:60s ribosomal protein [32e]] [gn:yl092w] [gic:10.4] [keggc:14.2] [sgfc:5.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG763	12501050_c2_21	5568	19671	372	124	YBL087C	583	9.9(10)-57	Saccharomyces cerevisiae	[ui:yl087c] [pn:ribosomal protein I23.e:60s ribosomal protein 117] [gn:pl17b:pl17a:yl0713] [gfc:10.4] [keggc:14.2] [sgfc:5.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG062	36367178_f3_4	5569	19672	627	209	YBL072C	697	8.1(10)-69	Saccharomyces cerevisiae	[ui:yl072c] [pn:ribosomal protein s8.e:40s ribosomal protein s8.s14:y59:pl19] [gn:ps8b:ps8a:yl0613:yl0613] [gfc:10.4] [keggc:14.2] [sgfc:5.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG44	24492149_c1_2	5570	19673	336	112	YBL027W	237	4.5(10)-20	Saccharomyces cerevisiae	[ui:yl027w] [pn:ribosomal protein I19:e:60s ribosomal protein I19:123.y14:tp33:tp15] [gn:pl19a:yl08abc:pl19b:ybr084c-a:yl0424] [gfc:10.4] [keggc:14.2] [sgfc:5.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]

CONTIG5370	9773444_c1_8	5571	19674	414	138	YBL027W	206	8.8(10)-17	Saccharomyces cerevisiae	[ui:ybl027w] [pn:ribosomal protein 119.e:60s ribosomal protein 119:123.y114:rp33:rp15]
									[gn:tpl19a:ybr084bc:tpl119b:ybr084c-a:ybl0424] [gicfc:10.4]	
									[keggfc:14.2] [sgdfc:5.1.0:9.2.0]	
									[db:gic-saccharomyces cerevisiae]	
CONTIG4531	22542162_c2_12	5572	19675	207	69	YBR031W	297	2.0(10)-26	Saccharomyces cerevisiae	[ui:ybr031w] [pn:ribosomal protein 12a:60s ribosomal protein 12a:rp2]
									[gn:tpl2a:tpl2:ybr0315] [gicfc:10.4]	
									[keggfc:14.2] [sgdfc:5.1.0:9.2.0]	
									[db:gic-saccharomyces cerevisiae]	
CONTIG4531	10984406_c2_11	5573	19676	252	84	YBR031W	143	2.1(10)-9	Saccharomyces cerevisiae	[ui:ybr031w] [pn:ribosomal protein 12a:60s ribosomal protein 12a:rp2]
									[gn:tpl2a:tpl2:ybr0315] [gicfc:10.4]	
									[keggfc:14.2] [sgdfc:5.1.0:9.2.0]	
									[db:gic-saccharomyces cerevisiae]	
b9x13909_x	14188817_f1_1	5574	19677	603	201	YBR031W	619	1.5(10)-60	Saccharomyces cerevisiae	[ui:ybr031w] [pn:ribosomal protein 12a:60s ribosomal protein 12a:rp2]
									[gn:tpl2a:tpl2:ybr0315] [gicfc:10.4]	
									[keggfc:14.2] [sgdfc:5.1.0:9.2.0]	
									[db:gic-saccharomyces cerevisiae]	
CONTIG4334	4475811_f3_4	5575	19678	423	141	YBR048W	574	8.9(10)-56	Saccharomyces cerevisiae	[ui:ybr048w] [pn:ribosomal protein s11.e:b.ribosomal protein rp41lys12:s18a/s18b]
									[gn:tps18b:ybr0501:tps18ayd9813]	
									[gicfc:10.4] [keggfc:14.2]	
									[sgdfc:5.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]	

CONTIG2123	10192175_f1_1	5576	19679	363	121	YBR181C	475	2.7(10)-45	Saccharomyces cerevisiae	[ui:ybr181c] [pn:ribosomal protein S6.e40s ribosomal protein S6.s10.y40s4.rp9] [gn:rps10a:rps6a:rps101:ybr1244] [gicfc: 10.4] [keggfc: 14.2] [sgdfc: 5.1.0.9.2.0] [db:gtsaccharomyces cerevisiae]
CONTIG2123	21901556_f3_7	5577	19680	204	68	YBR181C	164	2.5(10)-12	Saccharomyces cerevisiae	[ui:ybr181c] [pn:ribosomal protein S6.e40s ribosomal protein S6.s10.y40s4.rp9] [gn:rps10a:rps6a:rps101:ybr1244] [gicfc: 10.4] [keggfc: 14.2] [sgdfc: 5.1.0.9.2.0] [db:gtsaccharomyces cerevisiae]
CONTIG5383	19578141_c3_15	5578	19681	618	206	YBR189W	787	2.3(10)-78	Saccharomyces cerevisiae	[ui:ybr189w] [pn:ribosomal protein S9.e.b:40s ribosomal protein Yrs11:yp28.s13] [gn:rps13a:y511:a:rps13b:sup46:ybr1317] [gicfc: 10.4] [keggfc: 14.2] [sgdfc: 5.1.0.9.2.0] [db:gtsaccharomyces cerevisiae]
CONTIG2827	29511007_c1_4	5579	19682	216	72	YBR191W	220	2.8(10)-18	Saccharomyces cerevisiae	[ui:ybr191w] [pn:ribosomal protein I21.e:60s ribosomal protein I21e] [gn:urp1:a:urp1:ybr1401] [gicfc: 10.4] [keggfc: 14.2] [sgdfc: 5.1.0.9.2.0] [db:gtsaccharomyces cerevisiae]
CONTIG3383	33359385_c1_7	5580	19683	201	67	YBR191W	205	1.1(10)-16	Saccharomyces cerevisiae	[ui:ybr191w] [pn:ribosomal protein I21.e:60s ribosomal protein I21e] [gn:urp1:a:urp1:ybr1401] [gicfc: 10.4] [keggfc: 14.2] [sgdfc: 5.1.0.9.2.0] [db:gtsaccharomyces cerevisiae]

CONTIG5163	24414078_f1_1	5581	19684	900	300	YDL202W	466	2.5(10)-44	Saccharomyces cerevisiae	[ui:yd1202w] [pn:weak similarity to ribosomal protein] [gtcfc:10.4] [keggfc:14.2] [sgdfc:5.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5492	23486658_f2_2	5582	19685	360	120	YDL191W	376	8.5(10)-35	Saccharomyces cerevisiae	[ui:yd1191w] [pn:ribosomal protein] [gtcfc:10.4] [gn:sos1:d1249;sos2:d2170] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5216	23718757_f1_6	5583	19686	408	136	YDL083C	529	5.2(10)-51	Saccharomyces cerevisiae	[ui:yd1083c] [pn:ribosomal protein s16:e40s ribosomal protein rs16 homolog:rp61r homolog] [gn:rps16b:rps16a:rp61r:ym9375] [gtcfc:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5216	9770037_c2_13	5584	19687	669	223	YDL082W	658	1.1(10)-64	Saccharomyces cerevisiae	[ui:yd1082w] [pn:ribosomal protein l13] [gtcfc:10.4] [keggfc:14.2] [sgdfc:5.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1465	12922192_f1_1	5585	19688	402	134	YDL081C	204	1.3(10)-16	Saccharomyces cerevisiae	[ui:yd1081c] [pn:acidic ribosomal protein a1.60s acidic ribosomal protein p1-alpha:a1:112eia] [gn:rpl1:112eia:rpa1] [gtcfc:10.4;10.7] [keggfc:14.2] [sgdfc:5.1.0:5.2:0.9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5216	13703275_f1_3	5586	19689	333	111	YDL081C	262	1.0(10)-22	Saccharomyces cerevisiae	[uiydr081c] [pn:acidic ribosomal protein al:60s acidic ribosomal protein p1-alpha:a:112eia] [gn:rp1:a:112eia:rp1] [gicfc:10.4;10.7] [keggfc:14.2] [sgdfc:5.1.0:5.2.0:9.2.0] [db:gic-saccharomyces cerevisiae]
b2x14827.y	6145175_f3_2	5587	19690	201	67	YDL075W	206	8.8(10)-17	Saccharomyces cerevisiae	[uiydr075w] [pn:ribosomal protein [31 e:60s ribosomal protein [34:y128]]] [gn:rp134:rp134a:rp134b:8084] [gicfc:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG4967	36615676_f3_6	5588	19691	447	149	YDR041W	184	1.8(10)-14	Saccharomyces cerevisiae	[uiydr041w] [pn:weak similarity to bacterial ribosomal s10 proteins] [gicfc:10.4] [keggfc:14.2] [sgdfc:5.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG4935	4195268_f3_2	5589	19692	435	145	YDR064W	685	1.5(10)-67	Saccharomyces cerevisiae	[uiydr064w] [pn:ribosomal protein 40s ribosomal protein s13:ys15:s2:7a] [gn:ys15:rps13:yd96091] [gicfc:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5053	21604035_c2_11	5590	19693	405	135	YDR115W	197	7.9(10)-16	Saccharomyces cerevisiae	[uiydr115w] [pn:similarity to bacterial ribosomal 134 proteins] [gicfc:10.4] [keggfc:14.2] [sgdfc:5.1.0] [db:gic-saccharomyces cerevisiae]

CONTIG3607	25800716_c3_8	5591	19694	444	148	YDR116C	239	2.7(10)-20	Saccharomyces cerevisiae	[ui:ydr116c] [pn:similarity to bacterial ribosomal 11 proteins] [gtfc:10.4] [keggc:14.2] [sgfc:5.1.0] [db:gtc-saccharomyces cerevisiae]
b3x13209_x	23548178_f3_1	5592	19695	261	87	YDR237W	196	1.0(10)-15	Saccharomyces cerevisiae	[ui:ydr237w] [pn:similarity to bacterial ribosomal 15 protein:mitochondrial 60s ribosomal protein 17 precursor:ym17] [gn:mrp17.yd8419] [gtfc:10.4] [keggc:14.2] [sgfc:5.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4623	16286629_c1_5	5593	19696	615	205	YDR237W	459	1.3(10)-43	Saccharomyces cerevisiae	[ui:ydr237w] [pn:similarity to bacterial ribosomal 15 protein:mitochondrial 60s ribosomal protein 17 precursor:ym17] [gn:mrp17.yd8419] [gtfc:10.4] [keggc:14.2] [sgfc:5.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4056	19690675_c1_4	5594	19697	369	123	YDR382W	245	6.5(10)-21	Saccharomyces cerevisiae	[ui:ydr382w] [pn:acidic ribosomal protein:60s acidic ribosomal protein p2-beta:l45y/l44c:y/pal1:l12eia] [gn:rpl4:112eia:rpl45] [gtfc:10.4] [keggc:14.2] [sgfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3711	6031261_c1_7	5595	19698	354	118	YDR382W	188	7.0(10)-15	Saccharomyces cerevisiae	[ui:ydr382w] [pn:acidic ribosomal protein:60s acidic ribosomal protein p2-beta:l45y/l44c:y/pal1:l12eia] [gn:rpl4:112eia:rpl45] [gtfc:10.4] [keggc:14.2] [sgfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5811	12932805_f2_13	5596	19699	504	168	YDR418W	739	2.8(10)-73	Saccharomyces cerevisiae	[ui: ydr418w] [pn: ribosomal protein l12.e:60s ribosomal protein l12.y:15.y:23] [gn: rpl15b:rpl15a:d9461] [gtfc: 10.4] [keggfc: 14.2] [sgdfc: 5.1.0:9.2.0] [db: gtc-saccharomyces cerevisiae]
CONTIG5562	1031517_c3_15	5597	19700	408	136	YDR450W	540	3.6(10)-52	Saccharomyces cerevisiae	[ui: ydr450w] [pn: ribosomal protein s18.e:c4:ribosomal protein s18.e:c13:40s ribosomal protein s18e] [gn: rps18b:rps18a:rps13c:ydr064w:d9461] [gtfc: 10.4] [keggfc: 14.2] [sgdfc: 5.1.0:9.2.0] [db: gtc-saccharomyces cerevisiae]
CONTIG2546	6831302_f2_2	5598	19701	342	114	YDR500C	365	1.2(10)-33	Saccharomyces cerevisiae	[ui: ydr500c] [pn: ribosomal protein l37.e:60s ribosomal protein l37e:b:yp551] [gn: rpl35b:d9719] [gtfc: 10.4] [keggfc: 14.2] [sgdfc: 5.1.0:9.2.0] [db: gtc-saccharomyces cerevisiae]
CONTIG3339	26210927_c3_8	5599	19702	402	134	YDR500C	357	8.8(10)-33	Saccharomyces cerevisiae	[ui: ydr500c] [pn: ribosomal protein l37.c:60s ribosomal protein l37e:b:yp551] [gn: rpl35b:d9719] [gtfc: 10.4] [keggfc: 14.2] [sgdfc: 5.1.0:9.2.0] [db: gtc-saccharomyces cerevisiae]
CONTIG5720	26353216_c3_29	5600	19703	828	276	YELO50C	733	1.3(10)-72	Saccharomyces cerevisiae	[ui: yel050c] [pn: similarity to bacterial ribosomal l2 protein:putative 60s ribosomal protein yel050c] [gn: ygp-orf37] [gtfc: 10.4] [keggfc: 14.2] [sgdfc: 5.1.0] [db: gtc-saccharomyces cerevisiae]

CONTIG5720	26370418_c2_22	5601	19704	549	183	YELO50C	199	1.8(10)-15	Saccharomyces cerevisiae	[ui:ycf050c] [pn: similarity to bacterial ribosomal 12 protein:putative 60s ribosomal protein ycf050c] [gn:sygp-orf37] [gicfc:10.4] [keggfc:14.2] [sgdfc:5.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3279	2189062_f1_1	5602	19705	465	155	YER074W	498	1.0(10)-47	Saccharomyces cerevisiae	[ui:yer074w] [pn:ribosomal protein s24:e:40s ribosomal protein s24e:rp50] [gn:rp50:rp50b:rps24e:rps24eb] [gicfc:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5435	12926550_c2_14	5603	19706	366	122	YGL189C	522	2.8(10)-50	Saccharomyces cerevisiae	[ui:ygl189c] [pn:40s ribosomal protein s26e:c7:40s ribosomal protein s26e-a] [gn:rps26a:rps26:g:1355] [gicfc:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4954	10979677_c2_14	5604	19707	660	220	YGL135W	897	5.2(10)-90	Saccharomyces cerevisiae	[ui:ygl135w] [pn:ribosomal protein:60s ribosomal protein 110a] [gn:ssm1b:ssm2:g2834:ssm1a:yp1220w:ssm1] [gicfc:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5409	10975925_f2_7	5605	19708	756	252	YGL123W	836	1.5(10)-83	Saccharomyces cerevisiae	[ui:ygl123w] [pn:ribosomal protein:40s ribosomal protein s4; omnipotent suppressor protein sup44:rp12:s2e] [gn:sup44:g2893] [gicfc:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2928	26364033_c1_6	5606	19709	627	209	YGL076C	850	5.0(10)-85	Saccharomyces cerevisiae	[ui:yg 076c] [pn:ribosomal protein 17 e.a:60s ribosomal protein yl8:16:rp11]
									[gn:rp16a:rp16:rp18ay 8a]	
									[keggc:10.4] [keggc:14.2]	
									[sgdc:5.1.0-9.2.0] [db:gic-saccharomyces cerevisiae]	
CONTIG4731	5275312_f2_5	5607	19710	471	157	YGL031C	475	2.7(10)-45	Saccharomyces cerevisiae	[ui:yg 031c] [pn:ribosomal protein 124 e.a:60s ribosomal protein 130a:rp29:y121] [gn:rp30a:rp29]
									[gicfc:10.4] [keggc:14.2]	
									[sgdc:5.1.0-9.2.0] [db:gic-saccharomyces cerevisiae]	
CONTIG3829	30178908_c3_7	5608	19711	318	106	YGL030W	410	2.1(10)-38	Saccharomyces cerevisiae	[ui:yg 030w] [pn:ribosomal protein 130 e.a:60s ribosomal protein 130e:y132:rp73] [gn:rp32]
									[gicfc:10.4] [keggc:14.2]	
									[sgdc:5.1.0-9.2.0] [db:gic-saccharomyces cerevisiae]	
CONTIG545	10445193_c2_4	5609	19712	219	73	YGR027C	255	5.7(10)-22	Saccharomyces cerevisiae	[ui:yg 027c] [pn:ribosomal protein s25_e.c7] [gn:rp31a] [gicfc:10.4]
									[keggc:14.2] [sgdc:5.1.0-9.2.0]	
									[db:gic-saccharomyces cerevisiae]	
CONTIG5036	10739130_c1_8	5610	19713	522	174	YGR085C	789	1.5(10)-78	Saccharomyces cerevisiae	[ui:yg 085c] [pn:ribosomal protein y116_b:60s ribosomal protein 116y116:39a:rp39]
									[gn:rp116b:rp39b] [gicfc:10.4]	
									[keggc:14.2] [sgdc:5.1.0-9.2.0]	
									[db:gic-saccharomyces cerevisiae]	

CONTIG5247	35392568_c2_15	5611	19714	576	192	YGR118W	723	1.3(10)-71	Saccharomyces cerevisiae	[ui:ygr118w] [pn:ribosomal protein s28] [s23:e:40s ribosomal protein s28] [gn:ps28a:ps28;p9659] [gicfc:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]
b1x14649_x	11177068_f1_1	5612	19715	660	220	YGR214W	715	1.0(10)-70	Saccharomyces cerevisiae	[ui:ygr214w] [pn:40s ribosomal protein p40 homolog a:40s ribosomal protein sa homolog a:nucleic acid-binding protein nab1 a] [gn:mab1a:nab1:yst1] [gicfc:10.4;12.16] [keggfc:14.2] [sgdfc:5.1.0:6.4;0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5577	4820187_f1_2	5613	19716	231	77	YHL015W	243	1.1(10)-20	Saccharomyces cerevisiae	[ui:yhl015w] [pn:ribosomal protein:40s ribosomal protein] [gn:urp2] [gicfc:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5735	1564051_c2_17	5614	19717	393	131	YHR010W	458	1.7(10)-43	Saccharomyces cerevisiae	[ui:yhr010w] [pn:probable 60s ribosomal protein l27] [gn:pl27:a:rp127:rp127b:ydr471w:d8 035] [gicfc:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5339	23441910_f2_4	5615	19718	582	194	YHR148W	763	8.3(10)-76	Saccharomyces cerevisiae	[ui:yhr148w] [pn:similarity to ribosomal protein:putative 40s ribosomal protein yhr148w] [gicfc:0.4] [keggfc:14.2] [sgdfc:5.1.0] [db:gic-saccharomyces cerevisiae]

CONTIG5795	428_f3_20	5616	19719	708	236	YIL133C	766	4.0(10)-76	Saccharomyces cerevisiae	[ui:yil133c] [pn:ribosomal protein 60s ribosomal protein 113a:rpl22] [gn:rpl113a]
CONTIG3584	23546930_f2_2	5617	19720	789	263	YIL018W	1116	3.2(10)-113	Saccharomyces cerevisiae	[ui:yil18w] [pn:ribosomal protein 18 e:60s ribosomal protein yl6:15:rpl8]
CONTIG1243	4680_f2_1	5618	19721	327	109	YIL190C	434	6.0(10)-41	Saccharomyces cerevisiae	[gn:rpl190c] [pn:ribosomal protein s15a:e:c10-40s ribosomal protein s22:ys24:yp58]
CONTIG975	14882762_c2_3	5619	19722	186	62	YIL190C	208	5.4(10)-17	Saccharomyces cerevisiae	[gn:rps24a:rps24:j0355:rps24b:18039] [gicfc:10.4] [keggfc:14.2]
CONTIG5151	23837563_f2_2	5620	19723	354	118	YIL177W	359	5.4(10)-33	Saccharomyces cerevisiae	[ui:yil177w] [pn:ribosomal protein 117 e:60s ribosomal protein y117-b]

CONTIG3372	34433128_f3_5	5621	19724	210	70	YJL177W	129	1.3(10)-8	Saccharomyces cerevisiae	[ui:yj177w] [pn:ribosomal protein s117 e:60s ribosomal protein y17-b] [gn:rp120bj0493] [gicfc:10.4] [keggfc:14.2] [sgdfc:5.1.0-9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3328	20320378_c2_15	5622	19725	195	65	YJL136C	258	2.7(10)-22	Saccharomyces cerevisiae	[ui:yj136c] [pn:ribosomal protein s21.e] [gn:rps25b] [gicfc:10.4] [keggfc:14.2] [sgdfc:5.1.0-9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4189	10979656_c2_4	5623	19726	684	228	YJR123W	873	1.8(10)-87	Saccharomyces cerevisiae	[ui:yj123w] [pn:ribosomal protein s5.e:40s ribosomal protein s5:rp14:y8] [gn:rps5:j2045] [gicfc:10.4] [keggfc:14.2] [sgdfc:5.1.0-9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3175	32282527_c2_5	5624	19727	321	107	YIR145C	251	1.5(10)-21	Saccharomyces cerevisiae	[ui:yj145c] [pn:ribosomal protein s4.e:c10:40s ribosomal protein s4:s7:y56:rp5] [gn:rps7bj2:186] [gicfc:10.4] [keggfc:14.2] [sgdfc:5.1.0-9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5815	36366532_f2_15	5625	19728	795	265	YJR145C	1118	2.0(10)-113	Saccharomyces cerevisiae	[ui:yj145c] [pn:ribosomal protein s4.e:c10:40s ribosomal protein s4:s7:y56:rp5] [gn:rps7bj2:186] [gicfc:10.4] [keggfc:14.2] [sgdfc:5.1.0-9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4699	2117752_c3_9	5626	19729	357	119	YKL156W	316	1.8(10)-28	Saccharomyces cerevisiae	[ui:yk156w] [pn:ribosomal protein s27.e:40s ribosomal protein s27-1] [gn:rps27a] [gicfc:10.4] [keggfc:14.2] [sgdfc:5.1.0-9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5791	33306557_c2_24	5627	19730	696	232	YKL009W	862	2.7(10)-86	Saccharomyces cerevisiae	[ui:yl009w] [pn:weak similarity to red goosefoot acidic ribosomal protein p0 and m.jannaschii acidic ribosomal protein p0:hypothetical 27.1 kd protein uid4-cap1 intergenic region] [gn:yl160] [gtfc:10.4] [Regfc:14.2] [sgdc:5.1.0]
CONTIG3549	25431253_c2_5	5628	19731	285	95	YKL006W	255	5.7(10)-22	Saccharomyces cerevisiae	[ui:yl006w] [pn:probable 60s ribosomal protein 114ea] [gn:rp14a;yl153] [gtfc:10.4] [keggfc:14.2] [sgdfc:5.1.0;9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG3386	4081505_c1_3	5629	19732	609	203	YLL045C	840	5.7(10)-84	Saccharomyces cerevisiae	[ui:yl0045c] [pn:ribosomal protein 17a.e.b:60s ribosomal protein 17a-1:14-1.yl5:rp6] [gn:rp14b] [gtfc:10.4] [keggfc:14.2] [sgdfc:5.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG4586	4770001_c3_7	5630	19733	798	266	YLL045C	993	3.5(10)-100	Saccharomyces cerevisiae	[ui:yl0045c] [pn:ribosomal protein 17a.e.b:60s ribosomal protein 17a-1:14-1.yl5:rp6] [gn:rp14b] [gtfc:10.4] [keggfc:14.2] [sgdfc:5.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG2752	20423136_f1_1	5631	19734	612	204	YLR009W	544	1.3(10)-52	Saccharomyces cerevisiae	[ui:yl009w] [pn:similarity to ribosomal protein 124_c,b] [gtfc:10.4] [keggfc:14.2] [sgdfc:5.1.0] [db:gic-saccharomyces cerevisiae]

CONTIG5362	24797507_c2_15	5632	19735	363	121	YLR061W	231	2.0(10)-19	Saccharomyces cerevisiae	[uiylr061w] [pn:ribosomal protein 60s ribosomal protein y31] [gn:12168] [gicfc:10.4] [keggfc:14.2] [sgdfc:5.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG1362	1363817_f3_2	5633	19736	198	66	YLR075W	233	1.2(10)-19	Saccharomyces cerevisiae	[uiylr075w] [pn:ribosomal protein ubiquinol-cytochrome c reductase complex subunit vi requiring protein] [gn:qsr1:grc5] [gicfc:10.4;12.8] [keggfc:14.2] [sgdfc:3.8;0.5;1.0] [db:gic-saccharomyces cerevisiae]
CONTIG4663	4453427_f2_2	5634	19737	753	251	YLR075W	916	5.0(10)-92	Saccharomyces cerevisiae	[uiylr075w] [pn:ribosomal protein ubiquinol-cytochrome c reductase complex subunit vi requiring protein] [gn:qsr1:grc5] [gicfc:10.4;12.8] [keggfc:14.2] [sgdfc:3.8;0.5;1.0] [db:gic-saccharomyces cerevisiae]
CONTIG3605	21539018_f3_3	5635	19738	189	63	YLR287C-A	189	5.5(10)-15	Saccharomyces cerevisiae	[uiylr287c-a] [pn:ribosomal protein, strong similarity to human ubiquitin-like protein/ribosomal protein s30] [gn:rps30a;rps30b] [gicfc:10.4] [keggfc:14.2] [sgdfc:5.1.0] [db:gic-saccharomyces cerevisiae]
b3x14645.x	12672056_c3_2	5636	19739	264	88	YLR325C	206	8.8(10)-17	Saccharomyces cerevisiae	[uiylr325c] [pn:putative ribosomal protein 138;putative 60s ribosomal protein 138] [gn:18543] [gicfc:10.4] [keggfc:14.2] [sgdfc:5.1.0] [db:gic-saccharomyces cerevisiae]

CONTIG4548	29332305_c3_7	5637	19740	315	105	YLR340W	142	1.8(10)-9	Saccharomyces cerevisiae	[uii:ylr340w] [pn:acidic ribosomal protein 110.e:60s acidic ribosomal protein p0:1 0e] [gn:rpa0:rpa0:rp10e:110e:18300] [gicfc:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG4875	25835912_f3_5	5638	19741	525	175	YLR340W	594	6.7(10)-58	Saccharomyces cerevisiae	[uii:ylr340w] [pn:acidic ribosomal protein 110.e:60s acidic ribosomal protein p0:1 0e] [gn:rpa0:rpa0:rp10e:110e:18300] [gicfc:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG4263	24016512_c1_6	5639	19742	393	131	YLR344W	508	8.8(10)-49	Saccharomyces cerevisiae	[uii:ylr344w] [pn:ribosomal protein:60s ribosomal protein 126-a:y133] [gn:rpl33a:rpl26a:rp126:a:18300] [gicfc:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG4231	5338452_f1_1	5640	19743	399	133	YML073C	460	1.1(10)-43	Saccharomyces cerevisiae	[uii:yml073c] [pn:ribosomal protein:60s ribosomal protein] [gn:y116a] [gicfc:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG4687	13671937_c2_11	5641	19744	843	281	YML063W	961	8.6(10)-97	Saccharomyces cerevisiae	[uii:yml063w] [pn:ribosomal protein s.a.e:40s ribosomal protein rp10b] [gn:rp10b:rps10b:plc2] [gicfc:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]

CONTIG2652	13775442_f3_4	5642	19745	615	205	YMR121C	787	2.3(10)-78	Saccharomyces cerevisiae	[ui:ymr121c] [pn:ribosomal protein I15:e.c13:60s ribosomal protein y110 b:i13:rpl15r:yp18] [gn:rpl13b:rpl110b:y110b:ym8564] [gtcfc:10.4] [keggfc:14.2] [sgdfc:5.1.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
b1x10611.y	22742890_f2_2	5643	19746	324	108	YMR188C	174	2.2(10)-13	Saccharomyces cerevisiae	[ui:ymr188c] [pn:weak similarity to 30s ribosomal protein s17] [gtcfc:10.4] [keggfc:14.2] [sgdfc:5.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2692	15664802_c2_6	5644	19747	300	100	YMR194W	260	1.7(10)-22	Saccharomyces cerevisiae	[ui:ymr194w] [pn:ribosomal protein:60s ribosomal protein y39] [gn:rpl39a:rpl39b:ym9646] [gtcfc:10.4] [keggfc:14.2] [sgdfc:5.1.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3837	2928442_c3_9	5645	19748	342	114	YMR230W	292	6.7(10)-26	Saccharomyces cerevisiae	[ui:ymr230w] [pn:strong similarity to ribosomal protein s10;putative 40s ribosomal protein in mtl1 -mh1 intergenic region] [gn:ym9959] [gtcfc:10.4] [keggfc:14.2] [sgdfc:5.1.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3701	1054677_c2_7	5646	19749	561	187	YMR242C	738	3.7(10)-73	Saccharomyces cerevisiae	[ui:ymr242c] [pn:ribosomal protein:60s ribosomal protein 118a] [gn:rpl18a:rpl18a:ym9408] [gtcfc:10.4] [keggfc:14.2] [sgdfc:5.1.0.9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5802	24016500_f1_13	5647	19750	447	149	YNL302C	632	6.4(10)-62	Saccharomyces cerevisiae	[ui:ynl302c] [pn:ribosomal protein sl9:e:40s ribosomal protein sl9b:s16b:ys16:rp55] [gn:rp55b:rp516b:n0422] [gtfc:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3291	5132933_c3_9	5648	19751	495	165	YNL301C	571	1.8(10)-55	Saccharomyces cerevisiae	[ui:ynl301c] [pn:ribosomal protein sl8:e:ribosomal protein sl8:c:60s ribosomal protein sl8:rp28] [gn:rp28b:rp28a:n0425][gtfc:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5406	2189382_c3_12	5649	19752	864	288	YNL284C	650	7.9(10)-64	Saccharomyces cerevisiae	[ui:ynl284c] [pn:strong similarity to ribosomal protein 115:mitochondrial 60s ribosomal protein 110 precursor:ym110] [gn:mpf110:n0580][gtfc:10.4] [keggfc:14.2] [sgdfc:5.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1882	16605383_f1_2	5650	19753	393	131	YNL185C	359	5.4(10)-33	Saccharomyces cerevisiae	[ui:ynl185c] [pn:strong similarity to ribosomal protein 111:putative 60s mitochondrial ribosomal protein ynl185c] [gn:n1623][gtfc:10.4] [keggfc:14.2] [sgdfc:5.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3963	35672937_c2_5	5651	19754	192	64	YNL185C	154	2.8(10)-11	Saccharomyces cerevisiae	[ui:ynl185c] [pn:strong similarity to ribosomal protein 111:putative 60s mitochondrial ribosomal protein ynl185c] [gn:n1623][gtfc:10.4] [keggfc:14.2] [sgdfc:5.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG617	25565962_f2_2	5652	19755	561	187	YNL178W	568	3.7(10)-55	Saccharomyces cerevisiae	[ui:ynl178w] [pn:ribosomal protein s3.c:40s ribosomal protein s3.y3:rp13] [gn:rp3;sufl4:n1653] [gtcfc:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5558	29378811_f3_9	5653	19756	336	112	YNL162W	526	1.1(10)-50	Saccharomyces cerevisiae	[ui:ynl162w] [pn:ribosomal protein 36a.e] [gn:rp141.a] [gtcfc:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5165	4878516_f2_6	5654	19757	378	126	YNL081C	287	2.2(10)-25	Saccharomyces cerevisiae	[ui:ynl081c] [pn:similarity to ribosomal protein s13;putative 40s mitochondrial ribosomal protein ynl081c] [gn:n2322] [gtcfc:10.4] [keggfc:14.2] [sgdfc:5.1.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1297	31382010_f1_1	5655	19758	186	62	YNL067W	200	3.7(10)-16	Saccharomyces cerevisiae	[ui:ynl067w] [pn:ribosomal protein b.y111:rp25] [gn:rp19b.n2406.ynl2406w] [gtcfc:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3671	4954192_c2_3	5656	19759	399	133	YNL002C	156	5.7(10)-11	Saccharomyces cerevisiae	[ui:ynl002c] [pn:ribosomal protein 17.e:60s ribosomal protein 17] [gn:rp17:rp7.n2014] [gtcfc:10.4] [keggfc:14.2] [sgdfc:5.1.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5057	24428437_f2_2	5657	19760	381	127	YNL002C	146	7.5(10)-10	Saccharomyces cerevisiae	[ui:ynl002c] [pn:ribosomal protein I7.e:60s ribosomal protein [7] [gn:rp7:rp7:n2014] [gicfc:0.4] [keggfc:14.2] [sgdfc:5.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG1854	12610930_f1_1	5658	19761	591	197	YNR036C	423	8.9(10)-40	Saccharomyces cerevisiae	[ui:ynr036c] [pn:strong similarity to ribosomal protein s12:putative 40s mitochondrial ribosomal protein ynr036c] [gn:n3298] [gicfc:10.4] [keggfc:4.2] [sgdfc:5.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG63	12610930_f3_2	5659	19762	597	199	YNR036C	420	1.8(10)-39	Saccharomyces cerevisiae	[ui:ynr036c] [pn:strong similarity to ribosomal protein s12:putative 40s mitochondrial ribosomal protein ynr036c] [gn:n3298] [gicfc:10.4] [keggfc:4.2] [sgdfc:5.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG5496	1953127_c2_16	5660	19763	438	146	YOL127W	527	8.5(10)-51	Saccharomyces cerevisiae	[ui:yol127w] [pn:ribosomal protein I23.a.e:60s ribosomal protein I25.y!25:rp61] [gn:rp125] [gicfc:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG4890	24804625_c3_9	5661	19764	387	129	YOL040C	339	7.0(10)-31	Saccharomyces cerevisiae	[ui:yol040c] [pn:ribosomal protein I40s ribosomal protein s15:ys21:rp52:rig protein] [gn:rps15:rps21] [gicfc:10.4] [keggfc:14.2] [sgdfc:5.1:9.2.0] [db:gic-saccharomyces cerevisiae]

CONTIG3180	1408438_c2_9	5662	19765	426	142	YOR063W	466	2.5(10)-44	Saccharomyces cerevisiae	[ui:yor063w] [pn:ribosomal protein 13.e:60s ribosomal protein 13:trichodermin resistance protein.y11:rp1] [gn:icml:mak8] [gtcfc:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]
b1x11845.x	10167087_c2_1	5663	19766	801	267	YOR096W	666	1.6(10)-65	Saccharomyces cerevisiae	[ui:yor096w] [pn:ribosomal protein.40s ribosomal protein rp30] [gn:rp30:yor3177w:rp330] [gtcfc:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5608	4882938_c1_18	5664	19767	471	157	YOR369C	453	5.9(10)-43	Saccharomyces cerevisiae	[ui:yor369c] [pn:acidic ribosomal protein s12:40s ribosomal protein s12] [gn:rs12:rps12] [gtcfc:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5797	3906261_c3_33	5665	19768	318	106	YPL143W	445	4.2(10)-42	Saccharomyces cerevisiae	[ui:yp1143w] [pn:ribosomal protein 137a.y137.1:p47] [gn:yp137a:yp143w:p2625] [gtcfc:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5634	9791087_c3_29	5666	19769	408	136	YPL131W	331	5.0(10)-30	Saccharomyces cerevisiae	[ui:yp1131w] [pn:ribosomal protein 15.c:60s ribosomal 5 s rna-binding protein] [gn:rp11:yp1131w] [gtcfc:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]

CONTIG5634	12110026_c2_25	5667	19770	636	212	YPL131W	630	1.0(10)-61	Saccharomyces cerevisiae	[uii:ypl131w] [pn:ribosomal protein [15:e:60s ribosomal protein [11:15:y13:ribosomal] 5 s rna-binding protein] [gn:ypl1:ipl14w] [gicfc:10.4] [keggfc:14.2] [sgdgc:5.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG3400	31501_f3_4	5668	19771	300	100	YPR043W	259	2.1(10)-22	Saccharomyces cerevisiae	[uii:ypr043w] [pn:ribosomal protein [37a:e:probable 60s ribosomal protein [37a] [gn:yp9499] [gicfc:10.4] [keggfc:14.2] [sgdgc:5.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG3918	24432842_c3_6	5669	19772	870	290	YDL143W	881	2.6(10)-88	Saccharomyces cerevisiae	[uii:ydl143w] [pn:component of chaperonin-containing t-complex:tcp-1-complex protein 1, delta subunit:tcp-1-delta:cct-delta] [gn:cc14:tcp4:anc2] [gicfc:10.5:10.7:12.7] [keggfc:14.2] [sgdgc:6.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]
b9x11364.y	24665678_c3_2	5670	19773	555	185	YDL143W	705	1.2(10)-69	Saccharomyces cerevisiae	[uii:ydl143w] [pn:component of chaperonin-containing t-complex:tcp-1-complex protein 1, delta subunit:tcp-1-delta:cct-delta] [gn:cc14:tcp4:anc2] [gicfc:10.5:10.7:12.7] [keggfc:14.2] [sgdgc:6.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]

CONTIG4653	1179503_c3_10	5671	19774	246	82	YDR155C	227	5.2(10)-19	Saccharomyces cerevisiae	[ui:ydr155c] [pn:peptidyl[prolyl isomerase;peptidyl-prolyl cis-trans isomerase;piase:rotamase:cyclophilin:cyclosporin a-binding protein:cph:ppi-ii] [gn:spri:cyp1:cph1:sscl1:yd8358] [gicfc:10.5:10.7:12.7:13.2:14.1] [ec:5.2.1.8] [keggfc: [ec:5.2.1.8]
CONTIG5279	35781556_c1_11	5672	19775	207	69	YDR155C	236	5.7(10)-20	Saccharomyces cerevisiae	[ui:ydr155c] [pn:peptidyl[prolyl isomerase;peptidyl-prolyl cis-trans isomerase;piase:rotamase:cyclophilin:cyclosporin a-binding protein:cph:ppi-ii] [gn:spri:cyp1:cph1:sscl1:yd8358] [gicfc:10.5:10.7:12.7:13.2:14.1] [sgdfc:6.1.0:9.2.0] [keggfc: [ec:5.2.1.8]
CONTIG626	10761050_c2_4	5673	19776	1185	395	YDR188W	1303	5.0(10)-133	Saccharomyces cerevisiae	[ui:ydr188w] [pn:component of chaperonin-containing t-complex:zeta subunit:tcp-1-zeta:cct-zeta] [gn:cct6:tcp6:tcp20:yd9395] [gicfc:10.5:10.7:12.7] [keggfc:14.2] [sgdfc:6.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5630	4798262_f3_9	5674	19777	1677	559	YDR212W	2163	3.7(10)-224	Saccharomyces cerevisiae	[ui:ydr212w] [pn:component of chaperonin-containing t-complex:alpha complex protein 1, alpha subunit:tcp-1-alpha:cct-alpha] [gn:cct1:cpl1:yd8142] [gicfc:10.5:10.7:12.7] [keggfc:14.2] [sgdfc:6.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]

CONTIG4322	78192_c3_5	5675	19778	867	289	YDR304C	455	3.6(10)-43	Saccharomyces cerevisiae	[ui:ydr304c] [pn:cyclophilin d of the precursor:prolase:rotamase:cyclophilin d] [gn:cp5:cyp5:cypd:d9740] [gtfc: 0.5; 10.7; 12.16; 12.7] [ec:5.2.1.8] [keggfc: 14.1] [sgdfc: 6.1.0; 9.4.0] [db:gic-sacc]
CONTIG5744	32711061_c3_32	5676	19779	741	247	YDR304C	504	2.2(10)-48	Saccharomyces cerevisiae	[ui:ydr304c] [pn:cyclophilin d of the precursor:prolase:rotamase:cyclophilin d] [gn:cp5:cyp5:cypd:d9740] [gtfc: 10.5; 10.7; 12.16; 12.7] [ec:5.2.1.8] [keggfc: 14.1] [sgdfc: 6.1.0; 9.4.0] [db:gic-sacc]
CONTIG1065	23453438_c2_1	5677	19780	363	121	YDR519W	250	1.8(10)-21	Saccharomyces cerevisiae	[ui:ydr519w] [pn:R506/rapamycin-binding protein of the er:R506-binding protein precursor:Rkbp-13:Rkbp-15:peptidyl-prolyl cis-trans-isomerase:prolase] [gn:fpr2:fkb2:d9719] [gtfc: 10.5; 10.7; 12.16; 12.7; 13.2] [ec:5.2.1.8] [keggfc: 14.1] [sgdfc: 6.1.0; 9.4.0] [db:gic-sacc]
CONTIG2082	4688425_f3_1	5678	19781	927	309	YER048C	154	9.8(10)-9	Saccharomyces cerevisiae	[ui:yer048c] [pn:dnaj homolog:protein] [gn:caj1] [gtfc: 0.5; 10.7; 12.7] [keggfc: 14.2] [sgdfc: 6.1.0] [db:gic-saccharomyces cerevisiae]

CONTIG3227	3932812_f1_1	5679	19782	609	203	YER048C	163	3.2(10)-17	Saccharomyces cerevisiae	[ui:yer048c] [pn:dnaj homolog:protein] [gn:caj1] [gicfc:10.5:10.7:12.7] [keggfc:14.2] [sgdfc:6.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4756	3320192_c2_13	5680	19783	591	197	YER048C	215	2.8(10)-17	Saccharomyces cerevisiae	[ui:yer048c] [pn:dnaj homolog:protein] [gn:caj1] [gicfc:10.5:10.7:12.7] [keggfc:14.2] [sgdfc:6.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4772	34259382_c2_4	5681	19784	1017	339	YFR041C	334	2.3(10)-30	Saccharomyces cerevisiae	[ui:yfr041c] [pn:weak similarity to dnaj-like heat shock proteins] [hypothetical 34.2 kd protein in sap155-ymn31 intergenic region precursor] [gicfc:12.7] [keggfc:14.2] [sgdfc:6.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG833	8882781_c2_4	5682	19785	870	290	YIL142W	1022	3.0(10)-103	Saccharomyces cerevisiae	[ui:yil142w] [pn:chaperonin of the tcp1 ring complex, cytosolic:tcp1-complex protein 1, beta subunit:tcp1-beta:cc1-beta] [gn:cc2:tcp2:bin3] [gicfc:10.5:10.7:12.7] [keggfc:14.2] [sgdfc:6.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3227	24417882_f3_2	5683	19786	300	100	YIR004W	164	1.6(10)-11	Saccharomyces cerevisiae	[ui:yir004w] [pn:similarity to caj1p, ydj1p and to dnaj-like proteins] [hypothetical 48.6 kd protein in bet1-pan1 intergenic region] [gn:yib4w] [gicfc:10.5:10.7:12.7] [keggfc:14.2] [sgdfc:6.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3906	2834632_f1_1	5684	19787	1548	516	YIR004W	375	6.0(10)-86	Saccharomyces cerevisiae	[ui:yir004w] [pn:similarity to caj1p, ydj1p and to dnaj-like proteins; hypothetical 48.6 kd protein in bet1-pan1 intergenic region] [gn:yir004w] [gcfc:10.5:10.7:12.7] [keggfc:14.2] [sgdfc:6.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4172	9788936_c3_4	5685	19788	1461	487	YJL111W	1803	5.2(10)-186	Saccharomyces cerevisiae	[ui:yj111w] [pn:component of chaperonin-containing t-complex-t-complex protein 1, eta subunit;tcp-1-eta;cct7-eta] [gn:cct7;j3804] [gcfc:10.5:10.7:12.7] [keggfc:14.2] [sgdfc:6.1.0:9.2:0] [db:gtc-saccharomyces cerevisiae]
CONTIG5775	23829512_c2_26	5686	19789	2079	693	YJL034W	2374	1.6(10)-246	Saccharomyces cerevisiae	[ui:yj034w] [pn:nuclear fusion protein;78 kd glucose regulated protein homolog precursor;grp78;immunoglobulin heavy chain binding protein homolog;bip] [gn:kar2:ssd1.grp78;j1248] [gcfc:10.5:10.7:11.1:12.16:12.7:12.8] [keggfc:14.2] [
CONTIG204	21522577_c2_4	5687	19790	1590	530	YJL014W	2030	4.5(10)-210	Saccharomyces cerevisiae	[ui:yj014w] [pn:chaperonin of the tcp1 ring complex, cytosolic;t-complex protein 1, gamma subunit;tcp-1-gamma;cct-gamma] [gn:cct3:cp3:bin2;j1336] [gcfc:10.5:10.7:12.7] [keggfc:14.2] [sgdfc:6.1.0:9.2:0] [db:gtc-saccharomyces cerevi

CONTIG2981	24024074_c1_6	5688	19791	1473	491	YJL008C	1546	8.9(10)-159	Saccharomyces cerevisiae	[ui:yr008c] [pn:component of chaperonin-containing t-complex:tcp-1, theta subunit:tcp-1-theta:cct-theta] [gn:cet8,jl374] [gicfc:10.5:10.7:12.7] [keggfc:14.2] [sgdfc:6.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5230	22672051_c1_13	5689	19792	1701	567	YJR064W	2039	5.0(10)-211	Saccharomyces cerevisiae	[ui:yr064w] [pn:t-complex protein 1, epsilon subunit:tcp-1-epsilon:cct-epsilon] [gn:cet5/tcp5,jl1752] [gicfc:10.5:10.7:12.7] [keggfc:14.2] [sgdfc:6.1.0:9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5289	267012_f1_2	5690	19793	477	159	YJR097W	264	6.2(10)-23	Saccharomyces cerevisiae	[ui:yr097w] [pn:weak similarity to caj1p:hypothetical 20.0 kd protein in acr1-yuh1 intergenic region] [gn:j1931] [gicfc:10.5:10.7:12.7] [keggfc:14.2] [sgdfc:6.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG4803	10171900_c1_8	5691	19794	2055	685	YKL073W	692	2.7(10)-68	Saccharomyces cerevisiae	[ui:yl073w] [pn:chaperone of the heat shock protein 70 homolog lhs1 precursor] [gn:lhs1,ykl355] [gicfc:12.7:12.16:11.1] [keggfc:14.2] [sgdfc:6.1.0:6.2.0:9.4.0] [db:gic-saccharomyces cerevisiae]
CONTIG3857	4103453_f1_1	5692	19795	1107	369	YLR449W	476	8.0(10)-62	Saccharomyces cerevisiae	[ui:ylr449w] [pn:strong similarity to peptidyl/prolyl isomerase sfp3p] [gicfc:10.5:10.7:12.7] [keggfc:14.2] [sgdfc:6.1.0] [db:gic-saccharomyces cerevisiae]

CONTIG862	20431663_f3_2	5693	19796	564	188	YLR449W	95	0.023	Saccharomyces cerevisiae	[ui:yl449w] [pn:strong similarity to peptidylprolyl isomerase fp3p] [grfc:10.5;10.7;12.7] [keggfc:14.2] [sgdfc:6.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3583	30660886_f3_3	5694	19797	288	96	YMR161W	251	1.5(10)-21	Saccharomyces cerevisiae	[ui:ymr161w] [pn:similarity to dnaj proteins:hlj1 protein] [gn:hlj1;ymr8520] [grfc:0.5;10.7;12.7] [keggfc:14.2] [sgdfc:6.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4414	24390652_f1_1	5695	19798	357	119	YNL227C	280	8.0(10)-24	Saccharomyces cerevisiae	[ui:ynl227c] [pn:weak similarity to dnaj-like proteins:hypothetical 68.8 kd protein in ure2-ssu72 intergenic region] [gn:n1254] [grfc:10.5;10.7;12.7] [keggfc:14.2] [sgdfc:6.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4414	23923442_f2_3	5696	19799	1299	433	YNL227C	247	1.5(10)-41	Saccharomyces cerevisiae	[ui:ynl227c] [pn:weak similarity to dnaj-like proteins:hypothetical 68.8 kd protein in ure2-ssu72 intergenic region] [gn:n1254] [grfc:10.5;10.7;12.7] [keggfc:14.2] [sgdfc:6.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1898	15022061_f2_2	5697	19800	918	306	YOR288C	452	7.5(10)-43	Saccharomyces cerevisiae	[ui:yor288c] [pn:disulfide isomerase related protein] [gn:mpd1] [grfc:10.11;2.7] [keggfc:14.2] [sgdfc:6.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5499	12_c3_13	5698	19801	1992	664	YDR341C	1345	2.8(10)-209	Saccharomyces cerevisiae	[ui:ydr341c] [pn:strong similarity to arginine-trna ligase] [grfcf:10.6] [keggfc:14.2] [sgdfc:5.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5735	26798200_c1_13	5699	19802	642	214	YOL097C	690	4.5(10)-68	Saccharomyces cerevisiae	[ui:yol097c] [pn:tryptophan--trna ligase] [gn:wrs1] [gtcfc:10.6] [keggfc:4.2] [sgdfc:5.4.0-9.2.0]
CONTIG5735	26196061_c2_18	5700	19803	768	256	YOL097C	1010	5.5(10)-102	Saccharomyces cerevisiae	[ui:yol097c] [pn:tryptophan--trna ligase] [gn:wrs1] [gtcfc:10.6] [keggfc:14.2] [sgdfc:5.4.0-9.2.0]
CONTIG2571	24501442_f2_2	5701	19804	1308	436	YHR006W	393	1.3(10)-36	Saccharomyces cerevisiae	[ui:yhr006w] [pn:involved in pre-trna splicing; putative 60.8 kd zinc finger protein in gpa1-erg11 intergenic region] [gn:sp2] [gtcfc:10.6] [keggfc:14.2] [sgdfc:4.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG53303	9957192_c1_10	5702	19805	1329	443	YHR006W	354	3.2(10)-32	Saccharomyces cerevisiae	[ui:yhr006w] [pn:involved in pre-trna splicing; putative 60.8 kd zinc finger protein in gpa1-erg11 intergenic region] [gn:sp2] [gtcfc:10.6] [keggfc:14.2] [sgdfc:4.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5764	4895137_c3_31	5703	19806	1182	394	YHR006W	119	0.00023	Saccharomyces cerevisiae	[ui:yhr006w] [pn:involved in pre-trna splicing; putative 60.8 kd zinc finger protein in gpa1-erg11 intergenic region] [gn:sp2] [gtcfc:10.6] [keggfc:14.2] [sgdfc:4.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4159	79186_f1_1	5704	19807	774	258	YHR163W	497	1.3(10)-47	Saccharomyces cerevisiae	[ui:yhr163w] [pn:weak multicopy suppressor of los1-1 protein] [gn:sol3] [gtcfc:10.6] [keggfc:14.2] [sgdfc:4.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG5654	4735640_c3_17	5705	19808	1371	457	YLR375W	249	1.5(10)-20	Saccharomyces cerevisiae	[ui:yh375w] [pn:involved in pre-tma splicing and in uptake of branched-chain amino acids]
									[gn:stp3] [gicfc:10.6:12.1]	[keggfc:14.2] [sgdfc:1.1.3:4.5.0]
									[db:gic-saccharomyces cerevisiae]	
CONTIG4402	24489005_c1_4	5706	19809	1104	368	YNR034W	894	6.9(10)-100	Saccharomyces cerevisiae	[ui:ynr034w] [pn:multiplicity suppressor of los1::sol1 protein]
									[gn:sol1:n329] [gicfc:10.6]	[keggfc:14.2] [sgdfc:4.5.0]
									[db:gic-saccharomyces cerevisiae]	
CONTIG5140	4688933_c3_12	5707	19810	744	248	YOL102C	371	2.8(10)-34	Saccharomyces cerevisiae	[ui:yol102c] [pn:tRNA 2"-phosphotransferase] [gn:ipt1]
									[gicfc:10.6] [keggfc:14.2]	[sgdfc:4.5.0]
									[db:gic-saccharomyces cerevisiae]	
CONTIG3385	4492160_c2_12	5708	19811	1260	420	YFR010W	663	3.2(10)-65	Saccharomyces cerevisiae	[ui:yfr010w] [pn:similarity to c.elegans tRNA-guanine transglycosylase;putative ubiquitin carboxyl-terminal hydrolase yftf10w;ubiquitin thioesterase;ubiquitin-specific processing protease;deubiquitinating enzyme]
									[gicfc:10.6:10.11]	
CONTIG2795	36110408_c3_7	5709	19812	648	216	YGL105W	542	2.2(10)-52	Saccharomyces cerevisiae	[ui:ygl105w] [pn:protein with specific affinity for g4 quadruplex nucleic acids;gu4 nucleic-binding protein 1:p42:arc1 protein]
									[gn:g4p1:arc1:g3085] [gicfc:10.6]	[keggfc:14.2] [sgdfc:4.6.0]
									[db:gic-saccharomyces cerevisiae]	

CONTIG5624	26360285_f2_4	5710	19813	525	175	YGL105W	266	3.8(10)-23	Saccharomyces cerevisiae	[ui:ygl105w] [pn:protein with specific affinity for g4 quadruplex nucleic acids:gu4 nucleic-binding protein 1:p42:arc1 protein] [gn:g4p1:arc1:g3085] [gtcfc:10.6] [keggfc:14.2] [sgdfc:4.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG990	4768913_f2_1	5711	19814	690	230	YGL105W	191	1.2(10)-14	Saccharomyces cerevisiae	[ui:ygl105w] [pn:protein with specific affinity for g4 quadruplex nucleic acids:gu4 nucleic-binding protein 1:p42:arc1 protein] [gn:g4p1:arc1:g3085] [gtcfc:10.6] [keggfc:14.2] [sgdfc:4.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3516	23849143_c2_7	5712	19815	714	238	YAL003W	529	5.2(10)-51	Saccharomyces cerevisiae	[ui:yal003w] [pn:translation elongation factor eefl beta:elongation factor 1-beta:ef-1-beta] [gn:eefb1:tef5] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG292	14875252_f2_2	5713	19816	525	175	YBL091C	173	9.5(10)-13	Saccharomyces cerevisiae	[ui:ybl091c] [pn:methionine aminopeptidase, isoform 2:methionine aminopeptidase m 2] [gn:map2:ybl0701] [gtcfc:10.7] [ec:3.4.11.18] [keggfc:14.1] [sgdfc:5.2.0:6.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4487	I6828377_f3_1	5714	19817	1323	441	YBL091C	1062	1.7(10)-107	Saccharomyces cerevisiae	[ui:ybI091c] [pn:methionine aminopeptidase, isoform 2:methionine aminopeptidase m 2] [gn:map2:ybl0701] [gicfc:10.7] [ec:3.4.11.18] [keggic:14.1] [sgdfc:5.2.0;6.3.0] [db:gic-saccharomyces cerevisiae]
CONTIG3041	36362805_f1_2	5715	19818	615	205	YBR118W	923	9.3(10)-93	Saccharomyces cerevisiae	[ui:ybr118w] [pn:translation elongation factor eef1 alpha-a chain, cytosolic:elongation factor 1-alpha:ef-1-alpha] [gn:tef2:ybr0913:tef1:p9513] [gicfc:10.7] [keggic:14.2] [sgdfc:5.2.0;9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5539	36362805_f1_2	5716	19819	1383	461	YBR118W	2083	1.1(10)-215	Saccharomyces cerevisiae	[ui:ybr118w] [pn:translation elongation factor eef1 alpha-a chain, cytosolic:elongation factor 1-alpha:ef-1-alpha] [gn:tef2:ybr0913:tef1:p9513] [gicfc:10.7] [keggic:14.2] [sgdfc:5.2.0;9.2.0] [db:gic-saccharomyces cerevisiae]
CONTIG5583	4964037_c2_16	5717	19820	1320	440	YBR143C	1766	4.2(10)-182	Saccharomyces cerevisiae	[ui:ybr143c] [pn:translational release factor:eukaryotic peptide chain release factor subunit 1:erfl:omnipotent suppressor protein 1] [gn:sup1:sup45:sal4:ybr1120] [gicfc:10.7] [keggic:14.2] [sgdfc:5.2.0;9.2.0] [db:gic-saccharomyces ce]

CONTIG5804	21928252_c3_69	5718	19821	1086	362	YDL084W	1542	2.3(10)-158	Saccharomyces cerevisiae	[ui:yd 084w] [pn:strong similarity to nuclear rna helicase:dead family] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5804	5250252_c2_56	5719	19822	201	67	YDL084W	189	3.2(10)-14	Saccharomyces cerevisiae	[ui:yd 084w] [pn:strong similarity to nuclear rna helicase:dead family] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5421	26600300_c2_10	5720	19823	1206	402	YDR021W	1323	3.7(10)-135	Saccharomyces cerevisiae	[ui:yd 021w] [pn:strong similarity to human translation initiation factor elf4A homolog] [gtcfc:10.7] [keggfc:14.2][sgdfc:5.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG228	7276031_f3_3	5721	19824	477	159	YDR172W	117	3.7(10)-6	Saccharomyces cerevisiae	[ui:yd 172w] [pn:eukaryotic peptide chain release factor gtp-binding subunit:erf2:omnipotent suppressor protein 2:erf3:erf-3:g1 to s phase transition protein 1] [gn:sup2:sup35:suf12:gst1:sal3:pmn2:yd9395] [gtcfc:10.7:12.8] [keggfc:14.
CONTIG2600	433217_f1_1	5722	19825	420	140	YDR172W	129	1.8(10)-7	Saccharomyces cerevisiae	[ui:yd 172w] [pn:eukaryotic peptide chain release factor gtp-binding subunit:erf2:omnipotent suppressor protein 2:erf3:erf-3:g1 to s phase transition protein 1] [gn:sup2:sup35:suf12:gst1:sal3:pmn2:yd9395] [gtcfc:10.7:12.8] [keggfc:14.

CONTIG2600	22290936_f2_3	5723	19826	534	178	YDR172W	386	3.6(10)-35	Saccharomyces cerevisiae	[uiydr172w] [pn:eukaryotic peptide chain release factor gtp-binding subunit:erf2:omnipotent suppressor protein 2:erf3:erf-3:g1 to s phase transition protein 1] [gn:sup2:sup35:suf12:gst1:sal3:pmn2:yd9395] [gtcfc:10.7:12.8] [keggfc:14.
CONTIG2600	36032263_f3_5	5724	19827	192	64	YDR172W	300	8.0(10)-26	Saccharomyces cerevisiae	[uiydr172w] [pn:eukaryotic peptide chain release factor gtp-binding subunit:erf2:omnipotent suppressor protein 2:erf3:erf-3:g1 to s phase transition protein 1] [gn:sup2:sup35:suf12:gst1:sal3:pmn2:yd9395] [gtcfc:10.7:12.8] [keggfc:14.
CONTIG2600	9970452_f3_6	5725	19828	831	277	YDR172W	1032	2.6(10)-104	Saccharomyces cerevisiae	[uiydr172w] [pn:eukaryotic peptide chain release factor gtp-binding subunit:erf2:omnipotent suppressor protein 2:erf3:erf-3:g1 to s phase transition protein 1] [gn:sup2:sup35:suf12:gst1:sal3:pmn2:yd9395] [gtcfc:10.7:12.8] [keggfc:14.
CONTIG5345	14711558_03_21	5726	19829	2163	721	YDR211W	1422	1.2(10)-145	Saccharomyces cerevisiae	[uiydr211w] [pn:translation initiation factor eif2b epsilon, 81 kda subunit:translation initiation factor eif-2b- epsilon subunit:eif-2b gdp-gtp exchange factor:guanine nucleotide exchange factor subunit gcd6:gcd complex subunit gcd6]

CONTIG5306	10641063_3_16	5727	19830	1458	486	YDR385W	2139	1.3(10)-221	Saccharomyces cerevisiae	[ui:yd385w] [pn:translation elongation factor eef2:elongation factor 2:ef-2] [gn:eef2:eft1:0.33317] [gtfc:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5306	5100713_c3_15	5728	19831	714	238	YDR385W	1011	4.4(10)-102	Saccharomyces cerevisiae	[ui:yd385w] [pn:translation elongation factor eef2:elongation factor 2:ef-2] [gn:eef2:eft1:0.33317] [gtfc:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5306	6672140_c2_12	5729	19832	426	142	YDR385W	620	1.2(10)-60	Saccharomyces cerevisiae	[ui:yd385w] [pn:translation elongation factor eef2:elongation factor 2:ef-2] [gn:eef2:eft1:0.33317] [gtfc:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4326	25391536_f1_2	5730	19833	462	154	YEL034W	674	2.2(10)-66	Saccharomyces cerevisiae	[ui:yel034w] [pn:translation initiation factor eif5a.1:initiation factor 5a-2:eif5a:eif4d:hypusine containing protein hp2] [gn:hyp2:tif51a:sygp-orf21] [gtfc:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5665	20400292_f2_4	5731	19834	1596	532	YER025W	2098	2.7(10)-217	Saccharomyces cerevisiae	[ui:yer025w] [pn:translation initiation factor eif2 gamma chain:translational initiation factor 2 gamma subunit:eif2- gamma] [gn:ged11] [gtfc:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5017	24414661_c3_7	5732	19835	1200	400	YGL169W	850	1.1(10)-103	Saccharomyces cerevisiae	[ui:yg1169w] [pn:translation initiation protein:sua5 protein] [gn:sua5_g1660] [gicfc:10.7] [keggfc:14.2] [sgdfc:5.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2627	26367752_f2_1	5733	19836	645	215	YGL094C	501	6.2(10)-47	Saccharomyces cerevisiae	[ui:yg1094c] [pn:component of pab1 p-stimulated poly:a ribonuclease:pab-dependent poly:a-specific ribonuclease subunit:pab1 p-dependent poly:a-nuclease] [gn:pan2] [gicfc:10.7:10.9] [ec:3.1.13.4] [keggfc:14.1] [sgdfc:4.10.0.5.2.0] [db:gt]
CONTIG3648	210892_c3_6	5734	19837	945	315	YGL094C	171	2.1(10)-15	Saccharomyces cerevisiae	[ui:yg1094c] [pn:component of pab1 p-stimulated poly:a ribonuclease:pab-dependent poly:a-specific ribonuclease subunit:pab1 p-dependent poly:a-nuclease] [gn:pan2] [gicfc:10.7:10.9] [ec:3.1.13.4] [keggfc:14.1] [sgdfc:4.10.0.5.2.0] [db:gt]
CONTIG3648	21492182_c3_5	5735	19838	804	268	YGL094C	311	1.3(10)-26	Saccharomyces cerevisiae	[ui:yg1094c] [pn:component of pab1 p-stimulated poly:a ribonuclease:pab-dependent poly:a-specific ribonuclease subunit:pab1 p-dependent poly:a-nuclease] [gn:pan2] [gicfc:10.7:10.9] [ec:3.1.13.4] [keggfc:14.1] [sgdfc:4.10.0.5.2.0] [db:gt]

CONTIG2402	<u>16519663_f2_1</u>	5736	19839	1809	603	YGL049C	627	2.8(10)-73	Saccharomyces cerevisiae	[ui:yg 049c] [pn:mma cap-binding protein:eif4f, 130k subunit:eukaryotic initiation factor 4f subunit p130:eif-4f:mma cap-binding protein complex subunit p130] [gn:ti4632] [gtfc:10.7] [keggfc:14.2] [sgdfc:5.2:0:9.2.0] [db:gic-sacch]
CONTIG5035	<u>5937562_c1_11</u>	5737	19840	1563	521	YGR083C	567	3.0(10)-60	Saccharomyces cerevisiae	[ui:yg 083c] [pn:translation initiation factor eif2b, 71 kda:delta subunit:translation initiation factor eif-2b delta subunit:eif-2b Gdp-Gtp exchange factor:guanine nucleotide exchange factor subunit gcd2:gcd complex subunit gcd2] [gn:
CONTIG5278	<u>23470005_f1_1</u>	5738	19841	1221	407	YIL138C	1491	6.0(10)-153	Saccharomyces cerevisiae	[ui:yg 138c] [pn:translation initiation factor eif4a:translation initiation factor 4a:eukaryotic initiation factor 4a:eif-4a:stimulator factor i 37 kd component:p37] [gn:tf1:ti2; 0666] [gtfc:10.7] [keggfc:14.2] [sgdfc:5.2:0:9.2.0]
CONTIG4464	<u>24641888_c2_7</u>	5739	19842	531	177	YJR007W	462	6.5(10)-44	Saccharomyces cerevisiae	[ui:yg 007w] [pn:translation initiation factor eif2, alpha chain:translational initiation factor 2 alpha subunit:eif-2-alpha] [gn:su2;j 429] [gtfc:10.7:11.1] [keggfc:14.2] [sgdfc:5.2:0:9.1.0] [db:gic-saccharomyces cerevisiae]

CONTIG5702	13947217_c1_20	5740	19843	357	119	YJR007W	437	2.8(10)-41	Saccharomyces cerevisiae	[ui:yyj007w] [pn:translation initiation factor eif2, alpha chain:translational initiation factor 2 alpha subunit:eif- 2-alpha] [gn:sui2:j 429] [gicfc:10.7:11.1] [Keggfc:14.2] [sgdic:5.2:0:9.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG2481	4785900_f1_1	5741	19844	615	205	YKL173W	413	1.3(10)-37	Saccharomyces cerevisiae	[ui:yk1173w] [pn: similarity to elongation factor 2 eft1:gin10 protein] [gn:gin10:yk1637] [gicfc:10.7] [Keggfc:14.2] [sgdfc:5.2:0] [db:gic-saccharomyces cerevisiae]
CONTIG2814	26610288_f2_2	5742	19845	1557	519	YKL173W	433	6.9(10)-57	Saccharomyces cerevisiae	[ui:yk1173w] [pn: similarity to elongation factor 2 eft1:gin10 protein] [gn:gin10:yk1637] [gicfc:10.7] [Keggfc:14.2] [sgdfc:5.2:0] [db:gic-saccharomyces cerevisiae]
CONTIG4289	33593750_f1_2	5743	19846	690	230	YKL081W	283	6.0(10)-25	Saccharomyces cerevisiae	[ui:yk081w] [pn:translation elongation factor eef1, gamma chain:elongation factor 1-gamma 2:ef-1-gamma 2] [gn:lef4:efc1] [gicfc:10.7] [Keggfc:14.2] [sgdfc:5.2:0:9.2:0] [db:gic-saccharomyces cerevisiae]
CONTIG1883	23882758_c2_5	5744	19847	276	92	YKR026C	235	7.5(10)-20	Saccharomyces cerevisiae	[ui:yr026c] [pn:translation initiation factor eif2b, 34 kd, alpha subunit:translation initiation factor eif-2b alpha subunit:eif-2b gdp-gtp exchange factor:guanine nucleotide exchange factor subunit gen3:gcd complex subunit gen3:trans